



SEQUENCE LISTING

<100> MATSUDA, Akio et al.

<120> NF-kB ACTIVATING GENE

<130> 1254-0229P

<140> US 10/617,217

<141> 2003-07-11

<150> JP 2000-402288

<151> 2000-12-28

<150> JP 2001-088912

<151> 2001-03-26

<150> JP 2001-254018

<151> 2001-08-24

<150> US 60/258,315

<151> 2000-12-28

<150> US 60/278,640

<151> 2001-03-26

<150> US 60/314,385

<151> 2001-08-24

<160> 224

<170> PatentIn Ver. 2.0

<210> 1

<211> 167

<212> PRT

<213> Homo sapiens

<400> 1

Met Ser Gly Leu Ile Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val
1 5 10 15

Val Tyr Lys Leu Phe Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr
20 25 30

Ser Glu Tyr Pro Pro Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser
35 40 45

Ala Gly Pro Pro Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln
50 55 60

Asn Thr Gly His Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly
65 70 75 80

Gln Gln Gly Tyr Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly
85 90 95

Thr Gly Gly Ile Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr
 100 105 110
 Pro Phe Ser Asp Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro
 115 120 125
 Gly Thr Trp Asn Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser
 130 135 140
 Tyr Ser Val Cys Ser Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly
 145 150 155 160
 Tyr Gly Gly Thr Arg Arg Arg
 165

<210> 2
 <211> 1472
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (194)..(694)

<400> 2
 aaaaactgtg gtgagctgtg aaggctatga gtcctctgaa gaccagtatg tactaagagg 60
 ttcttgtggc ttggagtata atttagatta tacagaactt ggcctgcaga aactgaagga 120
 gtctggaaag cagcacggct ttgcctcttt ctctgattat tattataagt ggtcctcggc 180
 ggattcctgt aac atg agt gga ttg att acc atc gtg gta ctc ctt ggg 229
 Met Ser Gly Leu Ile Thr Ile Val Val Leu Leu Gly
 1 5 10
 atc gcc ttt gta gtc tat aag ctg ttc ctg agt gac ggg cag tat tct 277
 Ile Ala Phe Val Val Tyr Lys Leu Phe Leu Ser Asp Gly Gln Tyr Ser
 15 20 25
 cct cca ccg tac tct gag tat cct cca ttt tcc cac cgt tac cag aga 325
 Pro Pro Pro Tyr Ser Glu Tyr Pro Pro Phe Ser His Arg Tyr Gln Arg
 30 35 40
 ttc acc aac tca gca gga cct cct ccc cca ggc ttt aag tct gag ttc 373
 Phe Thr Asn Ser Ala Gly Pro Pro Pro Pro Gly Phe Lys Ser Glu Phe
 45 50 55 60
 aca gga cca cag aat act ggc cat ggt gca act tct ggt ttt ggc agt 421
 Thr Gly Pro Gln Asn Thr Gly His Gly Ala Thr Ser Gly Phe Gly Ser
 65 70 75
 gct ttt aca gga caa caa gga tat gaa aat tca gga cca ggg ttc tgg 469
 Ala Phe Thr Gly Gln Gln Gly Tyr Glu Asn Ser Gly Pro Gly Phe Trp
 80 85 90
 aca ggc ttg gga act ggt gga ata cta gga tat ttg ttt ggc agc aat 517

Thr Gly Leu Gly Thr Gly Gly Ile Leu Gly Tyr Leu Phe Gly Ser Asn
 95 100 105
 aga gcg gca aca ccc ttc tca gac tcg tgg tac tac ccg tcc tat cct 565
 Arg Ala Ala Thr Pro Phe Ser Asp Ser Trp Tyr Tyr Pro Ser Tyr Pro
 110 115 120
 ccc tcc tac cct ggc acg tgg aat agg gct tac tca ccc ctt cat gga 613
 Pro Ser Tyr Pro Gly Thr Trp Asn Arg Ala Tyr Ser Pro Leu His Gly
 125 130 135 140
 ggc tcg ggc agc tat tcg gta tgt tca aac tca gac acg aaa acc aga 661
 Gly Ser Gly Ser Tyr Ser Val Cys Ser Asn Ser Asp Thr Lys Thr Arg
 145 150 155
 act gca tca gga tat ggt ggt acc agg aga cga taaagtagaa agttggagtc 714
 Thr Ala Ser Gly Tyr Gly Gly Thr Arg Arg Arg
 160 165
 aaacactgga tgcagaaatt ttggatTTTT catcactttc tcttttagaaa aaaagtacta 774
 cctgttaaca attgggaaaa ggggatattc aaaagttcgg tgggtgttatg tccagtgtag 834
 ctttttgtat tctattattt gaggctaaaa gttgatgtgt gacaaaatac ttatgtgttg 894
 tatgtcagtg taacatgcag atgtatattg cagtttttga aagtgatcat tactgtggaa 954
 tgctaaaaat acattaattt ctaaacctg tgatgcccta agaagcatta agaatgaagg 1014
 tgttgtacta atagaaacta agtacagaaa atttcagttt taggtgggtg tagctgatga 1074
 gttattacct catagagact gtaatatctt atttggatt atattatttg atgtttgctg 1134
 ttcttcaaac atttaaacta agctttggac taattatgct aatttgtgag ttctgatcac 1194
 ttttgagctc tgaagctttg aatcattcag tgggtggagat ggccttctgg taactgaata 1254
 ttaccttctg taggaaaagg tggaaaataa gcatctagaa gggtgtgtg aatgactctg 1314
 tgctggcaaa aatgcttgaa acctctatat ttctttcggt cataagaggt aaaggtcaaa 1374
 tttttcaaca aaagtctttt aataacaaaa gcatgcagtt ctctgtgaaa tctcaaatat 1434
 tgttgtaata gtctgtttca atcttaaaaa gaatcaat 1472

<210> 3
 <211> 339
 <212> PRT
 <213> Homo sapiens

<400> 3
 Met Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Leu
 1 5 10 15
 Gly Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn
 20 25 30

Arg Arg Arg

<210> 4
 <211> 1924
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (115)..(1131)

<400> 4
 gttccttcgc cgccgccagg ggtagcggtg tagctgcgca gcgtcgcgcg cgctaccgca 60
 cccaggttcg gcccgtaggc gtctggcagc ccggcgccat cttcatcgag cgcc atg 117
 Met
 1
 gcc gca gcc tgc ggg ccg gga gcg gcc ggg tac tgc ttg ctc ctc ggc 165
 Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Leu Gly
 5 10 15
 ttg cat ttg ttt ctg ctg acc gcg ggc cct gcc ctg ggc tgg aac gac 213
 Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn Asp
 20 25 30
 cct gac aga atg ttg ctg cgg gat gta aaa gct ctt acc ctc cac tat 261
 Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His Tyr
 35 40 45
 gac cgc tat acc acc tcc cgc agg ctg gat ccc atc cca cag ttg aaa 309
 Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu Lys
 50 55 60 65
 tgt gtt gga ggc aca gct ggt tgt gat tct tat acc cca aaa gtc ata 357
 Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val Ile
 70 75 80
 cag tgt cag aac aaa ggc tgg gat ggg tat gat gta cag tgg gaa tgt 405
 Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu Cys
 85 90 95
 aag acg gac tta gat att gca tac aaa ttt gga aaa act gtg gtg agc 453
 Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val Ser
 100 105 110
 tgt gaa ggc tat gag tcc tct gaa gac cag tat gta cta aga ggt tct 501
 Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly Ser
 115 120 125
 tgt ggc ttg gag tat aat tta gat tat aca gaa ctt ggc ctg cag aaa 549
 Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln Lys
 130 135 140 145

ctg aag gag tct gga aag cag cac ggc ttt gcc tct ttc tct gat tat	597
Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp Tyr	
150 155 160	
tat tat aag tgg tcc tcg gcg gat tcc tgt aac atg agt gga ttg att	645
Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu Ile	
165 170 175	
acc atc gtg gta ctc ctt ggg atc gcc ttt gta gtc tat aag ctg ttc	693
Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu Phe	
180 185 190	
ctg agt gac ggg cag tat tct cct cca ccg tac tct gag tat cct cca	741
Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro Pro	
195 200 205	
ttt tcc cac cgt tac cag aga ttc acc aac tca gca gga cct cct ccc	789
Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro Pro	
210 215 220 225	
cca ggc ttt aag tct gag ttc aca gga cca cag aat act ggc cat ggt	837
Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His Gly	
230 235 240	
gca act tct ggt ttt ggc agt gct ttt aca gga caa caa gga tat gaa	885
Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr Glu	
245 250 255	
aat tca gga cca ggg ttc tgg aca ggc ttg gga act ggt gga ata cta	933
Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile Leu	
260 265 270	
gga tat ttg ttt ggc agc aat aga gcg gca aca ccc ttc tca gac tcg	981
Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp Ser	
275 280 285	
tgg tac tac ccg tcc tat cct ccc tcc tac cct ggc acg tgg aat agg	1029
Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn Arg	
290 295 300 305	
gct tac tca ccc ctt cat gga ggc tcg ggc agc tat tcg gta tgt tca	1077
Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys Ser	
310 315 320	
aac tca gac acg aaa acc aga act gca tca gga tat ggt ggt acc agg	1125
Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr Arg	
325 330 335	
aga cga taaagtagaa agttggagtc aaacactgga tgcagaaatt ttggattttt	1181
Arg Arg	
catcactttc tcttttagaaa aaaagtacta cctgttaaca attgggaaaa ggggatattc	1241
aaaagtccgg tgggtgttatg tccagtgtag ctttttgtat tctattattt gaggctaaaa	1301
gttgatgtgt gacaaaatac ttatgtgttg tatgtcagtg taacatgcag atgtatattg	1361

cagtttttga aagtgatcat tactgtggaa tgctaaaaat acattaattt ctaaaacctg 1421
 tgatgcccta agaagcatta agaatgaagg tgttgtacta atāgaaacta agtacagaaa 1481
 atttcagttt taggtgggtg tagctgatga gttattacct catagagact gtaatattct 1541
 atttggtatt atattatttg atgtttgctg ttcttcaaac atttaaataca agctttggac 1601
 taattatgct aatttgtgag ttctgatcac ttttgagctc tgaagctttg aatcattcag 1661
 tgggtggagat ggccttcttg taactgaata ttaccttctg taggaaaagg tggaaaataa 1721
 gcatctagaa gggtgtgtg aatgactctg tgctggcaaa aatgcttgaa acctctatat 1781
 ttctttcggt cataagaggt aaaggtcaaa tttttcaaca aaagtctttt aataacaaaa 1841
 gcatgcagtt ctctgtgaaa tctcaaatat tgttgtaata gtctgtttca atcttaaaaa 1901
 gaatcaataa aaacaaacaa ggg 1924

<210> 5
 <211> 127
 <212> PRT
 <213> Homo sapiens

<400> 5
 Met Ala Gly Ala Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile
 1 5 10 15
 Val Gly Gly Ile Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly
 20 25 30
 Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val
 35 40 45
 Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val
 50 55 60
 Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala
 65 70 75 80
 Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile
 85 90 95
 Pro Leu Pro His Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe
 100 105 110
 Ile Leu Gln Leu Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Ser
 115 120 125

<210> 6
 <211> 702
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (225)..(605)

<400> 6

acaatcacag ctccgggcat tgggggaacc cgagccggct gcgccggggg aatccgtgcg 60

ggcgtcttcc gtcccggtcc catcctcgcc gcgctccagc acctctgaag ttttgcagcg 120

cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcaccct 180

aaaacattta tttcaaggag aaaagaaaaa gggggggcgc aaaa atg gct ggg gca 236
Met Ala Gly Ala
1

att ata gaa aac atg agc acc aag aag ctg tgc att gtt ggt ggg att 284
Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile
5 10 15 20

ctg ctc gtg ttc caa atc atc gcc ttt ctg gtg gga ggc ttg att gct 332
Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala
25 30 35

cca ggg ccc aca acg gca gtg tcc tac atg tcg gtg aaa tgt gtg gat 380
Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp
40 45 50

gcc cgt aag aac cat cac aag aca aaa tgg ttc gtg cct tgg gga ccc 428
Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro
55 60 65

aat cat tgt gac aag atc cga gac att gaa gag gca att cca agg gaa 476
Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu
70 75 80

att gaa gcc aat gac atc gtg ttt tct gtt cac att ccc ctc ccc cac 524
Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His
85 90 95 100

atg gag atg agt cct tgg ttc caa ttc atg ctg ttt atc ctg cag ctg 572
Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe Ile Leu Gln Leu
105 110 115

gac att gcc ttc aag cta aac aac caa atc agt taagtgtact ctctctcat 625
Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Ser
120 125

ccctttcttc cctttgagca ttgccctctt tgggttcttt ttgagccaat tctaataaaa 685

gtaaaaatgg taatagt 702

<210> 7

<211> 233

<212> PRT

<213> Homo sapiens

<400> 7

Met Ala Gly Ala Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile
1 5 10 15

Val Gly Gly Ile Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly
20 25 30

Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val
35 40 45

Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val
50 55 60

Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala
65 70 75 80

Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile
85 90 95

Pro Leu Pro His Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe
100 105 110

Ile Leu Gln Leu Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Arg Glu
115 120 125

Asn Ala Glu Val Ser Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala
130 135 140

Phe Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro Arg Lys Leu
145 150 155 160

Lys Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr
165 170 175

Tyr Glu Cys Asp Val Leu Pro Tyr Ala Gln His Leu His His Tyr Gly
180 185 190

Val Val Leu Glu Glu Asp His His Asp Val Pro Thr Pro Ser Ala Ser
195 200 205

Gly Lys Ser His Leu Cys Pro Trp Asp Phe His Asp Leu Tyr Gln Tyr
210 215 220

Pro Ser Gly Met Val Phe His Arg Val
225 230

<210> 8

<211> 2409

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (225)..(923)

<400> 8

acaatcacag ctccgggcat tgggggaacc cgagccggct gcgccggggg aatccgtgcg 60

gag gat cac cat gat gtc ccg acc ccc agt gct tct gga aaa agt cat 860
Glu Asp His His Asp Val Pro Thr Pro Ser Ala Ser Gly Lys Ser His
200 205 210

ctt tgc cct tgg gat ttc cat gac ctt tat caa tat ccc agt gga atg 908
Leu Cys Pro Trp Asp Phe His Asp Leu Tyr Gln Tyr Pro Ser Gly Met
215 220 225

gtt ttc cat cgg gtt tgactggacc tggatgctgc tgtttggtga catccgacag 963
Val Phe His Arg Val
230

ggcatcttct atgcgatgct tctgtccttc tggatcatct tctgtggcga gcacatgatg 1023
gatcagcacg agcggaaacca catgcgaggg tattggaagc aagtcggacc cattgccgtt 1083
ggctccttct gcctcttcat atttgacatg tgtgagagag gggtaacaact cacgaatccc 1143
ttctacagta tctggactac agacattgga acagagctgg ccatggcctt catcatcgtg 1203
gctggaatct gcctctgcct ctacttctg tttctatgct tcatgggtatt tcaggtgttt 1263
cggaaacatca gtgggaagca gtccagcctg ccagctatga gcaaagtcg gcggctacac 1323
tatgaggggc taatttttag gttcaagttc ctcatgctta tcaccttggc ctgcgctgcc 1383
atgactgtca tcttcttcat cgttagtcag gtaacggaag gccattggaa atggggcggc 1443
gtcacagtcc aagtgaacag tgcccttttc acaggcatct atgggatgtg gaatctgtat 1503
gtctttgtct tgatgttctt gtatgcaaca tccataaaa actatggaga agaccagtcc 1563
aatggcgatc tgggtgtcca tagtggggaa gaactccagc tcaccaccac tatcaccat 1623
gtggacggac ccaactgagat ctacaagttg acccgcaagg agggccagga gtaggaggct 1683
gcagcgcccg gctgggacgg tctctccata cccagcccc tctaactaga gtggggagca 1743
tgccagagag agctcaatgt acaaatgaat gcctcatggc tcttagctgt ggtttcttgg 1803
accagcggca tggacatttg tcagtttgcc ttctgacggt agcttttgga ggaagattcc 1863
tgcagccact aatgcattgt gtatgataac aaaaactctg gtatgacaca ttttctgtga 1923
tcattgttaa ttagtgacat agtaacatct gtagcagctg gttagtaaac ctcatgtggg 1983
gggtgggtgg ggggtgtattc cttgggggat ggtttgggccc gaatggggag tggaatattt 2043
gacatttttc ctgttttaaa ttctaggata gattttaaca tcctttgcgg tccagtgcca 2103
aggtaggctg gtgtcatagt cttctcactc ctaatccatg accactgttt ttttctatt 2163
tatatcacca ggtagccac tgagttaata ttttaagttgt caatagataa gtgtccctgt 2223
tttgtggcat aatataactg aatttcatga gaagatttat tccaccaggg gtatttcagc 2283

tttgaaacca aatctgtgta tctaatacta accaatctgt tggatgtggg ttttaaaaaa 2343
 tgtttgctaa actaccaag taagatttac tgtattaaat ggccttcggg tctgaaaagc 2403
 tttttt 2409

<210> 9
 <211> 198
 <212> PRT
 <213> Homo sapiens

<400> 9
 Met Ala Thr Leu Trp Gly Gly Leu Leu Arg Leu Gly Ser Leu Leu Ser
 1 5 10 15
 Leu Ser Cys Leu Ala Leu Ser Val Leu Leu Leu Ala Gln Leu Ser Asp
 20 25 30
 Ala Ala Lys Asn Phe Glu Asp Val Arg Cys Lys Cys Ile Cys Pro Pro
 35 40 45
 Tyr Lys Glu Asn Ser Gly His Ile Tyr Asn Lys Asn Ile Ser Gln Lys
 50 55 60
 Asp Cys Asp Cys Leu His Val Val Glu Pro Met Pro Val Arg Gly Pro
 65 70 75 80
 Asp Val Glu Ala Tyr Cys Leu Arg Cys Glu Cys Lys Tyr Glu Glu Arg
 85 90 95
 Ser Ser Val Thr Ile Lys Val Thr Ile Ile Ile Tyr Leu Ser Ile Leu
 100 105 110
 Gly Leu Leu Leu Leu Tyr Met Val Tyr Leu Thr Leu Val Glu Pro Ile
 115 120 125
 Leu Lys Arg Arg Leu Phe Gly His Ala Gln Leu Ile Gln Ser Asp Asp
 130 135 140
 Asp Ile Gly Asp His Gln Pro Phe Ala Asn Ala His Asp Val Leu Ala
 145 150 155 160
 Arg Ser Arg Ser Arg Ala Asn Val Leu Asn Lys Val Glu Tyr Ala Gln
 165 170 175
 Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Ser Val Phe Asp
 180 185 190
 Arg His Val Val Leu Ser
 195

<210> 10
 <211> 1498
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (86)..(679)

<400> 10

```
gtgcctgagc ctgagcctga gcctgagccc gagccgggag ccggtcgcgg gggctccggg 60

ctgtgggacc gctgggcccc cagcgc atg gcg acc ctg tgg gga ggc ctt ctt 112
                               Met Ala Thr Leu Trp Gly Gly Leu Leu
                               1                               5

cgg ctt ggc tcc ttg ctc agc ctg tcg tgc ctg gcg ctt tcc gtg ctg 160
Arg Leu Gly Ser Leu Leu Ser Leu Ser Cys Leu Ala Leu Ser Val Leu
10                               15                               20                               25

ctg ctg gcg cag ctg tca gac gcc gcc aag aat ttc gag gat gtc aga 208
Leu Leu Ala Gln Leu Ser Asp Ala Ala Lys Asn Phe Glu Asp Val Arg
                               30                               35                               40

tgt aaa tgt atc tgc cct ccc tat aaa gaa aat tct ggg cat att tat 256
Cys Lys Cys Ile Cys Pro Pro Tyr Lys Glu Asn Ser Gly His Ile Tyr
                               45                               50                               55

aat aag aac ata tct cag aaa gat tgt gat tgc ctt cat gtt gtg gag 304
Asn Lys Asn Ile Ser Gln Lys Asp Cys Asp Cys Leu His Val Val Glu
                               60                               65                               70

ccc atg cct gtg cgg ggg cct gat gta gaa gca tac tgt cta cgc tgt 352
Pro Met Pro Val Arg Gly Pro Asp Val Glu Ala Tyr Cys Leu Arg Cys
75                               80                               85

gaa tgc aaa tat gaa gaa aga agc tct gtc aca atc aag gtt acc att 400
Glu Cys Lys Tyr Glu Glu Arg Ser Ser Val Thr Ile Lys Val Thr Ile
90                               95                               100                               105

ata att tat ctc tcc att ttg ggc ctt cta ctt ctg tac atg gta tat 448
Ile Ile Tyr Leu Ser Ile Leu Gly Leu Leu Leu Leu Tyr Met Val Tyr
                               110                               115                               120

ctt act ctg gtt gag ccc ata ctg aag agg cgc ctc ttt gga cat gca 496
Leu Thr Leu Val Glu Pro Ile Leu Lys Arg Arg Leu Phe Gly His Ala
125                               130                               135

cag ttg ata cag agt gat gat gat att ggg gat cac cag cct ttt gca 544
Gln Leu Ile Gln Ser Asp Asp Asp Ile Gly Asp His Gln Pro Phe Ala
140                               145                               150

aat gca cac gat gtg cta gcc cgc tcc cgc agt cga gcc aac gtg ctg 592
Asn Ala His Asp Val Leu Ala Arg Ser Arg Ser Arg Ala Asn Val Leu
155                               160                               165

aac aag gta gaa tat gca cag cag cgc tgg aag ctt caa gtc caa gag 640
Asn Lys Val Glu Tyr Ala Gln Gln Arg Trp Lys Leu Gln Val Gln Glu
170                               175                               180                               185

cag cga aag tct gtc ttt gac cgg cat gtt gtc ctc agc taattgggaa 689
```

Gln Arg Lys Ser Val Phe Asp Arg His Val Val Leu Ser
 190 195

ttgaattcaa ggtgactaga aagaaacagg cagacaactg gaaagaactg actggggttt 749
 gctgggtttc attttaatac ctgttgatt tcaccaactg ttgctggaag attcaaaact 809
 ggaagcaaaa acttgcttga ttttttttc ttgttaacgt aataatagag acatttttaa 869
 aagcacacag ctcaaagtca gccataagt cttttcctat ttgtgacttt tactaataaa 929
 aataaatctg cctgtaaatt atcttgaagt cctttacctg gaacaagcac tctctttttc 989
 accacatagt ttttaacttga ctttcaagat aattttcagg gtttttggtg ttgttggttt 1049
 ttgtttgttt gttttggtgg gagaggggag ggatgcctgg gaagtgggta acaacttttt 1109
 tcaagtcact ttactaaaca aacttttgta aatagacctt accttctatt ttogagtttc 1169
 atttatattt tgcagtgtag ccagcctcat caaagagctg acttactcat ttgacttttg 1229
 cactgactgt attatctggg tatctgctgt gtctgcactt catggtaaac gggatctaaa 1289
 atgcctggtg gcttttcaca aaaagcagat tttcttcatg tactgtgatg tctgatgcaa 1349
 tgcacccatg aacaaactgg ccatttgcta gtttactcta aagactaaac atagtcttgg 1409
 tgtgtgtggt cttactcatc ttctagtacc ttttaaggaca aatcctaagg acttgacac 1469
 ttgcaataaa gaaattttat tttaaacc 1498

<210> 11
 <211> 221
 <212> PRT
 <213> Homo sapiens

<400> 11
 Met Ala Leu Ala Leu Ala Ala Leu Ala Ala Val Glu Pro Ala Cys Gly
 1 5 10 15
 Ser Arg Tyr Gln Gln Leu Gln Asn Glu Glu Glu Ser Gly Glu Pro Glu
 20 25 30
 Gln Ala Ala Gly Asp Ala Pro Pro Pro Tyr Ser Ser Ile Ser Ala Glu
 35 40 45
 Ser Ala Ala Tyr Phe Asp Tyr Lys Asp Glu Ser Gly Phe Pro Lys Pro
 50 55 60
 Pro Ser Tyr Asn Val Ala Thr Thr Leu Pro Ser Tyr Asp Glu Ala Glu
 65 70 75 80
 Arg Thr Lys Ala Glu Ala Thr Ile Pro Leu Val Pro Gly Arg Asp Glu
 85 90 95
 Asp Phe Val Gly Arg Asp Asp Phe Asp Asp Ala Asp Gln Leu Arg Ile

100					105					110					
Gly	Asn	Asp	Gly	Ile	Phe	Met	Leu	Thr	Phe	Phe	Met	Ala	Phe	Leu	Phe
		115					120					125			
Asn	Trp	Ile	Gly	Phe	Phe	Leu	Ser	Phe	Cys	Leu	Thr	Thr	Ser	Ala	Ala
	130					135					140				
Gly	Arg	Tyr	Gly	Ala	Ile	Ser	Gly	Phe	Gly	Leu	Ser	Leu	Ile	Lys	Trp
145					150					155					160
Ile	Leu	Ile	Val	Arg	Phe	Ser	Thr	Tyr	Phe	Pro	Gly	Tyr	Phe	Asp	Gly
				165					170					175	
Gln	Tyr	Trp	Leu	Trp	Trp	Val	Phe	Leu	Val	Leu	Gly	Phe	Leu	Leu	Phe
			180					185					190		
Leu	Arg	Gly	Phe	Ile	Asn	Tyr	Ala	Lys	Val	Arg	Lys	Met	Pro	Glu	Thr
		195					200					205			
Phe	Ser	Asn	Leu	Pro	Arg	Thr	Arg	Val	Leu	Phe	Ile	Tyr			
	210					215					220				

<210> 12
 <211> 1864
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (153)..(815)

<400> 12
 ctgagaagag cgtctcgccc gggagcggcg gcggccatcg agaccacccc aaggcgcgtc 60
 cccctcggcc tcccagcgct cccaagcgcg agcggcgcg ccccttcagc tagctcgctc 120
 gctcgctctg cttccctgct gcgggctgcg cc atg gcg ttg gcg ttg gcg gcg 173
 Met Ala Leu Ala Leu Ala Ala
 1 5
 ctg gcg gcg gtc gag ccg gcc tgc ggc agc cgg tac cag cag ttg cag 221
 Leu Ala Ala Val Glu Pro Ala Cys Gly Ser Arg Tyr Gln Gln Leu Gln
 10 15 20
 aat gaa gaa gag tct gga gaa cct gaa cag gct gca ggt gat gct cct 269
 Asn Glu Glu Glu Ser Gly Glu Pro Glu Gln Ala Ala Gly Asp Ala Pro
 25 30 35
 cca cct tac agc agc att tct gca gag agc gca gca tat ttt gac tac 317
 Pro Pro Tyr Ser Ser Ile Ser Ala Glu Ser Ala Ala Tyr Phe Asp Tyr
 40 45 50 55
 aag gat gag tct ggg ttt cca aag ccc cca tct tac aat gta gct aca 365
 Lys Asp Glu Ser Gly Phe Pro Lys Pro Pro Ser Tyr Asn Val Ala Thr

	60	65	70	
aca-ctg ccc agt-tat gat gaa gcg gag agg acc aag gct gaa gct act				413
Thr Leu Pro Ser Tyr Asp Glu Ala Glu Arg Thr Lys Ala Glu Ala Thr				
	75	80	85	
atc cct ttg gtt cct ggg aga gat gag gat ttt gtg ggt cgg gat gat				461
Ile Pro Leu Val Pro Gly Arg Asp Glu Asp Phe Val Gly Arg Asp Asp				
	90	95	100	
ttt gat gat gct gac cag ctg agg ata gga aat gat ggg att ttc atg				509
Phe Asp Asp Ala Asp Gln Leu Arg Ile Gly Asn Asp Gly Ile Phe Met				
	105	110	115	
tta act ttt ttc atg gca ttc ctc ttt aac tgg att ggg ttt ttc ctg				557
Leu Thr Phe Phe Met Ala Phe Leu Phe Asn Trp Ile Gly Phe Phe Leu				
	120	125	130	135
tct ttt tgc ctg acc act tca gct gca gga agg tat ggg gcc att tca				605
Ser Phe Cys Leu Thr Thr Ser Ala Ala Gly Arg Tyr Gly Ala Ile Ser				
	140	145	150	
gga ttt ggt ctc tct cta att aaa tgg atc ctg att gtc agg ttt tcc				653
Gly Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser				
	155	160	165	
acc tat ttc cct gga tat ttt gat ggt cag tac tgg ctc tgg tgg gtg				701
Thr Tyr Phe Pro Gly Tyr Phe Asp Gly Gln Tyr Trp Leu Trp Trp Val				
	170	175	180	
ttc ctt gtt tta ggc ttt ctc ctg ttt ctc aga gga ttt atc aat tat				749
Phe Leu Val Leu Gly Phe Leu Leu Phe Leu Arg Gly Phe Ile Asn Tyr				
	185	190	195	
gca aaa gtt cgg aag atg cca gaa act ttc tca aat ctc ccc agg acc				797
Ala Lys Val Arg Lys Met Pro Glu Thr Phe Ser Asn Leu Pro Arg Thr				
	200	205	210	215
aga gtt ctc ttt att tat taaagatggt ttctggcaaa ggccttcctg				845
Arg Val Leu Phe Ile Tyr				
	220			
catttatgaa ttctctctca agaagcaaga gaacacctgc aggaagtgaa tcaagatgca				905
gaacacagag gaataatcac ctgctttaaa aaaataaagt actggttgaaa agatcatttc				965
tctctatttg ttcttaggtg taaaatttta atagttaatg cagaattctg taatcattga				1025
atcattagtg gttaatgttt gaaaaagctc ttgcaatcaa gtctgtgatg tattaataat				1085
gccttatata ttgtttgtag tcatttttaag tagcatgagc catgtccctg tagtcggtag				1145
ggggcagtct tgctttatcc atcctccatc tcaaaatgaa cttggaatta aatattgtaa				1205
gatatgtata atgctggcca ttttaaaggg gttttctcaa aagttaaact tttgctatga				1265
ctgtgttttt gcacataatc catatttgct gttcaagtta atctagaaat ttattcaatt				1325

ctgtatgaac acctggaagc aaaatcatag tgcaaaaata catttaaggt gtgggtcaaaa 1385
 ataagtcttt aattggtaaa taataagcat taatttttta tagcctgtat tcacaattct 1445
 gcggtacctt attgtaccta agggattcta aagggtgttg cactgtataa aacagaaagc 1505
 actaggatac aaatgaagct taattactaa aatgtaattc ttgacactct ttctataatt 1565
 agcgttcttc acccccaccc ccacccccac cccccttatt ttccctttgt ctccctgggtga 1625
 ttaggccaaa gtctgggagt aaggagagga ttaggtactt aggagcaaag aaagaagtag 1685
 cttggaactt ttgagatgat ccctaacata ctgtactact tgcttttaca atgtgttagc 1745
 agaaaccagt ggggttataat gtagaatgat gtgctttctg cccaagtggg aattcatctt 1805
 ggtttgctat gttaaaactg taaataacaac agaacattaa taaatatctc ttgtgtagc 1864

<210> 13
 <211> 242
 <212> PRT
 <213> Homo sapiens

<400> 13
 Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn
 1 5 10 15
 Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser
 20 25 30
 Asn Pro Ala Pro Gln Ile Val Gln Ala Ala Ser Ser Ala Pro Ala Leu
 35 40 45
 Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val
 50 55 60
 Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro
 65 70 75 80
 Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu
 85 90 95
 Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Glu Thr Ser Gln
 100 105 110
 Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala
 115 120 125
 Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe
 130 135 140
 Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile
 145 150 155 160
 Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu

	165	170	175	
--	Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr			--
	180	185	190	
	Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu			
	195	200	205	
	Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg			
	210	215	220	
	Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe			
	225	230	235	240

Leu Leu

<210> 14
 <211> 2324
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (13)..(738)

<400> 14
 gagccgggca gg atg gat cac cac cag ccg ggg act ggg cgc tac cag gtg 51
 Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val
 1 5 10

ctt ctt aat gaa gag gat aac tca gaa tca tcg gct ata gag cag cca 99
 Leu Leu Asn Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro
 15 20 25

cct act tca aac cca gca ccg cag att gtg cag gct gcg tct tca gca 147
 Pro Thr Ser Asn Pro Ala Pro Gln Ile Val Gln Ala Ala Ser Ser Ala
 30 35 40 45

cca gca ctt gaa act gac tct tcc cct cca cca tat agt agt att act 195
 Pro Ala Leu Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr
 50 55 60

gtg gaa gta cct aca act tca gat aca gaa gtt tac ggt gag ttt tat 243
 Val Glu Val Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr
 65 70 75

ccc gtg cca cct ccc tat agc gtt gct acc tct ctt cct aca tac gat 291
 Pro Val Pro Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp
 80 85 90

gaa gct gag aag gct aaa gct gct gca atg gca gct gca gca gca gaa 339
 Glu Ala Glu Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Glu
 95 100 105

aca tct caa aga att cag gag gaa gag tgt cca cca aga gat gac ttc 387

Thr	Ser	Gln	Arg	Ile	Gln	Glu	Glu	Glu	Cys	Pro	Pro	Arg	Asp	Asp	Phe	
110					115					120					125	
agt	gat	gca	gac	cag	ctc	aga	gtg	ggg	aat	gat	ggc	att	ttc	atg	ctg	435
Ser	Asp	Ala	Asp	Gln	Leu	Arg	Val	Gly	Asn	Asp	Gly	Ile	Phe	Met	Leu	
				130					135					140		
gca	ttt	ttc	atg	gca	ttt	att	ttc	aac	tgg	ctt	gga	ttt	tgt	tta	tcc	483
Ala	Phe	Phe	Met	Ala	Phe	Ile	Phe	Asn	Trp	Leu	Gly	Phe	Cys	Leu	Ser	
			145					150					155			
ttc	tgt	atc	acc	aat	acc	ata	gct	gga	agg	tat	ggg	gct	atc	tgc	gga	531
Phe	Cys	Ile	Thr	Asn	Thr	Ile	Ala	Gly	Arg	Tyr	Gly	Ala	Ile	Cys	Gly	
		160					165					170				
ttt	ggc	ctt	tcc	ttg	atc	aaa	tgg	atc	ctt	att	gtc	agg	ttt	tct	gat	579
Phe	Gly	Leu	Ser	Leu	Ile	Lys	Trp	Ile	Leu	Ile	Val	Arg	Phe	Ser	Asp	
	175					180					185					
tat	ttt	act	gga	tat	ttc	aat	gga	cag	tat	tgg	ctt	tgg	tgg	ata	ttt	627
Tyr	Phe	Thr	Gly	Tyr	Phe	Asn	Gly	Gln	Tyr	Trp	Leu	Trp	Trp	Ile	Phe	
190					195				200					205		
ctt	gta	ctt	ggc	ctg	ctc	ctt	ttc	ttc	aga	gga	ttt	gtt	aat	tat	cta	675
Leu	Val	Leu	Gly	Leu	Leu	Leu	Phe	Phe	Arg	Gly	Phe	Val	Asn	Tyr	Leu	
				210					215					220		
aaa	gtc	aga	aac	atg	tct	gaa	agt	atg	gca	gct	gct	cat	aga	aca	agg	723
Lys	Val	Arg	Asn	Met	Ser	Glu	Ser	Met	Ala	Ala	Ala	His	Arg	Thr	Arg	
			225					230					235			
tat	ttc	ttc	tta	ttg	tagagactgc	atcaaccgca	cattcctttc	ttataccaat								778
Tyr	Phe	Phe	Leu	Leu												
			240													
gtgaaatttc	cagatcatct	gtaaacctac	aactttaata	gaagactact	aataacagaa											838
gacaaattag	tgaagaaaag	acggagtttc	gaaattgaat	ggcaggggtgg	tttttgctta											898
caagccattt	ctgttcattc	tttaagtatc	tatatctcat	ttgttttgca	catatgcata											958
tgtgcccatt	taagatatct	gcatatactt	gatagaaacc	ataaagttgt	agcagtttaag											1018
tccagtcaca	tttggttaat	cagtgtttga	tataattgaa	agagttgagt	ggataaacag											1078
tcttccagct	tgtaaatgcc	attgacttct	gacctgacat	ttagtataat	aaaaatgaaa											1138
ttcttaacca	tgtcaaatga	tttagtttct	ggctcttaga	ctcatctggc	agttctacac											1198
atgaaacatc	ttttgttata	taggggtgtat	tgaacctgc	agtgtgtgatt	attagaaagg											1258
atttgtcaga	tttttgaaca	tgatatcttac	attattatct	aggaaaactc	ttcctgtaaa											1318
taaccatgca	taacttactt	tctgcaatgt	tttcttagaa	attgtgtcca	gatagctttc											1378
actaatctta	aattaagtga	actaaatata	tatgtgtata	tgtatacaca	tatatataca											1438

cacacacata tatatatatta gaaacgtgag tgttaaagat agaatttggt ttaggacaaa 1498
ttttaagaaa atgtgggaat accaaatgtc ctttataaga-aaaataaatt ttattttaag 1558
ggacatacta gttttagga ttttcagatg ggaagctgca tttttaggat tgcccatcct 1618
aagagatcct gcaggaagag attgtattag atattatatt tatttcattt aagataattt 1678
tcaaagttaa ttttctaaat aagataattc tcatttgtgt ttgtctttta aaaggccaat 1738
aaaatatcct tcagtatcat tgtaataatt ttttagagtt taatttgtaa agcttagcaa 1798
ataaaatcct gtactatgaa tagcttcttg ctttatgact ttaggattaa cttgtaaaaa 1858
acatatcctg aactgagata tgcaaaatac tcattttcaa gttatggaaa tgtgtttgtg 1918
gcatatagga ctgtggggtc tgtgtgtgta gtgagagtgt gtagccacta ttataactgg 1978
aatttaattt acattcataa actactatat ttcccatcct gcaaatcatt ttatgtctca 2038
tctgtttttc ctttcgggta tatctttggt tttgaatacc aacatttaaa atgatgggtat 2098
tttatctttt aaacttaaaa attatttaat acagctatat ggaccttata aaattgattt 2158
cttatttatt attagacatt actactaaaa ggtacatcta actattcagg gacatttttc 2218
catttccaaa aaataaaatt tattatgctt tataacctct tctgtatttt ctaatttttt 2278
cattgtcttt gataaataaa acagttttgt tttgctaata tagcct 2324

<210> 15
<211> 242
<212> PRT
<213> Homo sapiens

<400> 15
Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn
1 5 10 15
Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser
20 25 30
Asn Pro Ala Pro Gln Ile Val Gln Ala Val Ser Ser Ala Pro Ala Leu
35 40 45
Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val
50 55 60
Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro
65 70 75 80
Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu
85 90 95
Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Glu Thr Ser Gln
100 105 110


```

Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala
  115          120          125

Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe
  130          135          140

Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile
  145          150          155          160

Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu
  165          170          175

Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr
  180          185          190

Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu
  195          200          205

Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg
  210          215          220

Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe
  225          230          235          240

Leu Leu

```

```

<210> 16
<211> 2324
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (13)..(738)

```

```

<400> 16
gagccgggca gg atg gat cac cac cag ccg ggg act ggg cgc tac cag gtg 51
      Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val
        1          5          10

ctt ctt aat gaa gag gat aac tca gaa tca tcg gct ata gag cag cca 99
Leu Leu Asn Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro
  15          20          25

cct act tca aac cca gca ccg cag att gtg cag gct gtg tct tca gca 147
Pro Thr Ser Asn Pro Ala Pro Gln Ile Val Gln Ala Val Ser Ser Ala
  30          35          40          45

cca gca ctt gaa act gac tct tcc cct cca cca tat agt agt att act 195
Pro Ala Leu Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr
        50          55          60

gtg gaa gta cct aca act tca gat aca gaa gtt tac ggt gag ttt tat 243
Val Glu Val Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr

```

65	70	75	
ccc gtg cca cct ccc tat agc gtt gct acc tct ctt cct aca tac gat	291		
Pro Val Pro Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp			
80	85	90	
gaa gct gag aag gct aaa gct gct gca atg gca gct gca gca gca gaa	339		
Glu Ala Glu Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Glu			
95	100	105	
aca tct caa aga att cag gag gaa gag tgt cca cca aga gat gac ttc	387		
Thr Ser Gln Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe			
110	115	120	125
agt gat gca gac cag ctc aga gtg ggg aat gat ggc att ttc atg ctg	435		
Ser Asp Ala Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu			
130	135	140	
gca ttt ttc atg gca ttt att ttc aac tgg ctt gga ttt tgt tta tcc	483		
Ala Phe Phe Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser			
145	150	155	
ttc tgt atc acc aat acc ata gct gga agg tat ggt gct atc tgc gga	531		
Phe Cys Ile Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly			
160	165	170	
ttt ggc ctt tcc ttg atc aaa tgg atc ctt att gtc agg ttt tct gat	579		
Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp			
175	180	185	
tat ttt act gga tat ttc aat gga cag tat tgg ctt tgg tgg ata ttt	627		
Tyr Phe Thr Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe			
190	195	200	205
ctt gta ctt ggc ctg ctc ctt ttc ttc aga gga ttt gtt aat tat cta	675		
Leu Val Leu Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu			
210	215	220	
aaa gtc aga aac atg tct gaa agt atg gca gct gct cat aga aca agg	723		
Lys Val Arg Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg			
225	230	235	
tat ttc ttc tta ttg tagagactgc atcaaccoga cattcctttc ttataccaat	778		
Tyr Phe Phe Leu Leu			
240			
gtgaaatttc cagatcatct gtaaacctac aactttaata gaagactact aataacagaa	838		
gacaaattag tgaagaaaag acggagtttc gaaattgaat ggcagggtagg tttttgctta	898		
caagccattt ctgttcattc ttttaagtatc tatatttcat ttgttttgca catatgcata	958		
tgtgcccatt taagatattt gcatatactt gatagaaacc ataaagttgt agcagttaag	1018		
tccagtcaca tttggttaat cagtgtttga tataattgaa agagttgagt ggataaacag	1078		
tcttccagct tgtaaatgcc attgacttct gacctgacat ttagtataat aaaaatgaaa	1138		

ttcttaacca tgtcaaatga tttagtttct ggctcttaga ctcatctggc agttctacac 1198
 atgaaacatc ttttggtata taggggtgat tgaacctgc agtgctgatt attagaaagg 1258
 atttgtcaga tttttgaaca tgatatttac attattattt aggaaaactc ttcctgtaaa 1318
 taaccatgca taacttactt tctgcaatgt tttcttagaa atttgtgtcca gatagctttc 1378
 actaatttta aattaagtga actaaatata tatgtgtata tgtatacaca tatatatata 1438
 cacacacata tatatatatta gaaacgtgag tgttaaagat agaatttggt ttaggacaaa 1498
 ttttaagaaa atgtgggaat accaaatgtc ctttataaga aaaataaatt ttattttaag 1558
 ggacatacta gttttaggga ttttcagatg ggaagctgca tttttaggat tgcccatctt 1618
 aagagatctt gcaggaagag attgtattag atattatatt tatttcattt aagataattt 1678
 tcaaagttaa ttttctaaat aagataattc tcatttgtgt ttgtctttta aaaggccaat 1738
 aaaatatctt tcagtatcat tgtaataatt ttttagagtt taatttgtaa agcttagcaa 1798
 ataaaatctt gtactatgaa tagcttcttg ctttatgact ttaggattaa cttgtaaaaa 1858
 acatatcttg aactgagata tgcaaaatac tcattttcaa gttatggaaa tgtgtttgtg 1918
 gcatatagga ctgtggggtc tgtgtgtgta gtgagagtgt gtagccacta ttataactgg 1978
 aatttaattt acattcataa actactatat ttcccatctt gcaaatcatt ttatgtctca 2038
 tctgtttttc ctttcggtta tatctttggt tttgaatacc aacatttaaa atgatgggat 2098
 tttatctttt aaacttaaaa attatttaat acagctatat ggaccttata aaattgattt 2158
 cttatttatt attagacatt actactaaaa ggtacatcta actattcagg gacatttttc 2218
 catttccaaa aaataaaatt tattatgctt tataacctct tctgtatttt ctaatttttt 2278
 cattgtcttt gataaataaa acagttttgt tttgctaata tagcct 2324

<210> 17

<211> 336

<212> PRT

<213> Homo sapiens

<400> 17

Met Ala Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met
 1 5 10 15

Leu Asn Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr
 20 25 30

Asn Ala Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu
 35 40 45

Leu	Pro	Pro	Gly	Asp	Arg	Gly	Cys	Arg	Asn	Gly	Gly	Gly	Arg	Gly	Pro
50						55					60				
Ala	Ala	Thr	Thr	Ser	Ser	Thr	Gly	Val	Ala	Val	Gly	Ala	Glu	His	Gly
65					70					75					80
Glu	Asp	Ser	Leu	Ser	Arg	Lys	Pro	Asp	Pro	Glu	Pro	Gly	Arg	Met	Asp
				85					90					95	
His	His	Gln	Pro	Gly	Thr	Gly	Arg	Tyr	Gln	Val	Leu	Leu	Asn	Glu	Glu
			100					105					110		
Asp	Asn	Ser	Glu	Ser	Ser	Ala	Ile	Glu	Gln	Pro	Pro	Thr	Ser	Asn	Pro
		115					120					125			
Ala	Pro	Gln	Ile	Val	Gln	Ala	Val	Ser	Ser	Ala	Pro	Ala	Leu	Glu	Thr
	130					135					140				
Asp	Ser	Ser	Pro	Pro	Pro	Tyr	Ser	Ser	Ile	Thr	Val	Glu	Val	Pro	Thr
145					150					155					160
Thr	Ser	Asp	Thr	Glu	Val	Tyr	Gly	Glu	Phe	Tyr	Pro	Val	Pro	Pro	Pro
				165					170					175	
Tyr	Ser	Val	Ala	Thr	Ser	Leu	Pro	Thr	Tyr	Asp	Glu	Ala	Glu	Lys	Ala
			180					185					190		
Lys	Ala	Ala	Ala	Met	Ala	Ala	Ala	Ala	Ala	Glu	Thr	Ser	Gln	Arg	Ile
	195						200						205		
Gln	Glu	Glu	Glu	Cys	Pro	Pro	Arg	Asp	Asp	Phe	Ser	Asp	Ala	Asp	Gln
	210					215					220				
Leu	Arg	Val	Gly	Asn	Asp	Gly	Ile	Phe	Met	Leu	Ala	Phe	Phe	Met	Ala
225					230					235					240
Phe	Ile	Phe	Asn	Trp	Leu	Gly	Phe	Cys	Leu	Ser	Phe	Cys	Ile	Thr	Asn
				245					250					255	
Thr	Ile	Ala	Gly	Arg	Tyr	Gly	Ala	Ile	Cys	Gly	Phe	Gly	Leu	Ser	Leu
		260						265					270		
Ile	Lys	Trp	Ile	Leu	Ile	Val	Arg	Phe	Ser	Asp	Tyr	Phe	Thr	Gly	Tyr
		275					280					285			
Phe	Asn	Gly	Gln	Tyr	Trp	Leu	Trp	Trp	Ile	Phe	Leu	Val	Leu	Gly	Leu
	290					295					300				
Leu	Leu	Phe	Phe	Arg	Gly	Phe	Val	Asn	Tyr	Leu	Lys	Val	Arg	Asn	Met
305					310					315					320
Ser	Glu	Ser	Met	Ala	Ala	Ala	His	Arg	Thr	Arg	Tyr	Phe	Phe	Leu	Leu
				325					330					335	

<210> 18

<211> 2636

<212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (53)..(1060)

<400> 18
 cttactttttc catctcctcc caccagcta taccctccca ctggcggcgc gg atg gca 58
 Met Ala
 1

cgc cgg cgg agc cag cga gtc tgc gcg agc ggt ccg agc atg ctc aat 106
 Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met Leu Asn
 5 10 15

agc gcg cgc ggc gcc ccg gag ctt ctc cgc gga acc gcg acc aac gcg 154
 Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr Asn Ala
 20 25 30

gag gtc tcg gcg gcc gct gcg gga gcc aca gga agt gaa gag ctt ccg 202
 Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu Leu Pro
 35 40 45 50

ccg gga gac cgc ggc tgc agg aac gga ggc gga agg ggc cct gcg gcg 250
 Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Arg Gly Pro Ala Ala
 55 60 65

acg acg tcg tcg acg ggg gtg gcc gtg gga gct gag cac gga gaa gac 298
 Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly Glu Asp
 70 75 80

tcc ctc tct cgg aag ccg gat ccc gag ccg ggc agg atg gat cac cac 346
 Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp His His
 85 90 95

cag ccg ggg act ggg cgc tac cag gtg ctt ctt aat gaa gag gat aac 394
 Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu Asp Asn
 100 105 110

tca gaa tca tcg gct ata gag cag cca cct act tca aac cca gca ccg 442
 Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro Ala Pro
 115 120 125 130

cag att gtg cag gct gtg tct tca gca cca gca ctt gaa act gac tct 490
 Gln Ile Val Gln Ala Val Ser Ser Ala Pro Ala Leu Glu Thr Asp Ser
 135 140 145

tcc cct cca cca tat agt agt att act gtg gaa gta cct aca act tca 538
 Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr Thr Ser
 150 155 160

gat aca gaa gtt tac ggt gag ttt tat ccc gtg cca cct ccc tat agc 586
 Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro Tyr Ser
 165 170 175

gtt gct acc tct ctt cct aca tac gat gaa gct gag aag gct aaa gct 634

Val	Ala	Thr	Ser	Leu	Pro	Thr	Tyr	Asp	Glu	Ala	Glu	Lys	Ala	Lys	Ala		
180						185					190						
gct gca atg gca gct gca gca gca gaa aca tct caa aga att cag gag 682																	
Ala	Ala	Met	Ala	Ala	Ala	Ala	Ala	Glu	Thr	Ser	Gln	Arg	Ile	Gln	Glu		
195					200					205				210			
gaa gag tgt cca cca aga gat gac ttc agt gat gca gac cag ctc aga 730																	
Glu	Glu	Cys	Pro	Pro	Arg	Asp	Asp	Phe	Ser	Asp	Ala	Asp	Gln	Leu	Arg		
				215					220					225			
gtg ggg aat gat ggc att ttc atg ctg gca ttt ttc atg gca ttt att 778																	
Val	Gly	Asn	Asp	Gly	Ile	Phe	Met	Leu	Ala	Phe	Phe	Met	Ala	Phe	Ile		
			230					235					240				
ttc aac tgg ctt gga ttt tgt tta tcc ttc tgt atc acc aat acc ata 826																	
Phe	Asn	Trp	Leu	Gly	Phe	Cys	Leu	Ser	Phe	Cys	Ile	Thr	Asn	Thr	Ile		
		245					250					255					
gct gga agg tat ggt gct atc tgc gga ttt ggc ctt tcc ttg atc aaa 874																	
Ala	Gly	Arg	Tyr	Gly	Ala	Ile	Cys	Gly	Phe	Gly	Leu	Ser	Leu	Ile	Lys		
	260					265					270						
tgg atc ctt att gtc agg ttt tct gat tat ttt act gga tat ttc aat 922																	
Trp	Ile	Leu	Ile	Val	Arg	Phe	Ser	Asp	Tyr	Phe	Thr	Gly	Tyr	Phe	Asn		
275					280				285					290			
gga cag tat tgg ctt tgg tgg ata ttt ctt gta ctt ggc ctg ctc ctt 970																	
Gly	Gln	Tyr	Trp	Leu	Trp	Trp	Ile	Phe	Leu	Val	Leu	Gly	Leu	Leu	Leu		
				295					300					305			
ttc ttc aga gga ttt gtt aat tat cta aaa gtc aga aac atg tct gaa 1018																	
Phe	Phe	Arg	Gly	Phe	Val	Asn	Tyr	Leu	Lys	Val	Arg	Asn	Met	Ser	Glu		
			310					315					320				
agt atg gca gct gct cat aga aca agg tat ttc ttc tta ttg 1060																	
Ser	Met	Ala	Ala	Ala	His	Arg	Thr	Arg	Tyr	Phe	Phe	Leu	Leu				
		325				330						335					
tagagactgc atcaaccgca cattcctttc ttataccaat gtgaaatttc cagatcatct 1120																	
gtaaacctac aactttaata gaagactact aataacagaa gacaaattag tgaagaaaag 1180																	
acggagtttc gaaattgaat ggcagggtgg tttttgctta caagccattt ctgttcattc 1240																	
tttaagtatc tatatttcat ttgttttgca catatgcata tgtgccatt taagatattt 1300																	
gcatatactt gatagaaacc ataaagttgt agcagttaag tccagtcaca tttggttaat 1360																	
cagtgtttga tataattgaa agagttgagt ggataaacag tcttcagct tgtaaatgcc 1420																	
attgacttct gacctgacat ttagtataat aaaaatgaaa ttcttaacca tgtcaaatga 1480																	
tttagtttct ggctcttaga ctcatctggc agttctacac atgaaacatc ttttgttata 1540																	
taaggtgtat tgaaacctgc agtgctgatt attagaaagg atttgtcaga tttttgaaca 1600																	

tgatattttac attattatttt aggaaaactc ttccctgtaaa taaccatgca taacttactt 1660
 tctgcaatgt tttcttagaa attgtgtcca gatagctttc actaatTTta aattaagtga 1720
 actaaatata tatgtgtata tgtatacaca tatatataca cacacacata tatatatTTta 1780
 gaaacgtgag tgTTaaagat agaatttggt ttaggacaaa tTTtaagaaa atgtgggaat 1840
 accaaatgtc cTTtataaga aaaataaatt ttgtTTtaag ggacatacca gTTtttaggga 1900
 tTTtcagatg ggaagctgca tTTtttaggat tgcccatcct aagagatcct gcaggaagag 1960
 attgtattag atattatatt tatttcattt aagataattt tcaaagTTaa tTTtctaaat 2020
 aagataattc tcatttggtt ttgtcTTtta aaaggccaat aaaatatcct tcagtatcat 2080
 tgtaataatt tTTtagagtt taatttgtaa agcttagcaa ataaaatcct gtactatgaa 2140
 tagcttcttg cTTtatgact ttaggattaa cttgtaaaaa acatatcctg aactgagata 2200
 tgcaaaatac tcattttcaa gttatggaaa tgtgtttgtg gcatatagga ctgtgggggtc 2260
 tgtgtgtgta gtgagagtgt gtagccacta ttataactgg aatttaattt acattcataa 2320
 actactatat ttcccatcct gcaaatacatt ttatgtctca tctgtTTttc cTTtcggTTa 2380
 tatcTTtggt tttgaatacc aacatttaaa atgatggtat tttatcTTtt aaacttaaaa 2440
 attatttaat acagctatat ggaccttata aaattgattt cttatttatt attagacatt 2500
 actactaaaa ggtacatcta actattcagg gacattTTtc catttcctaaa aaataaaatt 2560
 tattatgctt tataacctct tctgtatttt ctaattTTtt cattgtcTTt gataaataaa 2620
 acagttttgt tttgct 2636

<210> 19
 <211> 336
 <212> PRT
 <213> Homo sapiens

<400> 19
 Met Ala Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met
 1 5 10 15
 Leu Asn Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr
 20 25 30
 Asn Ala Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu
 35 40 45
 Leu Pro Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro
 50 55 60
 Ala Ala Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly
 65 70 75 80

Glu	Asp	Ser	Leu	Ser	Arg	Lys	Pro	Asp	Pro	Glu	Pro	Gly	Arg	Met	Asp	
				85					90					95		
His	His	Gln	Pro	Gly	Thr	Gly	Arg	Tyr	Gln	Val	Leu	Leu	Asn	Glu	Glu	
			100					105					110			
Asp	Asn	Ser	Glu	Ser	Ser	Ala	Ile	Glu	Gln	Pro	Pro	Thr	Ser	Asn	Pro	
		115					120					125				
Ala	Pro	Gln	Ile	Val	Gln	Ala	Ala	Ser	Ser	Ala	Pro	Ala	Leu	Glu	Thr	
	130					135					140					
Asp	Ser	Ser	Pro	Pro	Pro	Tyr	Ser	Ser	Ile	Thr	Val	Glu	Val	Pro	Thr	
145					150					155					160	
Thr	Ser	Asp	Thr	Glu	Val	Tyr	Gly	Glu	Phe	Tyr	Pro	Val	Pro	Pro	Pro	
			165						170						175	
Tyr	Ser	Val	Ala	Thr	Ser	Leu	Pro	Thr	Tyr	Asp	Glu	Ala	Glu	Lys	Ala	
			180					185					190			
Lys	Ala	Ala	Ala	Met	Ala	Ala	Ala	Ala	Ala	Glu	Thr	Ser	Gln	Arg	Ile	
	195						200					205				
Gln	Glu	Glu	Glu	Cys	Pro	Pro	Arg	Asp	Asp	Phe	Ser	Asp	Ala	Asp	Gln	
	210					215					220					
Leu	Arg	Val	Gly	Asn	Asp	Gly	Ile	Phe	Met	Leu	Ala	Phe	Phe	Met	Ala	
225					230					235					240	
Phe	Ile	Phe	Asn	Trp	Leu	Gly	Phe	Cys	Leu	Ser	Phe	Cys	Ile	Thr	Asn	
			245						250					255		
Thr	Ile	Ala	Gly	Arg	Tyr	Gly	Ala	Ile	Cys	Gly	Phe	Gly	Leu	Ser	Leu	
			260					265					270			
Ile	Lys	Trp	Ile	Leu	Ile	Val	Arg	Phe	Ser	Asp	Tyr	Phe	Thr	Gly	Tyr	
		275					280					285				
Phe	Asn	Gly	Gln	Tyr	Trp	Leu	Trp	Trp	Ile	Phe	Leu	Val	Leu	Gly	Leu	
	290					295					300					
Leu	Leu	Phe	Phe	Arg	Gly	Phe	Val	Asn	Tyr	Leu	Lys	Val	Arg	Asn	Met	
305					310					315					320	
Ser	Glu	Ser	Met	Ala	Ala	Ala	His	Arg	Thr	Arg	Tyr	Phe	Phe	Leu	Leu	
			325						330					335		

<210> 20
 <211> 2636
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> (53).. (1060)

<400> 20

cttactttttc catctctctcc caccagcta taccctccca ctggcggcgc gg atg gca 58
Met Ala
1

cgc cgg cgg agc cag cga gtc tgc gcg agc ggt ccg agc atg ctc aat 106
Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met Leu Asn
5 10 15

agc gcg cgc ggc gcc ccg gag ctt ctc cgc gga acc gcg acc aac gcg 154
Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr Asn Ala
20 25 30

gag gtc tcg gcg gcc gct gcg gga gcc aca gga agt gaa gag ctt ccg 202
Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu Leu Pro
35 40 45 50

ccg gga gac cgc ggc tgc agg aac gga ggc gga agg ggc cct gcg gcg 250
Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro Ala Ala
55 60 65

acg acg tcg tcg acg ggg gtg gcc gtg gga gct gag cac gga gaa gac 298
Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly Glu Asp
70 75 80

tcc ctc tct cgg aag ccg gat ccc gag ccg ggc agg atg gat cac cac 346
Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp His His
85 90 95

cag ccg ggg act ggg cgc tac cag gtg ctt ctt aat gaa gag gat aac 394
Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu Asp Asn
100 105 110

tca gaa tca tcg gct ata gag cag cca cct act tca aac cca gca ccg 442
Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro Ala Pro
115 120 125 130

cag att gtg cag gct gcg tct tca gca cca gca ctt gaa act gac tct 490
Gln Ile Val Gln Ala Ala Ser Ser Ala Pro Ala Leu Glu Thr Asp Ser
135 140 145

tcc cct cca cca tat agt agt att act gtg gaa gta cct aca act tca 538
Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr Thr Ser
150 155 160

gat aca gaa gtt tac ggt gag ttt tat ccc gtg cca cct ccc tat agc 586
Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro Tyr Ser
165 170 175

gtt gct acc tct ctt cct aca tac gat gaa gct gag aag gct aaa gct 634
Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala Lys Ala
180 185 190

gct gca atg gca gct gca gca gca gaa aca tct caa aga att cag gag 682
Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile Gln Glu

-195-	-200-	-205-	-210-	
gaa gag tgt cca cca aga gat gac ttc agt gat gca gac cag ctc aga	730			
Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln Leu Arg				
215	220	225		
gtg ggg aat gat ggc att ttc atg ctg gca ttt ttc atg gca ttt att	778			
Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala Phe Ile				
230	235	240		
ttc aac tgg ctt gga ttt tgt tta tcc ttc tgt atc acc aat acc ata	826			
Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn Thr Ile				
245	250	255		
gct gga agg tat ggt gct atc tgc gga ttt ggc ctt tcc ttg atc aaa	874			
Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu Ile Lys				
260	265	270		
tgg atc ctt att gtc agg ttt tct gat tat ttt act gga tat ttc aat	922			
Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr Phe Asn				
275	280	285	290	
gga cag tat tgg ctt tgg tgg ata ttt ctt gta ctt ggc ctg ctc ctt	970			
Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu Leu Leu				
295	300	305		
ttc ttc aga gga ttt gtt aat tat cta aaa gtc aga aac atg tct gaa	1018			
Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met Ser Glu				
310	315	320		
agt atg gca gct gct cat aga aca agg tat ttc ttc tta ttg	1060			
Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu				
325	330	335		
tagagactgc atcaaccoga cattcctttc ttataccaat gtgaaatttc cagatcatct	1120			
gtaaacctac aactttaata gaagactact aataacagaa gacaaattag tgaagaaaag	1180			
acggagtttc gaaattgaat ggcagggtgg tttttgotta caagccattt ctgttcattc	1240			
tttaagtatc tatatttcatt ttgttttgca catatgcata tgtgcccatt taagatattt	1300			
gcatatactt gatagaaacc ataaagttgt agcagttaag tccagtcaca tttggttaat	1360			
cagtgtttga tataattgaa agagttgagt ggataaacag tcttcagct tgtaaatgcc	1420			
attgacttct gacctgacat ttagtataat aaaaatgaaa ttcttaacca tgtcaaatga	1480			
tttagtttct ggctcttaga ctcatctggc agttctacac atgaaacatc ttttgttata	1540			
taaggtgtat tgaaacctgc agtgctgatt attagaaagg atttgtcaga tttttgaaca	1600			
tgatatttac attattattt aggaaaactc ttctgtgaaa taaccatgca taacttactt	1660			
tctgcaatgt tttcttagaa attgtgtcca gatagctttc actaatttta aattaagtga	1720			
actaaatata tatgtgtata tgtatacaca tatatatata cacacacata tatatatatta	1780			

gaaacgtgag tgtaaagat agaatttggt ttaggacaaa ttttaagaaa atgtgggaat 1840
 accaaatgtc ctttataaga aaaataaatt ttgttttaag ggacatacca gttttaggga 1900
 ttttcagatg ggaagctgca tttttaggat tgcccatctt aagagatctt gcaggaagag 1960
 attgtattag atattatatt tatttcattt aagataattt tcaaagttaa ttttctaaat 2020
 aagataattc tcatttgtgt ttgtctttta aaaggccaat aaaatatctt tcagtatcat 2080
 tgtaataatt ttttagagtt taatttgtaa agcttagcaa ataaaatctt gtactatgaa 2140
 tagcttcttg ctttatgact ttaggattaa ctigtataaaa acatatcttg aactgagata 2200
 tgcaaaatac tcattttcaa gttatggaaa tgtgtttgtg gcatatagga ctgtgggggc 2260
 tgtgtgtgta gtgagagtgt gtagccacta ttataactgg aatttaattt acattcataa 2320
 actactatat ttcccatctt gcaaatcatt ttatgtctca tctgtttttc ctttcgggta 2380
 tatctttggg tttgaatacc aacatttaaa atgatgggat tttatctttt aaacttaaaa 2440
 attatttaat acagctatat ggacctata aaattgattt cttatttatt attagacatt 2500
 actactaaaa ggtacatcta actattcagg gacatttttc catttcocaa aaataaaatt 2560
 tattatgctt tataacctct tctgtatttt ctaatttttt cattgtcttt gataaataaa 2620
 acagttttgt tttgct 2636

<210> 21
 <211> 76
 <212> PRT
 <213> Homo sapiens

<400> 21
 Met Val Cys Ile Pro Cys Ile Val Ile Pro Val Leu Leu Trp Ile Tyr
 1 5 10 15
 Lys Lys Phe Leu Glu Pro Tyr Ile Tyr Pro Leu Val Ser Pro Phe Val
 20 25 30
 Ser Arg Ile Trp Pro Lys Lys Ala Ile Gln Glu Ser Asn Asp Thr Asn
 35 40 45
 Lys Gly Lys Val Asn Phe Lys Gly Ala Asp Met Asn Gly Leu Pro Thr
 50 55 60
 Lys Gly Pro Thr Glu Ile Cys Asp Lys Lys Lys Asp
 65 70 75

<210> 22
 <211> 1085
 <212> DNA

```

<213> Homo sapiens -
<220>
<221> CDS
<222> (176)..(403)

<400> 22
gggctagcgg cctggggttg gctttgtagc tgctccgcag gccagcccc ggccgcgctc 60
gcagagtccct aggcgggtgcg cggcctcctg cctcctccct cctcggcggt cgcgccccgc 120
cggcctccgc ggtgcctgcc ttgcgtctca gggtgaggag ctcaagcttg ggaaa atg 178
                                         Met
                                         1
gtg tgc att cct tgt atc gtc att cca gtt ctg ctc tgg atc tac aaa 226
Val Cys Ile Pro Cys Ile Val Ile Pro Val Leu Leu Trp Ile Tyr Lys
          5                      10                      15
aaa ttc ctg gag cca tat ata tac cct ctg gtt tcc ccc ttc gtt agt 274
Lys Phe Leu Glu Pro Tyr Ile Tyr Pro Leu Val Ser Pro Phe Val Ser
          20                      25                      30
cgt ata tgg cct aag aaa gca ata caa gaa tcc aat gat aca aac aaa 322
Arg Ile Trp Pro Lys Lys Ala Ile Gln Glu Ser Asn Asp Thr Asn Lys
          35                      40                      45
ggc aaa gta aac ttt aag ggt gca gac atg aat gga tta cca aca aaa 370
Gly Lys Val Asn Phe Lys Gly Ala Asp Met Asn Gly Leu Pro Thr Lys
          50                      55                      60                      65
gga cca aca gaa atc tgt gat aaa aag aaa gac taaagaaatt ttctaaagg 423
Gly Pro Thr Glu Ile Cys Asp Lys Lys Lys Asp
          70                      75
accccatcat ttaaaaaatg gacctgataa tatgaagcat ctctcttgta attgtctctg 483
acctttttat ctgagaccgg aattcaggat aggagtctag atatttacct gatactaatac 543
aggaaatata tgatatccgt atttaaaatg tagttagtta tatttaatga cctcattcct 603
aagttccttt ttcgttaatg tagctttcat ttctgttatt gctgtttgaa taatatgatt 663
aaatagaagg tttgtgccag tagacattat gttactaaat cagcacttta aaatctttgg 723
ttctctaatt catatgaatt tgctgtttgc tctaatttct ttgggctctt ctaatttgag 783
tgaggtacaa ttttgtttgt aaacagtcca gtgaaactgt gcagggaaat gaaggtagaa 843
ttttgggagg taataatgat gtgaaacata aagatttaat aattactgtc caacacagtg 903
gagcagcttg tccacaaata tagtaattac tatttattgc tctaaggaag attaaaaaaa 963
gatagggaaa aggggggaaac ttctttgaaa aatgaaacat ctgttacatt aatgtctaata 1023
tataaaatth taatccttac tgcatttctt ctgttctac aaatgtatta aacattcagt 1083

```

<210> 23
 <211> 84
 <212> PRT
 <213> Homo sapiens

<400> 23
 Met Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile Leu
 1 5 10 15
 Pro Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys Val
 20 25 30
 Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile
 35 40 45
 Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Phe Tyr Trp
 50 55 60
 Met Arg Val Ile Leu Ala Ser Asn Arg Gly Thr Leu Met Glu His Ser
 65 70 75 80
 Leu Ser Gly Leu

<210> 24
 <211> 1593
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (65)..(316)

<400> 24
 agcgtgcgct cacgcggagc agagctgagc tgaagcggga cccggagccc gagcagccgc 60
 cgcc atg gca atc aaa ttt ctg gaa gtc atc aag ccc ttc tgt gtc atc 109
 Met Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile
 1 5 10 15
 ctg ccg gaa att cag aag cca gag agg aag att cag ttt aag gag aaa 157
 Leu Pro Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys
 20 25 30
 gtg ctg tgg acc gct atc acc ctc ttt atc ttc tta gtg tgc tgc cag 205
 Val Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln
 35 40 45
 att ccc ctg ttt ggg atc atg tct tca gat tca gct gac cct ttc tat 253
 Ile Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Phe Tyr
 50 55 60
 tgg atg aga gtg att cta gcc tct aac aga ggc aca ttg atg gag cac 301

Trp Met Arg Val Ile Leu Ala Ser Asn Arg Gly Thr Leu Met Glu His -- -- -- -- --
65 70 75

tct ctc tct ggc ctt tagggagtcc cctcttagga caggcactgc ccagcagcaa 356
Ser Leu Ser Gly Leu
80

gggcagcaga gttgggtgct aagatcctga ggagctcgag gtttcgagct ggcttttagac 416
attggtggga ccaaggatgt tttgcaggat gccctgatcc taagaagggg gcctgggggt 476
gcgtgcagcc tgtcggggag accccactct gtgcacctat tggctcttct agctgactct 536
tctcgttggg cttagagtct gccctgtttct gctagctccg tgttttagtcc acttgggtca 596
tcagctctgc caagctgagc ctggccaagc taggtggaca gacccttgca gtgatgtccg 656
tttgtccaga ttctgccagt catcactgga cacgtctcct cgcagctgcc ctagcaaggg 716
gagacattgt ggtagctatc agacatggac agaaactgac ttagtgctca caagccccta 776
caccttctgg gctgaagatc acccagctgt gttcagaatt ttcttactgt gcttaggact 836
gcacgcaagt gagcagacac caccgacttc ctttctgcgt caccagtgtc gtcagcagag 896
agaggacagc acaggctcaa ggttggtagt gaagtcaggt tcgggggtgca tgggctgtgg 956
tggtggtgat cagttgctcc agtggttgaa ataagaagac tcatgtttat gtctggaata 1016
agttctgttt gtgctgacag gtgaccttgc tggcagtgct agccaggaaa cagagtgacc 1076
aagggacaag aagggaactg cctaaagcca ccagcaact cagcagcaga accaagatgg 1136
gccccaggct cctccatatg gcccagggt taccacccta tcacacgtgg ccttgtctag 1196
accagtcct gagcagggga gaggtctttg agacctgatg ccctcctacc cacatgggtc 1256
tcccactgcc ctgtctgtc tgctgctaca gaggggcagg gcctcccca gccacgctt 1316
aggaatgctt ggctctggc aggcaggcag ctgtacccaa gctggtgggc agggggctgg 1376
aaggcaccag gcctcaggag gagccccata gtcccgctg cagcctgtaa ccatcggtg 1436
ggccctgcaa ggcccacact cagccctgt gggatgatgg caggtgggt ggggtggggc 1496
tgaccccagc ttccagggga ctgtcactgt ggacgcaaaa atggcataac tgagataagg 1556
tgaataagtg acaaataaag ccagtttttt acaaggt 1593

<210> 25
<211> 179
<212> PRT
<213> Homo sapiens

<400> 25
Met Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile Leu

Glu	Ile	Gln	Lys	Pro	Glu	Arg	Lys	Ile	Gln	Phe	Lys	Glu	Lys	Val	Leu	
	20						25					30				
tgg	acc	gct	atc	acc	ctc	ttt	atc	ttc	tta	gtg	tgc	tgc	cag	att	ccc	260
Trp	Thr	Ala	Ile	Thr	Leu	Phe	Ile	Phe	Leu	Val	Cys	Cys	Gln	Ile	Pro	
	35					40					45					
ctg	ttt	ggg	atc	atg	tct	tca	gat	tca	gct	gac	ccg	gtc	cat	gca	gtt	308
Leu	Phe	Gly	Ile	Met	Ser	Ser	Asp	Ser	Ala	Asp	Pro	Val	His	Ala	Val	
	50				55					60					65	
gta	tac	ata	gtg	ttc	atg	ctg	ggc	tcc	tgt	gca	ttc	ttc	tcc	aaa	acg	356
Val	Tyr	Ile	Val	Phe	Met	Leu	Gly	Ser	Cys	Ala	Phe	Phe	Ser	Lys	Thr	
				70					75					80		
tgg	att	gag	gtc	tca	ggg	tcc	tct	gcc	aaa	gat	gtt	gca	aag	cag	ctg	404
Trp	Ile	Glu	Val	Ser	Gly	Ser	Ser	Ala	Lys	Asp	Val	Ala	Lys	Gln	Leu	
			85					90					95			
aag	gag	cag	cag	atg	gtg	atg	aga	ggc	cac	cga	gag	acc	tcc	atg	gtc	452
Lys	Glu	Gln	Gln	Met	Val	Met	Arg	Gly	His	Arg	Glu	Thr	Ser	Met	Val	
		100					105					110				
cat	gaa	ctc	aac	cgg	tac	atc	ccc	aca	gcc	gcg	gcc	ttt	ggg	ggg	ctg	500
His	Glu	Leu	Asn	Arg	Tyr	Ile	Pro	Thr	Ala	Ala	Ala	Phe	Gly	Gly	Leu	
	115					120					125					
tgc	atc	ggg	gcc	ctc	tgc	gtc	ctg	gct	gac	ttc	cta	ggc	gcc	att	ggg	548
Cys	Ile	Gly	Ala	Leu	Ser	Val	Leu	Ala	Asp	Phe	Leu	Gly	Ala	Ile	Gly	
	130				135				140					145		
tct	gga	acc	ggg	atc	ctg	ctc	gca	gtc	aca	atc	atc	tac	cag	tac	ttt	596
Ser	Gly	Thr	Gly	Ile	Leu	Leu	Ala	Val	Thr	Ile	Ile	Tyr	Gln	Tyr	Phe	
				150					155					160		
gag	atc	ttc	gtt	aag	gag	caa	agc	gag	gtt	ggc	agc	atg	ggg	gcc	ctg	644
Glu	Ile	Phe	Val	Lys	Glu	Gln	Ser	Glu	Val	Gly	Ser	Met	Gly	Ala	Leu	
			165				170					175				
ctc	ttc	tgagcccgtc	tcccggacag	gttgaggaag	ctgctccaga	agcgccctcg										700
Leu	Phe															
aaggggagct	ctcatcatgg	cgcgtgctgc	tgccgcatat	ggacttttaa	taatgttttt											760
gaatttcgta	ttctttcatt	ccactgtgta	aagtgtaga	cattttccaa	tttaaaattt											820
tgctttttat	cctggcactg	gcaaaaagaa	ctgtgaaagt	gaattttattc	agccgactgc											880
cagagaagtg	ggaatggtat	aggattgtcc	ccaagtgtcc	atgtaacttt	tgttttaacc											940
tttgcacctt	ctcagtgtg	tatgcccgtg	cagccgtctc	acctgtttcc	ccacaaaggg											1000
aatttctcac	tctgggttga	agcacaacaa	ctgaaatgtc	tacgtttcat	tttggcagta											1060
gggtgtgaag	ctgggagcag	atcatgtatt	tcccggagac	atgggacctt	gctggcatgt											1120
ctccttcaca	atcaggcgtg	ggaatatctg	gcttaggact	gtttctctct	aagacaccat											1180

tgttttccct tattttaaaa gtgatttttt taaggacaga acttcttcca aaagagaggg 1240
 atggctttcc cagaagacac tctggagacc ttgctggcag tgctagccag gaaacagagt 1300
 gaccaaggga caagaaggga cttgcctaaa gccacccagc aactcagcag cagaaccaag 1360
 atggggcccca ggctcctcca tatggcccag ggcttaccac cctatcacac gtggccttgt 1420
 ctagaccagc tcctgagcag gggagaggct cttgagacct gatgccctcc taccacatg 1480
 gttctcccac tgccctgtct gctctgctgc tacaragggg cagggcctcc ccagcccccac 1540
 gcttaggaat gcttggcctc tggcaggcag gcagctgtac ccaagctggt gggcaggggg 1600
 ctggaaggca ccaggcctca ggaggagccc catagtcccg cctgcagcct gtaaccatcg 1660
 gctggggcct gcaaggccca cactcacgcc ctgtgggtga tggtcacggt gggtaggggg 1720
 gggctgaccc cagcttccag gggactgtca ctgtggacgc caaatggca taactsasat 1780
 aaggtgaata agtgacaaat aaagccagtt ttttacaagg 1820

<210> 27
 <211> 279
 <212> PRT
 <213> Homo sapiens

<400> 27
 Met Glu Ala Val Val Asn Leu Tyr Gln Glu Val Met Lys His Ala Asp
 1 5 10 15
 Pro Arg Ile Gln Gly Tyr Pro Leu Met Gly Ser Pro Leu Leu Met Thr
 20 25 30
 Ser Ile Leu Leu Thr Tyr Val Tyr Phe Val Leu Ser Leu Gly Pro Arg
 35 40 45
 Ile Met Ala Asn Arg Lys Pro Phe Gln Leu Arg Gly Phe Met Ile Val
 50 55 60
 Tyr Asn Phe Ser Leu Val Ala Leu Ser Leu Tyr Ile Val Tyr Glu Phe
 65 70 75 80
 Leu Met Ser Gly Trp Leu Ser Thr Tyr Thr Trp Arg Cys Asp Pro Val
 85 90 95
 Asp Tyr Ser Asn Ser Pro Glu Ala Leu Arg Met Val Arg Val Ala Trp
 100 105 110
 Leu Phe Leu Phe Ser Lys Phe Ile Glu Leu Met Asp Thr Val Ile Phe
 115 120 125
 Ile Leu Arg Lys Lys Asp Gly Gln Val Thr Phe Leu His Val Phe His
 130 135 140

His	Ser	Val	Leu	Pro	Trp	Ser	Trp	Trp	Trp	Gly	Val	Lys	Ile	Ala	Pro
145					150					155					160
Gly	Gly	Met	Gly	Ser	Phe	His	Ala	Met	Ile	Asn	Ser	Ser	Val	His	Val
				165					170					175	
Ile	Met	Tyr	Leu	Tyr	Tyr	Gly	Leu	Ser	Ala	Phe	Gly	Pro	Val	Ala	Gln
			180					185					190		
Pro	Tyr	Leu	Trp	Trp	Lys	Lys	His	Met	Thr	Ala	Ile	Gln	Leu	Ile	Gln
		195					200					205			
Phe	Val	Leu	Val	Ser	Leu	His	Ile	Ser	Gln	Tyr	Tyr	Phe	Met	Ser	Ser
	210					215					220				
Cys	Asn	Tyr	Gln	Tyr	Pro	Val	Ile	Ile	His	Leu	Ile	Trp	Met	Tyr	Gly
225					230					235					240
Thr	Ile	Phe	Phe	Met	Leu	Phe	Ser	Asn	Phe	Trp	Tyr	His	Ser	Tyr	Thr
				245					250					255	
Lys	Gly	Lys	Arg	Leu	Pro	Arg	Ala	Leu	Gln	Gln	Asn	Gly	Ala	Pro	Gly
			260					265					270		
Ile	Ala	Lys	Val	Lys	Ala	Asn									
		275													

<210> 28
 <211> 1472
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (119)..(955)

<400> 28
 gccacgacaga tgaggaagtg gcaggcaggc aggctggccc cggggacttc tctctggccc 60
 tgctccctcc gagcgctccg ccgttgcccg cctggcccct acggagtcct tagccagg 118
 atg gag gct gtt gtg aac ttg tac caa gag gtg atg aag cac gca gat 166
 Met Glu Ala Val Val Asn Leu Tyr Gln Glu Val Met Lys His Ala Asp
 1 5 10 15
 ccc cgg atc cag ggc tac cct ctg atg ggg tcc ccc ttg cta atg acc 214
 Pro Arg Ile Gln Gly Tyr Pro Leu Met Gly Ser Pro Leu Leu Met Thr
 20 25 30
 tcc att ctc ctg acc tac gtg tac ttc gtt ctc tca ctt ggg cct cgc 262
 Ser Ile Leu Leu Thr Tyr Val Tyr Phe Val Leu Ser Leu Gly Pro Arg
 35 40 45
 atc atg gct aat cgg aag ccc ttc cag ctc cgt ggc ttc atg att gtc 310
 Ile Met Ala Asn Arg Lys Pro Phe Gln Leu Arg Gly Phe Met Ile Val
 50 55 60

tac aac ttc tca ctg gtg gca ctc tcc ctc tac att gtc tat gag ttc	358
Tyr Asn Phe Ser Leu Val Ala Leu Ser Leu Tyr Ile Val Tyr Glu Phe	
65 70 75 80	
ctg atg tcg ggc tgg ctg agc acc tat acc tgg cgc tgt gac cct gtg	406
Leu Met Ser Gly Trp Leu Ser Thr Tyr Thr Trp Arg Cys Asp Pro Val	
85 90 95	
gac tat tcc aac agc cct gag gca ctt agg atg gtt cgg gtg gcc tgg	454
Asp Tyr Ser Asn Ser Pro Glu Ala Leu Arg Met Val Arg Val Ala Trp	
100 105 110	
ctc ttc ctc ttc tcc aag ttc att gag ctg atg gac aca gtg atc ttt	502
Leu Phe Leu Phe Ser Lys Phe Ile Glu Leu Met Asp Thr Val Ile Phe	
115 120 125	
att ctc cga aag aaa gac ggg cag gtg acc ttc cta cat gtc ttc cat	550
Ile Leu Arg Lys Lys Asp Gly Gln Val Thr Phe Leu His Val Phe His	
130 135 140	
cac tct gtg ctt ccc tgg agc tgg tgg tgg ggg gta aag att gcc ccg	598
His Ser Val Leu Pro Trp Ser Trp Trp Trp Gly Val Lys Ile Ala Pro	
145 150 155 160	
gga gga atg ggc tct ttc cat gcc atg ata aac tct tcc gtg cat gtc	646
Gly Gly Met Gly Ser Phe His Ala Met Ile Asn Ser Ser Val His Val	
165 170 175	
ata atg tac ctg tac tac gga tta tct gcc ttt ggc cct gtg gca caa	694
Ile Met Tyr Leu Tyr Tyr Gly Leu Ser Ala Phe Gly Pro Val Ala Gln	
180 185 190	
ccc tac ctt tgg tgg aaa aag cac atg aca gcc att cag ctg atc cag	742
Pro Tyr Leu Trp Trp Lys Lys His Met Thr Ala Ile Gln Leu Ile Gln	
195 200 205	
ttt gtc ctg gtc tca ctg cac atc tcc cag tac tac ttt atg tcc agc	790
Phe Val Leu Val Ser Leu His Ile Ser Gln Tyr Tyr Phe Met Ser Ser	
210 215 220	
tgt aac tac cag tac cca gtc att att cac ctc atc tgg atg tat ggc	838
Cys Asn Tyr Gln Tyr Pro Val Ile Ile His Leu Ile Trp Met Tyr Gly	
225 230 235 240	
acc atc ttc ttc atg ctg ttc tcc aac ttc tgg tat cac tct tat acc	886
Thr Ile Phe Phe Met Leu Phe Ser Asn Phe Trp Tyr His Ser Tyr Thr	
245 250 255	
aag ggc aag cgg ctg ccc cgt gca ctt cag caa aat gga gct cca ggt	934
Lys Gly Lys Arg Leu Pro Arg Ala Leu Gln Gln Asn Gly Ala Pro Gly	
260 265 270	
att gcc aag gtc aag gcc aac tgagaagcat ggcctagata ggcgccacc	985
Ile Ala Lys Val Lys Ala Asn	
275	

```

--taagtgcctc-aggactgcac-cttagggcag-tgtccgtcag-tgccctctcc acctacacct 1045
gtgaccaagg cttatgtggt caggactgag caggggactg gccctcccct ccccacagct 1105
gctctacagg gaccacggct ttggttcctc acccacttcc cccgggcagc tccagggatg 1165
tggcctcatt gctgtctgcc actccagagc tgggggctaa aagggtgta cagttatttc 1225
cccctccctg ccttaaaact tgggagagga gcactcaggg ctggccccac aaaggtctc 1285
gtggcctttt tcctcacaca gaagaggtca gcaataatgt cactgtggac ccagtctcac 1345
tcctccacco cacacactga agcagtagct tctgggccaa aggtcagggg gggcgggggc 1405
ctgggaatac agcctgtgga ggctgcttac tcaacttggt tcttaattaa aagtgcaga 1465
ggaacc 1472

```

```

<210> 29
<211> 137
<212> PRT
<213> Homo sapiens

```

```

<400> 29
Met Gly Phe Gly Ala Thr Leu Ala Val Gly Leu Thr Ile Phe Val Leu
  1             5             10            15
Ser Val Val Thr Ile Ile Ile Cys Phe Thr Cys Ser Cys Cys Cys Leu
          20             25             30
Tyr Lys Thr Cys Arg Arg Pro Arg Pro Val Val Thr Thr Thr Thr Ser
      35             40             45
Thr Thr Val Val His Ala Pro Tyr Pro Gln Pro Pro Ser Val Pro Pro
  50             55             60
Ser Tyr Pro Gly Pro Ser Tyr Gln Gly Tyr His Thr Met Pro Pro Gln
  65             70             75             80
Pro Gly Met Pro Ala Ala Pro Tyr Pro Met Gln Tyr Pro Pro Pro Tyr
          85             90             95
Pro Ala Gln Pro Met Gly Pro Pro Ala Tyr His Glu Thr Leu Ala Gly
      100             105             110
Gly Ala Ala Ala Pro Tyr Pro Ala Ser Gln Pro Pro Tyr Asn Pro Ala
      115             120             125
Tyr Met Asp Ala Pro Lys Ala Ala Leu
      130             135

```

```

<210> 30
<211> 1788
<212> DNA
<213> Homo sapiens

```

$\langle 222 \rangle$ (145) .. (555)

gtgcttcctg tggctgacgt catctggagg agatttgctt tctttttctc caaaagggga 60

ctctgggtga aggcagaggc taac atg ggg ttc gga gcg acc ttg gcc gtt 171
Met Gly Phe Gly Ala Thr Leu Ala Val
1 5

ggc ctg acc atc ttt gtg ctg tct gtc gtc act atc atc atc tgc ttc 219
Gly Leu Thr Ile Phe Val Leu Ser Val Val Thr Ile Ile Ile Cys Phe
10 15 20 25

acc tgc tcc tgc tgc tgc ctt tac aag acg tgc cgc cga cca cgt ccg 267
Thr Cys Ser Cys Cys Cys Leu Tyr Lys Thr Cys Arg Arg Pro Arg Pro
30 35 40

gtt gtc acc acc acc aca tcc acc act gtg gtg cat gcc cct tat cct 315
Val Val Thr Thr Thr Thr Ser Thr Thr Val Val His Ala Pro Tyr Pro
45 50 55

cag cct cca agt gtg ccg ccc agc tac cct gga cca agc tac cag ggc 363
Gln Pro Pro Ser Val Pro Pro Ser Tyr Pro Gly Pro Ser Tyr Gln Gly
60 65 70

tac	cac	acc	atg	ccg	cct	cag	cca	ggg	atg	cca	gca	gca	ccc	tac	cca	411
Tyr	His	Thr	Met	Pro	Pro	Gln	Pro	Gly	Met	Pro	Ala	Ala	Pro	Tyr	Pro	
	75					80					85					

atg cag tac cca cca cct tac cca gcc cag ccc atg ggc cca ccg gcc 459
Met Gln Tyr Pro Pro Pro Tyr Pro Ala Gln Pro Met Gly Pro Pro Ala
90 95 100 105

tac cac gag acc ctg gct gga gga gca gcc gcg ccc tac ccc gcc agc 507
 Tyr His Glu Thr Leu Ala Gly Gly Ala Ala Ala Pro Tyr Pro Ala Ser
 110 115 120

cag cct cct tac aac ccg gcc tac atg gat gcc ccg aag gcg gcc ctc 555
Gln Pro Pro Tyr Asn Pro Ala Tyr Met Asp Ala Pro Lys Ala Ala Leu
125 130 135

tgagcattcc ctggcctctc tggctgccac ttggttatgt tgtgtgtgtg cgtgagtggg 615

gtgcaggcgc ggttccttac gccccatgtg tgctgtgtgt gtccaggcac ggttccttac 675

gccccatgtg tgctgtgtgt gtcctgcctg tataatgtggc ttcctctgat gctgacaagg 735

tggggaacaa tccttgccag agtgggctgg gaccagactt tgttctcttc ctcacctgaa 795

attatgcttc ctaaaatctc aagccaaact caaagaatgg ggtggtgggg ggcaccctgt 855

gaggtggccc ctgagaggtg ggggcctctc cagggcacat ctggagtctt tctccagctt 915

accctagggg gaccaagtag ggccctgtcac accaggggtgg cgcagctttc tgtgtgatgc 975
 agatgtgtcc tggtttcggc agcgtagcca gctgctgctt gaggccatgg ctcgcccccg 1035
 gagttggggg taccggttgc agagccaggg acatgatgca ggccaagctt gggatctggc 1095
 caagttggac tttgatcctt tgggcagatg tcccattgct ccctggagcc tgtcatgcct 1155
 gttggggatc aggcagcctc ctgatgccag aacacctcag gcagagccct actcagctgt 1215
 acctgtctgc ctggactgtc ccctgtcccc gcatctcccc tgggaccagc tggagggcca 1275
 catgcacaca cagcctagct gccccaggg agctctgctg cccttgctgg ccctgccctt 1335
 cccacaggtg agcagggctc ctgtccacca gcacactcag ttctcttccc tgcagtgttt 1395
 tcattttatt ttagccaaac attttgctg ttttctgttt caaacatkat agttgatatg 1455
 agactgaaac ccctggggtt tggagggaaa ttggctcaga gatggacaac ctggcaactg 1515
 tgagtccctg cttcccgaca ccagcctcat ggaatatgca acaactcctg taccocagtc 1575
 cacggtgttc tggcagcagg gacacctggg ccaatgggcc atctggacca aaggtggggg 1635
 gtggggccct ggatggcagc tctggcccag acatgaatac ctgctgttcc tcctccctct 1695
 attactgttt caccagagct gtcttagctc aaatctgttg tgtttctgag tctaggggtct 1755
 gtacacttgt ttataataaa tgcaatcggt tgg 1788

<210> 31
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 31
 Met Gly Phe Gly Ala Thr Leu Ala Val Gly Leu Thr Ile Phe Val Leu
 1 5 10 15
 Ser Val Val Thr Ile Ile Ile Cys Phe Thr Cys Ser Cys Cys Cys Leu
 20 25 30
 Tyr Lys Thr Cys Arg Arg Pro Arg Pro Val Val Thr Thr Thr Thr Ser
 35 40 45
 Thr Thr Val Val His Ala Pro Tyr Pro Gln Pro Pro Ser Val Pro Pro
 50 55 60
 Ser Tyr Pro Gly Pro Ser Tyr Gln Gly Tyr His Thr Met Pro Pro Gln
 65 70 75 80
 Pro Gly Met Pro Ala Ala Pro Tyr Pro Met Gln Tyr Pro Pro Pro Tyr
 85 90 95
 Pro Ala Gln Pro Met Gly Pro Pro Ala Tyr His Glu Thr Leu Ala Gly

```

100      105      110
Glu Cys Pro Cys Gln Leu
115

<210> 32
<211> 1908
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (91)..(444)

<400> 32
gggggaggaa attgaaactg agtggccac gatgggaaga ggggaaagcc caggggtaca 60

ggaggcctct ggggtgaaggc agaggctaac atg ggg ttc gga gcg acc ttg gcc 114
Met Gly Phe Gly Ala Thr Leu Ala
1 5

gtt ggc ctg acc atc ttt gtg ctg tct gtc gtc act atc atc atc tgc 162
Val Gly Leu Thr Ile Phe Val Leu Ser Val Val Thr Ile Ile Ile Cys
10 15 20

ttc acc tgc tcc tgc tgc tgc ctt tac aag acg tgc cgc cga cca cgt 210
Phe Thr Cys Ser Cys Cys Cys Leu Tyr Lys Thr Cys Arg Arg Pro Arg
25 30 35 40

ccg gtt gtc acc acc acc aca tcc acc act gtg gtg cat gcc cct tat 258
Pro Val Val Thr Thr Thr Thr Ser Thr Thr Val Val His Ala Pro Tyr
45 50 55

cct cag cct cca agt gtg ccg ccc agc tac cct gga cca agc tac cag 306
Pro Gln Pro Pro Ser Val Pro Pro Ser Tyr Pro Gly Pro Ser Tyr Gln
60 65 70

ggc tac cac acc atg ccg cct cag cca ggg atg cca gca gca ccc tac 354
Gly Tyr His Thr Met Pro Pro Gln Pro Gly Met Pro Ala Ala Pro Tyr
75 80 85

cca atg cag tac cca cca cct tac cca gcc cag ccc atg ggc cca ccg 402
Pro Met Gln Tyr Pro Pro Pro Tyr Pro Ala Gln Pro Met Gly Pro Pro
90 95 100

gcc tac cac gag acc ctg gct ggt gag tgc ccc tgc caa ctc 444
Ala Tyr His Glu Thr Leu Ala Gly Glu Cys Pro Cys Gln Leu
105 110 115

tagccctgcc cgacttcccg agtctctgcc agcatccctc gggcacccat cccaaactac 504

atcactcaac aggctctctgc ccctttctgc ttgcctgcc ctcacacggc agcccaccat 564

gctcacagcc aaccagggtc ctctctgctt tcaggaggag cagccgcgcc ctaccccgcc 624

agccagcctc cttacaaccc ggcctacatg gatgccccga aggcggccct ctgagcattc 684

```

cctggcctct ctggctgcca cttgggttatg ttgtgtgtgt gcgtgagtgg tgtgcaggcg 744
cggttcctta cgcccatgt gtgctgtgtg tgtccaggca cggttcctta cgcccatgt 804
gtgctgtgtg tgtcctgcct gtatatgtgg ctctctctga tgcctgacaag gtggggaaca 864
atccttgcca gagggtggctg ggaccagact ttgttctctt cctcacctga aattatgctt 924
cctaaaatct caagccaaac tcaaagaatg ggggtggtggg gggcaccctg tgaggtggcc 984
cctgagaggt gggggcctct ccagggcaca tctggagttc ttctccagct taccctaggg 1044
tgaccaagta gggcctgtca caccagggtg gcgcagcttt ctgtgtgatg cagatgtgtc 1104
ctgggttctgg cagcgtagcc agctgctgct tgaggccatg gctcgtcccc ggagttgggg 1164
gtaccogttg cagagccagg gacatgatgc aggcgaagct tgggatctgg ccaagttgga 1224
ctttgatcct ttgggcagat gtcccattgc tccctggagc ctgtcatgcc tgttggggat 1284
caggcagcct cctgatgcca gaacacctca ggcagagccc tactcagctg tacctgtctg 1344
cctggactgt cccctgtccc cgcctctccc ctgggaccag ctggagggcc acatgcacac 1404
acagcctagc tgccccaggg gagctctgct gcccttgctg gccctgccct tcccacaggt 1464
gagcagggtt cctgtccacc agcacactca gttctcttcc ctgcagtgtt ttcattttat 1524
tttagccaaa cattttgcct gttttctgtt tcaaacatga tagttgatat gagactgaaa 1584
cccctgggtt gtggagggaa attggctcag agatggacaa cctggcaact gtgagtcctt 1644
gcttcccgac accagcctca tggaatatgc aacaactcct gtaccccagt ccacggtgtt 1704
ctggcagcag ggacacctgg gccaatgggc catctggacc aaagggtgggg tgtggggccc 1764
tggatggcag ctctggccca gacatgaata cctcgtgttc ctccctccctc tattactgtt 1824
tcaccagagc tgtcttagct caaatctgtt gtgtttctga gtctagggtc tgtacacttg 1884
tttataataa atgcaatcgt ttgg 1908

<210> 33

<211> 168

<212> PRT

<213> Homo sapiens

<400> 33

Met	Asn	Ser	Lys	Gly	Gln	Tyr	Pro	Thr	Gln	Pro	Thr	Tyr	Pro	Val	Gln
1				5					10					15	

Pro	Pro	Gly	Asn	Pro	Val	Tyr	Pro	Gln	Thr	Leu	His	Leu	Pro	Gln	Ala
			20					25					30		

Pro	Pro	Tyr	Thr	Asp	Ala	Pro	Pro	Ala	Tyr	Ser	Glu	Leu	Tyr	Arg	Pro
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35 40 45

Ser Phe Val His Pro Gly Ala Ala Thr Val Pro Thr Met Ser Ala Ala
50 55 60

Phe Pro Gly Ala Ser Leu Tyr Leu Pro Met Ala Gln Ser Val Ala Val
65 70 75 80

Gly Pro Leu Gly Ser Thr Ile Pro Met Ala Tyr Tyr Pro Val Gly Pro
85 90 95

Ile Tyr Pro Pro Gly Ser Thr Val Leu Val Glu Gly Gly Tyr Asp Ala
100 105 110

Gly Ala Arg Phe Gly Ala Gly Ala Thr Ala Gly Asn Ile Pro Pro Pro
115 120 125

Pro Pro Gly Cys Pro Pro Asn Ala Ala Gln Leu Ala Val Met Gln Gly
130 135 140

Ala Asn Val Leu Val Thr Gln Arg Lys Gly Asn Phe Phe Met Gly Gly
145 150 155 160

Ser Asp Gly Gly Tyr Thr Ile Trp
165

<210> 34
<211> 1897
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (70)..(573)

<400> 34
ctccgaacag gaagaggacg aaaaaaataa ccgtccgcga cgccgagaca aaccggaccc 60

gcaaccacc atg aac agc aaa ggt caa tat cca aca cag cca acc tac cct 111
Met Asn Ser Lys Gly Gln Tyr Pro Thr Gln Pro Thr Tyr Pro
1 5 10

gtg cag cct cct ggg aat cca gta tac cct cag acc ttg cat ctt cct 159
Val Gln Pro Pro Gly Asn Pro Val Tyr Pro Gln Thr Leu His Leu Pro
15 20 25 30

cag gct cca ccc tat acc gat gct cca cct gcc tac tca gag ctc tat 207
Gln Ala Pro Pro Tyr Thr Asp Ala Pro Pro Ala Tyr Ser Glu Leu Tyr
35 40 45

cgt ccg agc ttt gtg cac cca ggg gct gcc aca gtc ccc acc atg tca 255
Arg Pro Ser Phe Val His Pro Gly Ala Ala Thr Val Pro Thr Met Ser
50 55 60

gcc gca ttt cct gga gcc tct ctg tat ctt ccc atg gcc cag tct gtg 303
Ala Ala Phe Pro Gly Ala Ser Leu Tyr Leu Pro Met Ala Gln Ser Val

65 70 75
 gct gtt ggg cct tta ggt tcc aca atc ccc atg gct tat tat cca gtc 351
 Ala Val Gly Pro Leu Gly Ser Thr Ile Pro Met Ala Tyr Tyr Pro Val
 80 85 90
 ggt ccc atc tat cca cct ggc tcc aca gtg ctg gtg gaa gga ggg tat 399
 Gly Pro Ile Tyr Pro Pro Gly Ser Thr Val Leu Val Glu Gly Gly Tyr
 95 100 105 110
 gat gca ggt gcc aga ttt gga gct ggg gct act gct ggc aac att cct 447
 Asp Ala Gly Ala Arg Phe Gly Ala Gly Ala Thr Ala Gly Asn Ile Pro
 115 120 125
 cct cca cct cct gga tgc cct ccc aat gct gct cag ctt gca gtc atg 495
 Pro Pro Pro Pro Gly Cys Pro Pro Asn Ala Ala Gln Leu Ala Val Met
 130 135 140
 cag gga gcc aac gtc ctc gta act cag cgg aag ggg aac ttc ttc atg 543
 Gln Gly Ala Asn Val Leu Val Thr Gln Arg Lys Gly Asn Phe Phe Met
 145 150 155
 ggt ggt tca gat ggt ggc tac acc atc tgg tgaggaacca aggccacctc 593
 Gly Gly Ser Asp Gly Gly Tyr Thr Ile Trp
 160 165
 tgtgcgggga aagacatcac ataccttcag cacttctcac aatgtaactg ctttagtcat 653
 attaacctga agttgcagtt tagacacatg ttgttgggggt gtctttctgg tgcccaaact 713
 ttcaggcact ttctaaatct aataaggaac catgtaatgg tagcagtacc tccctaaagc 773
 attttgaggt aggggaggta tccattcata aatgaatgt ggggtgaagcc gccctaagga 833
 ttttccttta atttctctgg agtaatactg taccatactg gtctttgctt ttagtaataa 893
 aacatcaaat taggtttgga gggaactttg atcttcttaa gaattaaagt tgccaaatta 953
 ttctgattgg tctttaatct cctttaagtc tttgatatat attacttggt ataaatggaa 1013
 cgcattagtt gtctgccttt tcttttccat cctttgcccc acccatccca tctccaaccc 1073
 tagtcttcca tttcctcccg ccagtctcca ttgaatcaat ggtgcaggac agaaagccag 1133
 tcagactaat ttccttcttt cctcgcaactt ctccccactc gtcacttttt aactagtgtt 1193
 tcacaaggat cctctgaaac cctctctgtg ccccaagtac agatgccatt acttctgctt 1253
 tcgtatctcc tcaggcaaaa gtggaggggtg ccttatgggc cctcctcata gggtgtctct 1313
 gcatacacga acctaacca aatttgcttt ggtgccagaa aaactgagct atgtttgaac 1373
 aaagatgtcg tgcaaactgt actgtgaaca acagttgggt taaaatatga ggggcaagga 1433
 ggaggatgca ttctaaaagc ttgattgatg tgttcagagc taaattaaga ggagttttca 1493
 gatcaaaaac tggttacat tttttgtcag agtgtctgat gcggccactc attcggtctc 1553

ccagaattcc tagactgggt taataggggtc atattgtgaa tgtctcacta caaaatgact 1613
 tgagtccagt gaaatctcat tagggtttaa gaatatttca gggatcctta atgttttgat 1673
 ttttgttttc tgaaattgga ttttatttta ttttatctta taatttcagt tcatctaaat 1733
 tgtgtgttct gtacatgtga tgtttgactg taccattgac tgttatggaa gttcagcgtt 1793
 gtatgtctct ctctacactg tggtgcactt aacttgaggga atttttatac taaaaatgta 1853
 gaataaagac tattttgaag atttgaataa agtgatgaag ttgc 1897

<210> 35
 <211> 455
 <212> PRT
 <213> Homo sapiens

<400> 35
 Met Ser Phe Leu Ile Asp Ser Ser Ile Met Ile Thr Ser Gln Ile Leu
 1 5 10 15
 Phe Phe Gly Phe Gly Trp Leu Phe Phe Met Arg Gln Leu Phe Lys Asp
 20 25 30
 Tyr Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser Val Thr Phe
 35 40 45
 Ala Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe Glu Ile Leu Gly
 50 55 60
 Val Leu Asn Ser Ser Ser Arg Tyr Phe His Trp Lys Met Asn Leu Cys
 65 70 75 80
 Val Ile Leu Leu Ile Leu Val Phe Met Val Pro Phe Tyr Ile Gly Tyr
 85 90 95
 Phe Ile Val Ser Asn Ile Arg Leu Leu His Lys Gln Arg Leu Leu Phe
 100 105 110
 Ser Cys Leu Leu Trp Leu Thr Phe Met Tyr Phe Phe Trp Lys Leu Gly
 115 120 125
 Asp Pro Phe Pro Ile Leu Ser Pro Lys His Gly Ile Leu Ser Ile Glu
 130 135 140
 Gln Leu Ile Ser Arg Val Gly Val Ile Gly Val Thr Leu Met Ala Leu
 145 150 155 160
 Leu Ser Gly Phe Gly Ala Val Asn Cys Pro Tyr Thr Tyr Met Ser Tyr
 165 170 175
 Phe Leu Arg Asn Val Thr Asp Thr Asp Ile Leu Ala Leu Glu Arg Arg
 180 185 190
 Leu Leu Gln Thr Met Asp Met Ile Ile Ser Lys Lys Lys Arg Met Ala

- - - 195 - - - - 200 - - - - 205 - - - -
 Met Ala Arg Arg Thr Met Phe Gln Lys Gly Glu Val His Asn Lys Pro
 210 215 220
 Ser Gly Phe Trp Gly Met Ile Lys Ser Val Thr Thr Ser Ala Ser Gly
 225 230 235 240
 Ser Glu Asn Leu Thr Leu Ile Gln Gln Glu Val Asp Ala Leu Glu Glu
 245 250 255
 Leu Ser Arg Gln Leu Phe Leu Glu Thr Ala Asp Leu Tyr Ala Thr Lys
 260 265 270
 Glu Arg Ile Glu Tyr Ser Lys Thr Phe Lys Gly Lys Tyr Phe Asn Phe
 275 280 285
 Leu Gly Tyr Phe Phe Ser Ile Tyr Cys Val Trp Lys Ile Phe Met Ala
 290 295 300
 Thr Ile Asn Ile Val Phe Asp Arg Val Gly Lys Thr Asp Pro Val Thr
 305 310 315 320
 Arg Gly Ile Glu Ile Thr Val Asn Tyr Leu Gly Ile Gln Phe Asp Val
 325 330 335
 Lys Phe Trp Ser Gln His Ile Ser Phe Ile Leu Val Gly Ile Ile Ile
 340 345 350
 Val Thr Ser Ile Arg Gly Leu Leu Ile Thr Leu Thr Lys Phe Phe Tyr
 355 360 365
 Ala Ile Ser Ser Ser Lys Ser Ser Asn Val Ile Val Leu Leu Leu Ala
 370 375 380
 Gln Ile Met Gly Met Tyr Phe Val Ser Ser Val Leu Leu Ile Arg Met
 385 390 395 400
 Ser Met Pro Leu Glu Tyr Arg Thr Ile Ile Thr Glu Val Leu Gly Glu
 405 410 415
 Leu Gln Phe Asn Phe Tyr His Arg Trp Phe Asp Val Ile Phe Leu Val
 420 425 430
 Ser Ala Leu Ser Ser Ile Leu Phe Leu Tyr Leu Ala His Lys Gln Ala
 435 440 445
 Pro Glu Lys Gln Met Ala Pro
 450 455

<210> 36
 <211> 1903
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
 <222> (116)..(1480)

<400> 36

agtccccggct gcagcacctg ggagaaggca gaccgtgtga gggggcctgt ggccccagcg 60

tgctgtggcc tcggggagtg ggaagtggag gcaggagcct tccttacact tcgcc atg 118
 Met
 1

agt ttc ctc atc gac tcc agc atc atg att acc tcc cag ata cta ttt 166
 Ser Phe Leu Ile Asp Ser Ser Ile Met Ile Thr Ser Gln Ile Leu Phe
 5 10 15

ttt gga ttt ggg tgg ctt ttc ttc atg cgc caa ttg ttt aaa gac tat 214
 Phe Gly Phe Gly Trp Leu Phe Phe Met Arg Gln Leu Phe Lys Asp Tyr
 20 25 30

gag ata cgt cag tat gtt gta cag gtg atc ttc tcc gtg acg ttt gca 262
 Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser Val Thr Phe Ala
 35 40 45

ttt tct tgc acc atg ttt gag ctc atc atc ttt gaa atc tta gga gta 310
 Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe Glu Ile Leu Gly Val
 50 55 60 65

ttg aat agc agc tcc cgt tat ttt cac tgg aaa atg aac ctg tgt gta 358
 Leu Asn Ser Ser Ser Arg Tyr Phe His Trp Lys Met Asn Leu Cys Val
 70 75 80

att ctg ctg atc ctg gtt ttc atg gtg cct ttt tac att ggc tat ttt 406
 Ile Leu Leu Ile Leu Val Phe Met Val Pro Phe Tyr Ile Gly Tyr Phe
 85 90 95

att gtg agc aat atc cga cta ctg cat aaa caa cga ctg ctt ttt tcc 454
 Ile Val Ser Asn Ile Arg Leu Leu His Lys Gln Arg Leu Leu Phe Ser
 100 105 110

tgt ctc tta tgg ctg acc ttt atg tat ttc ttc tgg aaa cta gga gat 502
 Cys Leu Leu Trp Leu Thr Phe Met Tyr Phe Phe Trp Lys Leu Gly Asp
 115 120 125

ccc ttt ccc att ctc agc cca aaa cat ggg atc tta tcc ata gaa cag 550
 Pro Phe Pro Ile Leu Ser Pro Lys His Gly Ile Leu Ser Ile Glu Gln
 130 135 140 145

ctc atc agc cgg gtt ggt gtg att gga gtg act ctc atg gct ctt ctt 598
 Leu Ile Ser Arg Val Gly Val Ile Gly Val Thr Leu Met Ala Leu Leu
 150 155 160

tct gga ttt ggt gct gtc aac tgc cca tac act tac atg tct tac ttc 646
 Ser Gly Phe Gly Ala Val Asn Cys Pro Tyr Thr Tyr Met Ser Tyr Phe
 165 170 175

ctc agg aat gtg act gac acg gat att cta gcc ctg gaa cgg cga ctg 694
 Leu Arg Asn Val Thr Asp Thr Asp Ile Leu Ala Leu Glu Arg Arg Leu
 180 185 190

ctg	caa	acc	atg	gat	atg	atc	ata	agc	aaa	aag	aaa	agg	atg	gca	atg	742
Leu	Gln	Thr	Met	Asp	Met	Ile	Ile	Ser	Lys	Lys	Lys	Arg	Met	Ala	Met	
	195					200					205					
gca	cgg	aga	aca	atg	ttc	cag	aag	ggg	gaa	gtg	cat	aac	aaa	cca	tca	790
Ala	Arg	Arg	Thr	Met	Phe	Gln	Lys	Gly	Glu	Val	His	Asn	Lys	Pro	Ser	
210					215					220				225		
ggg	ttc	tgg	gga	atg	ata	aaa	agt	gtt	acc	act	tca	gca	tca	gga	agt	838
Gly	Phe	Trp	Gly	Met	Ile	Lys	Ser	Val	Thr	Thr	Ser	Ala	Ser	Gly	Ser	
				230					235					240		
gaa	aat	ctt	act	ctt	att	caa	cag	gaa	gtg	gat	gct	ttg	gaa	gaa	tta	886
Glu	Asn	Leu	Thr	Leu	Ile	Gln	Gln	Glu	Val	Asp	Ala	Leu	Glu	Glu	Leu	
			245					250					255			
agc	agg	cag	ctt	ttt	ctg	gaa	aca	gct	gat	cta	tat	gct	acc	aag	gag	934
Ser	Arg	Gln	Leu	Phe	Leu	Glu	Thr	Ala	Asp	Leu	Tyr	Ala	Thr	Lys	Glu	
		260					265					270				
aga	ata	gaa	tac	tcc	aaa	acc	ttc	aag	ggg	aaa	tat	ttt	aat	ttt	ctt	982
Arg	Ile	Glu	Tyr	Ser	Lys	Thr	Phe	Lys	Gly	Lys	Tyr	Phe	Asn	Phe	Leu	
	275					280					285					
ggg	tac	ttt	ttc	tct	att	tac	tgt	gtt	tgg	aaa	att	ttc	atg	gct	acc	1030
Gly	Tyr	Phe	Phe	Ser	Ile	Tyr	Cys	Val	Trp	Lys	Ile	Phe	Met	Ala	Thr	
290					295					300					305	
atc	aat	att	gtt	ttt	gat	cga	gtt	ggg	aaa	acg	gat	cct	gtc	aca	aga	1078
Ile	Asn	Ile	Val	Phe	Asp	Arg	Val	Gly	Lys	Thr	Asp	Pro	Val	Thr	Arg	
				310					315					320		
ggc	att	gag	atc	act	gtg	aat	tat	ctg	gga	atc	caa	ttt	gat	gtg	aag	1126
Gly	Ile	Glu	Ile	Thr	Val	Asn	Tyr	Leu	Gly	Ile	Gln	Phe	Asp	Val	Lys	
			325					330					335			
ttt	tgg	tcc	caa	cac	att	tcc	ttc	att	ctt	gtt	gga	ata	atc	atc	gtc	1174
Phe	Trp	Ser	Gln	His	Ile	Ser	Phe	Ile	Leu	Val	Gly	Ile	Ile	Ile	Val	
		340					345					350				
aca	tcc	atc	aga	gga	ttg	ctg	atc	act	ctt	acc	aag	ttc	ttt	tat	gcc	1222
Thr	Ser	Ile	Arg	Gly	Leu	Leu	Ile	Thr	Leu	Thr	Lys	Phe	Phe	Tyr	Ala	
	355					360					365					
atc	tct	agc	agt	aag	tcc	tcc	aat	gtc	att	gtc	ctg	cta	tta	gca	cag	1270
Ile	Ser	Ser	Ser	Lys	Ser	Ser	Asn	Val	Ile	Val	Leu	Leu	Leu	Ala	Gln	
370					375					380					385	
ata	atg	ggc	atg	tac	ttt	gtc	tcc	tct	gtg	ctg	ctg	atc	cga	atg	agt	1318
Ile	Met	Gly	Met	Tyr	Phe	Val	Ser	Ser	Val	Leu	Leu	Ile	Arg	Met	Ser	
				390					395					400		
atg	cct	tta	gaa	tac	cgc	acc	ata	atc	act	gaa	gtc	ctt	gga	gaa	ctg	1366
Met	Pro	Leu	Glu	Tyr	Arg	Thr	Ile	Ile	Thr	Glu	Val	Leu	Gly	Glu	Leu	
			405					410					415			

cag ttc aac ttc tat cac cgt tgg ttt gat gtg atc ttc ctg gtc agc 1414
 Gln Phe Asn Phe Tyr His Arg Trp Phe Asp Val Ile Phe Leu Val Ser
 420 425 430

gct ctc tct agc ata ctc ttc ctc tat ttg gct cac aaa cag gca cca 1462
 Ala Leu Ser Ser Ile Leu Phe Leu Tyr Leu Ala His Lys Gln Ala Pro
 435 440 445

gag aag caa atg gca cct tgaacttaag cctactacag actgttagag 1510
 Glu Lys Gln Met Ala Pro
 450 455

gccagtgggtt tcaaaatttta gatataagag ggggggaaaaa tggaaccagg gcctgacatt 1570

ttataaaciaa acaaaatgct atggttagcat ttttcacctt catagcatac tccttccccg 1630

tcaggtgata ctatgaccat gagtagcatc agccagaaca tgagagggag aactaactca 1690

agacaatact cagcagagag catcccggtgt ggatatgagg ctggtgtaga ggcggagagg 1750

agccaagaaa ctaaagggtga aaaatacact ggaactctgg ggcaagacat gtctatggta 1810

gctgagccaa acacgtagga tttccgtttt aagggttcaca tggaaaagggt tatagctttg 1870

ccttgagatt gactcattaa aatcagagac tgt 1903

<210> 37

<211> 322

<212> PRT

<213> Homo sapiens

<400> 37

Met Ser Ser Leu Gly Gly Gly Ser Gln Asp Ala Gly Gly Ser Ser Ser
 1 5 10 15

Ser Ser Thr Asn Gly Ser Gly Gly Ser Gly Ser Ser Gly Pro Lys Ala
 20 25 30

Gly Ala Ala Asp Lys Ser Ala Val Val Ala Ala Ala Ala Pro Ala Ser
 35 40 45

Val Ala Asp Asp Thr Pro Pro Pro Glu Arg Arg Asn Lys Ser Gly Ile
 50 55 60

Ile Ser Glu Pro Leu Asn Lys Ser Leu Arg Arg Ser Arg Pro Leu Ser
 65 70 75 80

His Tyr Ser Ser Phe Gly Ser Ser Gly Gly Ser Gly Gly Gly Ser Met
 85 90 95

Met Gly Gly Glu Ser Ala Asp Lys Ala Thr Ala Ala Ala Ala Ala Ala
 100 105 110

Ser Leu Leu Ala Asn Gly His Asp Leu Ala Ala Ala Met Ala Val Asp
 115 120 125

Lys	Ser	Asn	Pro	Thr	Ser	Lys	His	Lys	Ser	Gly	Ala	Val	Ala	Ser	Leu
130						135					140				
Leu	Ser	Lys	Ala	Glu	Arg	Ala	Thr	Glu	Leu	Ala	Ala	Glu	Gly	Gln	Leu
145					150					155					160
Thr	Leu	Gln	Gln	Phe	Ala	Gln	Ser	Thr	Glu	Met	Leu	Lys	Arg	Val	Val
				165					170					175	
Gln	Glu	His	Leu	Pro	Leu	Met	Ser	Glu	Ala	Gly	Ala	Gly	Leu	Pro	Asp
			180					185					190		
Met	Glu	Ala	Val	Ala	Gly	Ala	Glu	Ala	Leu	Asn	Gly	Gln	Ser	Asp	Phe
	195						200					205			
Pro	Tyr	Leu	Gly	Ala	Phe	Pro	Ile	Asn	Pro	Gly	Leu	Phe	Ile	Met	Thr
	210						215					220			
Pro	Ala	Gly	Val	Phe	Leu	Ala	Glu	Ser	Ala	Leu	His	Met	Ala	Gly	Leu
225					230					235					240
Ala	Glu	Tyr	Pro	Met	Gln	Gly	Glu	Leu	Ala	Ser	Ala	Ile	Ser	Ser	Gly
				245					250					255	
Lys	Lys	Lys	Arg	Lys	Arg	Cys	Gly	Met	Cys	Ala	Pro	Cys	Arg	Arg	Arg
			260					265					270		
Ile	Asn	Cys	Glu	Gln	Cys	Ser	Ser	Cys	Arg	Asn	Arg	Lys	Thr	Gly	His
	275						280					285			
Gln	Ile	Cys	Lys	Phe	Arg	Lys	Cys	Glu	Glu	Leu	Lys	Lys	Lys	Pro	Ser
	290					295					300				
Ala	Ala	Leu	Glu	Lys	Val	Met	Leu	Pro	Thr	Gly	Ala	Ala	Phe	Arg	Trp
305					310					315					320

Phe Gln

<210> 38
 <211> 1448
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (292)..(1257)

<400> 38
 tactgtctggc ggctggagcg gagcgcaccg cggcgggtggt gccagagcg gagcgcagct 60
 ccctgccccg cccctcccc tggcctcgc gggaacggcg gcggtggcgg cttggacgac 120
 tcggagagcc gagtgaagac atttccacct ggacacctga ccatgtgcct gccctgagca 180


```

--gcgaggecca ccaggcatct-ctgttgtggg cagcagggcc aggtcctggt ctgtggaccc 240
tcggcagttg gcaggctccc tctgcagtgg ggtctggggc tcggccccac c atg tcg 297
Met Ser
1
agc ctc ggc ggt ggc tcc cag gat gcc ggc ggc agt agc agc agc agc 345
Ser Leu Gly Gly Gly Ser Gln Asp Ala Gly Gly Ser Ser Ser Ser Ser
5 10 15
acc aat ggc agc ggt ggc agt ggc agc agt ggc cca aag gca gga gca 393
Thr Asn Gly Ser Gly Gly Ser Gly Ser Ser Gly Pro Lys Ala Gly Ala
20 25 30
gca gac aag agt gca gtg gtg gct gcc gcc gca cca gcc tca gtg gca 441
Ala Asp Lys Ser Ala Val Val Ala Ala Ala Ala Pro Ala Ser Val Ala
35 40 45 50
gat gac aca cca ccc ccc gag cgt cgg aac aag agc ggt atc atc agt 489
Asp Asp Thr Pro Pro Pro Glu Arg Arg Asn Lys Ser Gly Ile Ile Ser
55 60 65
gag ccc ctc aac aag agc ctg cgc cgc tcc cgc ccg ctc tcc cac tac 537
Glu Pro Leu Asn Lys Ser Leu Arg Arg Ser Arg Pro Leu Ser His Tyr
70 75 80
tct tct ttt ggc agc agt ggt ggt agt ggc ggt ggc agc atg atg ggc 585
Ser Ser Phe Gly Ser Ser Gly Gly Ser Gly Gly Gly Ser Met Met Gly
85 90 95
gga gag tct gct gac aag gcc act gcg gct gca gcc gct gcc tcc ctg 633
Gly Glu Ser Ala Asp Lys Ala Thr Ala Ala Ala Ala Ala Ala Ser Leu
100 105 110
ttg gcc aat ggg cat gac ctg gcg gcg gcc atg gcg gtg gac aaa agc 681
Leu Ala Asn Gly His Asp Leu Ala Ala Ala Met Ala Val Asp Lys Ser
115 120 125 130
aac cct acc tca aag cac aaa agt ggt gct gtg gcc agc ctg ctg agc 729
Asn Pro Thr Ser Lys His Lys Ser Gly Ala Val Ala Ser Leu Leu Ser
135 140 145
aag gca gag cgg gcc acg gag ctg gca gcc gag gga cag ctg acg ctg 777
Lys Ala Glu Arg Ala Thr Glu Leu Ala Ala Glu Gly Gln Leu Thr Leu
150 155 160
cag cag ttt gcg cag tcc aca gag atg ctg aag cgc gtg gtg cag gag 825
Gln Gln Phe Ala Gln Ser Thr Glu Met Leu Lys Arg Val Val Gln Glu
165 170 175
cat ctc ccg ctg atg agc gag gcg ggt gct ggc ctg cct gac atg gag 873
His Leu Pro Leu Met Ser Glu Ala Gly Ala Gly Leu Pro Asp Met Glu
180 185 190
gct gtg gca ggt gcc gaa gcc ctc aat ggc cag tcc gac ttc ccc tac 921
Ala Val Ala Gly Ala Glu Ala Leu Asn Gly Gln Ser Asp Phe Pro Tyr
195 200 205 210

```

ctg ggc gct ttc ccc atc aac cca ggc ctc ttc att atg acc ccg gca 969
 Leu Gly Ala Phe Pro Ile Asn Pro Gly Leu Phe Ile Met Thr Pro Ala
 215 220 225
 ggt gtg ttc ctg gcc gag agc gcg ctg cac atg gcg ggc ctg gct gag 1017
 Gly Val Phe Leu Ala Glu Ser Ala Leu His Met Ala Gly Leu Ala Glu
 230 235 240
 tac ccc atg cag gga gag ctg gcc tct gcc atc agc tcc ggc aag aag 1065
 Tyr Pro Met Gln Gly Glu Leu Ala Ser Ala Ile Ser Ser Gly Lys Lys
 245 250 255
 aag cgg aaa cgc tgc ggc atg tgc gcg ccc tgc cgg cgg cgc atc aac 1113
 Lys Arg Lys Arg Cys Gly Met Cys Ala Pro Cys Arg Arg Arg Ile Asn
 260 265 270
 tgc gag cag tgc agc agt tgt agg aat cga aag act ggc cat cag att 1161
 Cys Glu Gln Cys Ser Ser Cys Arg Asn Arg Lys Thr Gly His Gln Ile
 275 280 285 290
 tgc aaa ttc aga aaa tgt gag gaa ctc aaa aag aag cct tcc gct gct 1209
 Cys Lys Phe Arg Lys Cys Glu Glu Leu Lys Lys Lys Pro Ser Ala Ala
 295 300 305
 ctg gag aag gtg atg ctt ccg acg gga gcc gcc ttc cgg tgg ttt cag 1257
 Leu Glu Lys Val Met Leu Pro Thr Gly Ala Ala Phe Arg Trp Phe Gln
 310 315 320
 tgacggcggc ggaacccaaa gctgccctct ccgtgcaatg tcaactgctcg tgtgggtctcc 1317
 agcaagggat tcgggcgaag acaaacggat gcacccgtct ttagaaccaa aaatattctc 1377
 tcacagattt cattcctggt tttatatata ttttttttgt tgtcgtttta acatctccac 1437
 gtccctagca t 1448

<210> 39
 <211> 313
 <212> PRT
 <213> Homo sapiens

<400> 39
 Met Ala Gly Gln Pro Gly His Met Pro His Gly Gly Ser Ser Asn Asn
 1 5 10 15
 Leu Cys His Thr Leu Gly Pro Val His Pro Pro Asp Pro Gln Arg His
 20 25 30
 Pro Asn Thr Leu Ser Phe Arg Cys Ser Leu Ala Asp Phe Gln Ile Glu
 35 40 45
 Lys Lys Ile Gly Arg Gly Gln Phe Ser Glu Val Tyr Lys Ala Thr Cys
 50 55 60
 Leu Leu Asp Arg Lys Thr Val Ala Leu Lys Lys Val Gln Ile Phe Glu


```

<400> 40
ggcggaaccg agctgacggg cgtgcggccg ctgcgccgca aactcgtgtg ggacgcaccg 60

ctccagccgc ccgcggggcca gcgcaccggt cccccagcgg cagccgagcc cgcccgcgcg 120

ccgttcgtgc cctcgtgagg ctggcatgca gg atg gca gga cag ccc ggc cac 173
                               Met Ala Gly Gln Pro Gly His
                               1                               5

atg ccc cat gga ggg agt tcc aac aac ctc tgc cac acc ctg ggg cct 221
Met Pro His Gly Gly Ser Ser Asn Asn Leu Cys His Thr Leu Gly Pro
      10                               15                               20

gtg cat cct cct gac cca cag agg cat ccc aac acg ctg tct ttt cgc 269
Val His Pro Pro Asp Pro Gln Arg His Pro Asn Thr Leu Ser Phe Arg
      25                               30                               35

tgc tcg ctg gcg gac ttc cag atc gaa aag aag ata ggc cga gga cag 317
Cys Ser Leu Ala Asp Phe Gln Ile Glu Lys Lys Ile Gly Arg Gly Gln
      40                               45                               50                               55

ttc agc gag gtg tac aag gcc acc tgc ctg ctg gac agg aag aca gtg 365
Phe Ser Glu Val Tyr Lys Ala Thr Cys Leu Leu Asp Arg Lys Thr Val
      60                               65                               70

gct ctg aag aag gtg cag atc ttt gag atg atg gac gcc aag gcg agg 413
Ala Leu Lys Lys Val Gln Ile Phe Glu Met Met Asp Ala Lys Ala Arg
      75                               80                               85

cag gac tgt gtc aag gag atc ggc ctc ttg aag caa ctg aac cac cca 461
Gln Asp Cys Val Lys Glu Ile Gly Leu Leu Lys Gln Leu Asn His Pro
      90                               95                               100

aat atc atc aag tat ttg gac tcg ttt atc gaa gac aac gag ctg aac 509
Asn Ile Ile Lys Tyr Leu Asp Ser Phe Ile Glu Asp Asn Glu Leu Asn
      105                               110                               115

att gtg ctg gag ttg gct gac gca ggg gac ctc tcg cag atg atc aag 557
Ile Val Leu Glu Leu Ala Asp Ala Gly Asp Leu Ser Gln Met Ile Lys
      120                               125                               130                               135

tac ttt aag aag cag aag cgg ctc atc ccg gag agg aca gta tgg aag 605
Tyr Phe Lys Lys Gln Lys Arg Leu Ile Pro Glu Arg Thr Val Trp Lys
      140                               145                               150

tac ttt gtg cag ctg tgc agc gcc gtg gag cac atg cat tca cgc cgg 653
Tyr Phe Val Gln Leu Cys Ser Ala Val Glu His Met His Ser Arg Arg
      155                               160                               165

gtg atg cac cga gac atc aag cct gcc aac gtg ttc atc aca gcc acg 701
Val Met His Arg Asp Ile Lys Pro Ala Asn Val Phe Ile Thr Ala Thr
      170                               175                               180

ggc gtc gtg aag ctc ggt gac ctt ggt ctg ggc cgc ttc ttc agc tct 749
Gly Val Val Lys Leu Gly Asp Leu Gly Leu Gly Arg Phe Phe Ser Ser
      185                               190                               195

```

```

gag acc acc gca gcc cac tcc cta gtg ggg acg ccc tac tac atg tca 797
Glu Thr Thr Ala Ala His Ser Leu Val Gly Thr Pro Tyr Tyr Met Ser
200 205 210 215

ccg gag agg atc cat gag aac ggc tac aac ttc aag tcc gac atc tgg 845
Pro Glu Arg Ile His Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp
220 225 230

tcc ttg ggc tgt ctg ctg tac gag atg gca gcc ctc cag agc ccc ttc 893
Ser Leu Gly Cys Leu Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe
235 240 245

tat gga gat aag atg aat ctc ttc tcc ctg tgc cag aag atc gag cag 941
Tyr Gly Asp Lys Met Asn Leu Phe Ser Leu Cys Gln Lys Ile Glu Gln
250 255 260

tgt gac tac ccc cca ctc ccc ggg gag cac tac tcc gag aag tta cga 989
Cys Asp Tyr Pro Pro Leu Pro Gly Glu His Tyr Ser Glu Lys Leu Arg
265 270 275

gaa ctg gtc agc atg tgc atc tgc cct gac ccc cac cag aga cct gac 1037
Glu Leu Val Ser Met Cys Ile Cys Pro Asp Pro His Gln Arg Pro Asp
280 285 290 295

atc gga tac gtg cac cag gtg gcc aag cag atg cac atc tgg atg tcc 1085
Ile Gly Tyr Val His Gln Val Ala Lys Gln Met His Ile Trp Met Ser
300 305 310

agc acc tgagcgtgga tgcaccgtgc cttatcaaag ccagcaccac tttgccttac 1141
Ser Thr

ttgagtcgtc ttctcttcga gtggccacct ggtagcctag aacagctaag accacagggt 1201

tcagcagggt ccccaaaagg ctgcccagcc ttacagcaga tgctgaaggc agagcagctg 1261

agggaggggc gctggccaca tgtcactgat ggtcagattc caaagtcctt tctttatact 1321

gttggtggaca atctcagctg ggtcaataag ggcaggtggt tcagcgagcc acggcagccc 1381

cctgtatctg gattgtaatg tgaatcttta gggtaatcc tccagtgacc tgtcaaggct 1441

tatgctaaca ggagacttgc aggagaccgt gtgatttggt tagtgagcct ttgaaaatgg 1501

ttagtaccgg gttcagttta gttcttggt tcttttcaat caagctgtgt gcttaattta 1561

ctctgttgta aagggataaa gtggaaatca tttttt 1597

```

```

<210> 41
<211> 371
<212> PRT
<213> Homo sapiens

```

```

<400> 41
Met Ser His Glu Lys Ser Phe Leu Val Ser Gly Asp Asn Tyr Pro Pro
1 5 10 15

```

Pro-Asn Pro Gly Tyr Pro Gly Gly Pro Gln Pro Pro-Met Pro Pro Tyr
 20 25 30
 Ala Gln Pro Pro Tyr Pro Gly Ala Pro Tyr Pro Gln Pro Pro Phe Gln
 35 40 45
 Pro Ser Pro Tyr Gly Gln Pro Gly Tyr Pro His Gly Pro Ser Pro Tyr
 50 55 60
 Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Gly Gly Tyr Pro
 65 70 75 80
 Gln Gly Pro Tyr Pro Gln Glu Gly Tyr Pro Gln Gly Pro Tyr Pro Gln
 85 90 95
 Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Ser Pro Phe Pro Pro Asn
 100 105 110
 Pro Tyr Gly Gln Pro Gln Val Phe Pro Gly Gln Asp Pro Asp Ser Pro
 115 120 125
 Gln His Gly Asn Tyr Gln Glu Gly Pro Pro Ser Tyr Tyr Asp Asn
 130 135 140
 Gln Asp Phe Pro Ala Thr Asn Trp Asp Asp Lys Ser Ile Arg Gln Ala
 145 150 155 160
 Phe Ile Arg Lys Val Phe Leu Val Leu Thr Leu Gln Leu Ser Val Thr
 165 170 175
 Leu Ser Thr Val Ser Val Phe Thr Phe Val Ala Glu Val Lys Gly Phe
 180 185 190
 Val Arg Glu Asn Val Trp Thr Tyr Tyr Val Ser Tyr Ala Val Phe Phe
 195 200 205
 Ile Ser Leu Ile Val Leu Ser Cys Cys Gly Asp Phe Arg Arg Lys His
 210 215 220
 Pro Trp Asn Leu Val Ala Leu Ser Val Leu Thr Ala Ser Leu Ser Tyr
 225 230 235 240
 Met Val Gly Met Ile Ala Ser Phe Tyr Asn Thr Glu Ala Val Ile Met
 245 250 255
 Ala Val Gly Ile Thr Thr Ala Val Cys Phe Thr Val Val Ile Phe Ser
 260 265 270
 Met Gln Thr Arg Tyr Asp Phe Thr Ser Cys Met Gly Val Leu Leu Val
 275 280 285
 Ser Met Val Val Leu Phe Ile Phe Ala Ile Leu Cys Ile Phe Ile Arg
 290 295 300
 Asn Arg Ile Leu Glu Ile Val Tyr Ala Ser Leu Gly Ala Leu Leu Phe
 305 310 315 320

```

--- Thr Cys Phe-Leu Ala-Val Asp-Thr Gln Leu Leu Leu Gly-Asn Lys-Gln ---
      325                               330                               335

Leu Ser Leu Ser Pro Glu Glu Tyr Val Phe Ala Ala Leu Asn Leu Tyr
      340                               345                               350

Thr Asp Ile Ile Asn Ile Phe Leu Tyr Ile Leu Thr Ile Ile Gly Arg
      355                               360                               365

Ala Lys Glu
      370

```

```

<210> 42
<211> 1781
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (91)..(1203)

```

```

<400> 42
attggccatc accgcgcggc cgcgcagcgg acaccgtgcg taccggcctg cggcgccccg 60

ccaccggggc ggaccgcgga acccgaggcc atg tcc cat gaa aag agt ttt ttg 114
                               Met Ser His Glu Lys Ser Phe Leu
                               1                               5

gtg tct ggg gac aac tat cct ccc ccc aac cct gga tat ccg ggg ggg 162
Val Ser Gly Asp Asn Tyr Pro Pro Pro Asn Pro Gly Tyr Pro Gly Gly
      10                               15                               20

ccc cag cca ccc atg ccc ccc tat gct cag cct ccc tac cct ggg gcc 210
Pro Gln Pro Pro Met Pro Pro Tyr Ala Gln Pro Pro Tyr Pro Gly Ala
      25                               30                               35                               40

cct tac cca cag ccc cct ttc cag ccc tcc ccc tac ggt cag cca ggg 258
Pro Tyr Pro Gln Pro Pro Phe Gln Pro Ser Pro Tyr Gly Gln Pro Gly
                               45                               50                               55

tac ccc cat ggc ccc agc ccc tac ccc caa ggg ggc tac cca cag ggt 306
Tyr Pro His Gly Pro Ser Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly
                               60                               65                               70

ccc tac ccc caa ggg ggc tac cca cag ggc ccc tac cca caa gag ggc 354
Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Glu Gly
      75                               80                               85

tac cca cag ggc ccc tac ccc caa ggg ggc tac ccc cag ggg cca tat 402
Tyr Pro Gln Gly Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr
      90                               95                               100

ccc cag agc ccc ttc ccc ccc aac ccc tat gga cag cca cag gtc ttc 450
Pro Gln Ser Pro Phe Pro Pro Asn Pro Tyr Gly Gln Pro Gln Val Phe
105                               110                               115                               120

```

cca-gga caa-gac-cct gac-tca ccc cag cat gga-aac tac cag gag gag	498
Pro Gly Gln Asp Pro Asp Ser Pro Gln His Gly Asn Tyr Gln Glu Glu	
125 130 135	
ggt ccc cca tcc tac tat gac aac cag gac ttc cct gcc acc aac tgg	546
Gly Pro Pro Ser Tyr Tyr Asp Asn Gln Asp Phe Pro Ala Thr Asn Trp	
140 145 150	
gat gac aag agc atc cga cag gcc ttc atc cgc aag gtg ttc cta gtg	594
Asp Asp Lys Ser Ile Arg Gln Ala Phe Ile Arg Lys Val Phe Leu Val	
155 160 165	
ctg acc ttg cag ctg tcg gtg acc ctg tcc acg gtg tct gtg ttc act	642
Leu Thr Leu Gln Leu Ser Val Thr Leu Ser Thr Val Ser Val Phe Thr	
170 175 180	
ttt gtt gcg gag gtg aag ggc ttt gtc cgg gag aat gtc tgg acc tac	690
Phe Val Ala Glu Val Lys Gly Phe Val Arg Glu Asn Val Trp Thr Tyr	
185 190 195 200	
tat gtc tcc tat gct gtc ttc ttc atc tct ctc atc gtc ctc agc tgt	738
Tyr Val Ser Tyr Ala Val Phe Phe Ile Ser Leu Ile Val Leu Ser Cys	
205 210 215	
tgt ggg gac ttc cgg cga aag cac ccc tgg aac ctt gtt gca ctg tcg	786
Cys Gly Asp Phe Arg Arg Lys His Pro Trp Asn Leu Val Ala Leu Ser	
220 225 230	
gtc ctg acc gcc agc ctg tcg tac atg gtg ggg atg atc gcc agc ttc	834
Val Leu Thr Ala Ser Leu Ser Tyr Met Val Gly Met Ile Ala Ser Phe	
235 240 245	
tac aac acc gag gca gtc atc atg gcc gtg ggc atc acc aca gcc gtc	882
Tyr Asn Thr Glu Ala Val Ile Met Ala Val Gly Ile Thr Thr Ala Val	
250 255 260	
tgc ttc acc gtc gtc atc ttc tcc atg cag acc cgc tac gac ttc acc	930
Cys Phe Thr Val Val Ile Phe Ser Met Gln Thr Arg Tyr Asp Phe Thr	
265 270 275 280	
tca tgc atg ggc gtg ctc ctg gtg agc atg gtg gtg ctc ttc atc ttc	978
Ser Cys Met Gly Val Leu Leu Val Ser Met Val Val Leu Phe Ile Phe	
285 290 295	
gcc att ctc tgc atc ttc atc cgg aac cgc atc ctg gag atc gtg tac	1026
Ala Ile Leu Cys Ile Phe Ile Arg Asn Arg Ile Leu Glu Ile Val Tyr	
300 305 310	
gcc tca ctg ggc gct ctg ctc ttc acc tgc ttc ctc gca gtg gac acc	1074
Ala Ser Leu Gly Ala Leu Leu Phe Thr Cys Phe Leu Ala Val Asp Thr	
315 320 325	
cag ctg ctg ctg ggg aac aag cag ctg tcc ctg agc cca gaa gag tat	1122
Gln Leu Leu Leu Gly Asn Lys Gln Leu Ser Leu Ser Pro Glu Glu Tyr	
330 335 340	
gtg ttt gct gcg ctg aac ctg tac aca gac atc atc aac atc ttc ctg	1170

Val Phe Ala Ala Leu Asn Leu Tyr Thr Asp Ile Ile Asn Ile Phe Leu
 345 350 355 360
 tac atc ctc acc atc att ggc cgc gcc aag gag tagccgagct ccagctcgct 1223
 Tyr Ile Leu Thr Ile Ile Gly Arg Ala Lys Glu
 365 370
 gtgcccgcctc aggtggcacg gctggcctgg accctgcccc tggcacggca gtgccagctg 1283
 tacttcccct ctctcttgtc ccaggcaca gcctagggaa aaggatgcct ctctccaacc 1343
 ctctgtatg tacactgcag atacttccat ttggaccgc tgtggccaca gcatggcccc 1403
 tttagtcctc ccgccccgc caaggggcag caaggccacg tttccgtgcc acctcctgtc 1463
 tactcattgt tgcattgagc ctgtctgcca gccacccca gggactgggg gcagcaccag 1523
 gtcccgggga gagggattga gccaaagggt gaggggtgcac gtcttcctc ctgtcccagc 1583
 tccccagcct ggcgtagagc acccctcccc tccccccac cccctggag tgctgccctc 1643
 tggggacatg cggagtgggg gtcttatccc tgtgctgagc cctgagggca gagaggatgg 1703
 catgtttcag gggaggggga agccttcctc tcaatttggt gtcagtga aa ttccaataaa 1763
 tgggatttgc tctctgcc 1781

<210> 43
 <211> 393
 <212> PRT
 <213> Homo sapiens

<400> 43
 Met Ser Asp Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala
 1 5 10 15
 Ser Ser Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro
 20 25 30
 Ala Ala Ser Glu Gly Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu
 35 40 45
 Arg Cys Leu Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu
 50 55 60
 Gln Ser Arg Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr
 65 70 75 80
 Leu Arg Leu Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg
 85 90 95
 Gln Gly Leu Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met
 100 105 110
 Glu Gly Ala Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg
 115 120 125

Lys Ala Gly Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln
 130 135 140
 Glu Glu Val Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala
 145 150 155 160
 Met Thr Phe Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala
 165 170 175
 Tyr Met Val Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val
 180 185 190
 Leu Val His Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu
 195 200 205
 Cys Arg Thr Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser
 210 215 220
 Lys His Glu Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr
 225 230 235 240
 His Thr Thr Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly
 245 250 255
 Val Asp Ile Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly
 260 265 270
 Tyr Asn Leu Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala
 275 280 285
 Asn Leu Leu Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr
 290 295 300
 Trp Trp Asn Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn
 305 310 315 320
 Arg Ala Val Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu
 325 330 335
 Leu Val Ser Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly
 340 345 350
 His Ile Lys Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala
 355 360 365
 Asp Ala Met Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu
 370 375 380
 Leu Val Pro Gly Pro Glu Lys Glu Asn
 385 390

<210> 44
 <211> 2396
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (50)..(1228)

<400> 44

agctgtgcac tctccatcca gctgtgcgct ctcgtcgggga gtcccagcc atg tcc gac 58
Met Ser Asp
1

gag aga gag gta gcc gag gca gcg acc ggg gaa gac gcc tct tcg ccg 106
Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala Ser Ser Pro
5 10 15

cct ccg aaa acc gag gca gcg agc gac ccc cag cat ccc gcg gcc tcc 154
Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro Ala Ala Ser
20 25 30 35

gaa ggg gcc gcc gcc gcc gcc gcc tcc ccg cca ctg ctg cgc tgc cta 202
Glu Gly Ala Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu Arg Cys Leu
40 45 50

gtg ctc acc ggc ttt gga ggc tac gac aag gtg aag ctg cag agc cgg 250
Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu Gln Ser Arg
55 60 65

ccg gca gcg ccc ccg gcc cct ggg ccc ggc cag ctg acg ctg cgt ctg 298
Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr Leu Arg Leu
70 75 80

cgg gcc tgc ggg ctc aac ttc gca gac ctc atg gct agg cag ggg ctg 346
Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg Gln Gly Leu
85 90 95

tac gac cgt ctc ccg cct ctg cct gtc act ccg ggc atg gag ggc gcg 394
Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met Glu Gly Ala
100 105 110 115

ggt gtt gtg atc gca gtg ggc gag gga gtc agc gac cgc aag gca gga 442
Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg Lys Ala Gly
120 125 130

gac cgg gtg atg gtg ttg aac cgg tca ggg atg tgg cag gaa gag gtg 490
Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln Glu Glu Val
135 140 145

act gtg ccc tcg gtc cag acc ttc ctg att cct gag gcc atg acc ttt 538
Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala Met Thr Phe
150 155 160

gag gaa gct gct gcc ttg ctc gtc aat tac att aca gcc tac atg gtc 586
Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala Tyr Met Val
165 170 175

ctc ttt gac ttc ggc aac cta cag cct ggc cac agc gtc ttg gta cac 634
Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val Leu Val His
180 185 190 195

atg gct gca ggg ggt gtg ggt atg gct gcc gtg cag ctg tgc cgt aca	682
Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu Cys Arg Thr	
200 205 210	
gtg gag aat gtg aca gtg ttc gga acg gcc tcg gcc agc aag cac gag	730
Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser Lys His Glu	
215 220 225	
gca ctg aag gag aat ggg gtc aca cat ccc atc gac tat cac acg act	778
Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr His Thr Thr	
230 235 240	
gac tac gtg gat gag atc aag aag att tcc cct aaa gga gtg gac att	826
Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly Val Asp Ile	
245 250 255	
gtc atg gac cct ctg ggt ggg tca gat act gcc aag ggc tac aac ctc	874
Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly Tyr Asn Leu	
260 265 270 275	
ctg aaa ccc atg ggc aaa gtc gtc acc tat gga atg gcc aac ctg ctg	922
Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala Asn Leu Leu	
280 285 290	
acg ggc ccc aaa cgg aac ctg atg gcc ctg gcc cgg aca tgg tgg aat	970
Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr Trp Trp Asn	
295 300 305	
cag ttc agc gtg aca gct ctg cag ctg ctg cag gcc aac cgg gct gtg	1018
Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn Arg Ala Val	
310 315 320	
tgt ggc ttc cac ctg ggc tac ctg gat ggt gag gtg gag ctg gtc agt	1066
Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu Leu Val Ser	
325 330 335	
ggt gtg gtg gcc cgc ctc ctg gct ctg tac aac cag ggc cac atc aag	1114
Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly His Ile Lys	
340 345 350 355	
ccc cac att gac tca gtc tgg ccc ttc gag aag gtg gct gat gcc atg	1162
Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala Asp Ala Met	
360 365 370	
aaa cag atg cag gag aag aag aat gtg ggc aag gtc ctc ctg gtt cca	1210
Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu Leu Val Pro	
375 380 385	
ggg cca gag aag gag aac tagggcaagt ggctgtgaga ccctagagac	1258
Gly Pro Glu Lys Glu Asn	
390	
cagcgaaggg agaagttggg aagctacgtt ctgttggtcca ccagacttgc atttcagcct	1318
ctgtcataat gctctgccct cccctccccg aagttctctg tggatgatgac cgctctcccc	1378

- tgccccctccc cgcttctga cctctgaaga ggttggaag tgaaccatttg gatgtctggg 1438
 ccttgccaag gcgacaggga gggtcagagg gaggcgggct gcttcttgcc cccacccttt 1498
 ccccgggcct gctgtgctgc ttttgtgcca aggttagcca gtccccctg ttgtgttcca 1558
 tgtgttttca cctctgcctc atctttctc ccgtccctgc cccgccacct ccccaaagaa 1618
 ttgaaacgtc agctcaggat atggggccaa tctctgtgag tccagcatgt acctgtctct 1678
 ccctagtgtc ccttcagcct gggctgacca gtgccgcct ctgggcttga ccagttccca 1738
 atctogtct ctgtcccaa cttcttaagc acaattgggc ttcttccatc tccaggtttt 1798
 ctgccattct taaccaaggc agccccaagc ctctgggga ggcagggcaa aaacagggtgc 1858
 cctcatcgtg gtctgtgcca tgtcccgct ctatggtggt tgaggagaaa ggcggggaag 1918
 ctctctcagc cttgcagata tgtgtggcat ttactagcca gagctctgaa aggcagtgtc 1978
 gtctgtttct tgtactggga ccaaagtaaa aatccaagca cattcccctt gcagttaggg 2038
 gaggcctac tgccttctca aagcagagag gcagcttctc aaactcagcc caaaactctg 2098
 tttacatggg tggggagatg gagcaggga gtacagagtg ggatggtcag gacctgggcc 2158
 attgcaacca aaatggggac ttctgggta gggaggtcac tccctctact cactgagcta 2218
 ggattaggga gggttattgc cccaaccatt gcaatgggag gtggagggac aggctcagcc 2278
 tctcattgt ctaaagagg cctaaatgtg tgaagtgcga tttctgcttt tgtgtacccc 2338
 accacccat taccacagct gcctttgtgt gtttgtgtca ataaaaagcc aaaccctg 2396

<210> 45
 <211> 393
 <212> PRT
 <213> Homo sapiens

<400> 45
 Met Ser Asp Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala
 1 5 10 15
 Ser Ser Pro Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro
 20 25 30
 Ala Ala Ser Glu Gly Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu
 35 40 45
 Arg Cys Leu Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu
 50 55 60
 Gln Ser Arg Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr
 65 70 75 80
 Leu Arg Leu Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg

			85				90				95				
Gln	Gly	Leu	Tyr 100	Asp	Arg	Leu	Pro	Pro 105	Leu	Pro	Val	Thr	Pro 110	Gly	Met
Glu	Gly	Ala 115	Gly	Val	Val	Ile	Ala 120	Val	Gly	Glu	Gly	Val 125	Ser	Asp	Arg
Lys	Ala 130	Gly	Asp	Arg	Val	Met 135	Val	Leu	Asn	Arg	Ser 140	Gly	Met	Trp	Gln
Glu 145	Glu	Val	Thr	Val	Pro 150	Ser	Val	Gln	Thr	Phe 155	Leu	Ile	Pro	Glu	Ala 160
Met	Thr	Phe	Glu	Glu 165	Ala	Ala	Ala	Leu	Leu 170	Val	Asn	Tyr	Ile	Thr 175	Ala
Tyr	Met	Val	Leu 180	Phe	Asp	Phe	Gly	Asn 185	Leu	Gln	Pro	Gly	His 190	Ser	Val
Leu	Val	His 195	Met	Ala	Ala	Gly	Gly 200	Val	Gly	Met	Ala	Ala 205	Val	Gln	Leu
Cys	Arg 210	Thr	Val	Glu	Asn	Val 215	Thr	Val	Phe	Gly	Thr 220	Ala	Ser	Ala	Ser
Lys 225	His	Glu	Ala	Leu	Lys 230	Glu	Asn	Gly	Val	Thr 235	His	Pro	Ile	Asp	Tyr 240
His	Thr	Thr	Asp	Tyr 245	Val	Asp	Glu	Ile	Lys 250	Lys	Ile	Ser	Pro	Lys 255	Gly
Val	Asp	Ile	Val 260	Met	Asp	Pro	Leu	Gly 265	Gly	Ser	Asp	Thr	Ala 270	Lys	Gly
Tyr	Asn	Leu 275	Leu	Lys	Pro	Met	Gly 280	Lys	Val	Val	Thr	Tyr 285	Gly	Met	Ala
Asn	Leu 290	Leu	Thr	Gly	Pro	Lys 295	Arg	Asn	Leu	Met	Ala 300	Leu	Ala	Arg	Thr
Trp 305	Trp	Asn	Gln	Phe	Ser 310	Val	Thr	Ala	Leu	Gln 315	Leu	Leu	Gln	Ala	Asn 320
Arg	Ala	Val	Cys	Gly 325	Phe	His	Leu	Gly	Tyr 330	Leu	Asp	Gly	Glu	Val 335	Glu
Leu	Val	Ser	Gly 340	Val	Val	Ala	Arg	Leu 345	Leu	Ala	Leu	Tyr	Asn 350	Gln	Gly
His	Ile	Lys 355	Pro	His	Ile	Asp	Ser 360	Val	Trp	Pro	Phe	Glu 365	Lys	Val	Ala
Asp	Ala 370	Met	Lys	Gln	Met	Gln 375	Glu	Lys	Lys	Asn	Val 380	Gly	Lys	Val	Leu
Leu	Val	Pro	Gly	Pro	Glu	Lys	Gln	Asn							

385- -390-

<210> 46
 <211> 2396
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (50)..(1228)

<400> 46
 agctgtgcac tctccatcca gctgtgcgct ctcgtcgga gtcccagcc atg tcc gac 58
 Met Ser Asp
 1

gag aga gag gta gcc gag gca gcg acc ggg gaa gac gcc tct tcg ccg 106
 Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala Ser Ser Pro
 5 10 15

cct ccg aaa acc gag gca gcg agc gac ccc cag cat ccc gcg gcc tcc 154
 Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro Ala Ala Ser
 20 25 30 35

gaa ggg gcc gcc gcc gcc gcc gcc tgc ccg cca ctg ctg cgc tgc cta 202
 Glu Gly Ala Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu Arg Cys Leu
 40 45 50

gtg ctc acc ggc ttt gga ggc tac gac aag gtg aag ctg cag agc cgg 250
 Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu Gln Ser Arg
 55 60 65

ccg gca gcg ccc ccg gcc cct ggg ccc ggc cag ctg acg ctg cgt ctg 298
 Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr Leu Arg Leu
 70 75 80

cgg gcc tgc ggg ctc aac ttc gca gac ctc atg gct agg cag ggg ctg 346
 Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg Gln Gly Leu
 85 90 95

tac gac cgt ctc ccg cct ctg cct gtc act ccg ggc atg gag ggc gcg 394
 Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met Glu Gly Ala
 100 105 110 115

ggg gtt gtg atc gca gtg ggc gag gga gtc agc gac cgc aag gca gga 442
 Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg Lys Ala Gly
 120 125 130

gac cgg gtg atg gtg ttg aac cgg tca ggg atg tgg cag gaa gag gtg 490
 Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln Glu Glu Val
 135 140 145

act gtg ccc tcg gtc cag acc ttc ctg att cct gag gcc atg acc ttt 538
 Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala Met Thr Phe
 150 155 160

gag gaa gct gct gcc ttg-ctc gtc aat tac att aca gcc tac atg gtc	586
Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala Tyr Met Val	
165 170 175	
ctc ttt gac ttc ggc aac cta cag cct ggc cac agc gtc ttg gta cac	634
Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val Leu Val His	
180 185 190 195	
atg gct gca ggg ggt gtg ggt atg gct gcc gtg cag ctg tgc cgt aca	682
Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu Cys Arg Thr	
200 205 210	
gtg gag aat gtg aca gtg ttc gga acg gcc tcg gcc agc aag cac gag	730
Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser Lys His Glu	
215 220 225	
gca ctg aag gag aat ggg gtc aca cat ccc atc gac tat cac acg act	778
Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr His Thr Thr	
230 235 240	
gac tac gtg gat gag atc aag aag att tcc cct aaa gga gtg gac att	826
Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly Val Asp Ile	
245 250 255	
gtc atg gac cct ctg ggt ggg tca gat act gcc aag ggc tac aac ctc	874
Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly Tyr Asn Leu	
260 265 270 275	
ctg aaa ccc atg ggc aaa gtc gtc acc tat gga atg gcc aac ctg ctg	922
Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala Asn Leu Leu	
280 285 290	
acg ggc ccc aaa cgg aac ctg atg gcc ctg gcc cgg aca tgg tgg aat	970
Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr Trp Trp Asn	
295 300 305	
cag ttc agc gtg aca gct ctg cag ctg ctg cag gcc aac cgg gct gtg	1018
Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn Arg Ala Val	
310 315 320	
tgt ggc ttc cac ctg ggc tac ctg gat ggt gag gtg gag ctg gtc agt	1066
Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu Leu Val Ser	
325 330 335	
ggt gtg gtg gcc cgc ctc ctg gct ctg tac aac cag ggc cac atc aag	1114
Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly His Ile Lys	
340 345 350 355	
ccc cac att gac tca gtc tgg ccc ttc gag aag gtg gct gat gcc atg	1162
Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala Asp Ala Met	
360 365 370	
aaa cag atg cag gag aag aag aat gtg ggc aag gtc ctc ctg gtt cca	1210
Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu Leu Val Pro	
375 380 385	
ggg cca gag aag cag aac tagggcaagt ggctgtgaga ccctagagac	1258

Gly Pro Glu Lys Gln Asn -
390

cagcgaaggg agaagttggg aagctacgtt ctggtggcca ccagacttgc atttcagcct 1318
ctgtcataat gctctgccct ccctcccccg aagttctctg tggatgatgac cgtctctccc 1378
tgccccctcc cgcttctga cctctgaaga ggttgggaag tgaccatttg gatgtctggg 1438
ccctgccaaag ggcacagggg gggtcagagg gaggcgggt gcttctgcc cccacccttt 1498
ccccgggcct gctgtgctgc ttttgtgcca aggttagcca gtccccctg ttgtgttcca 1558
tgtgttttca cctctgcctc atctttctc cgtccctgc ccgccaact ccccaaagaa 1618
ttgaaacgtc agctcaggat atggggccaa tctctgtgag tccagcatgt acctgtctct 1678
ccctagtgtc ccttcagcct gggctgacca gtgcccgcct ctgggcttga ccagttccca 1738
atctcgtcct ctgtcccaa cttcttaagc acaattgggc ttcttccatc tccaggtttt 1798
ctgccattct taaccaaggc agccccaagc ctctgggga ggcagggcaa aaacaggtgc 1858
cctcatcgtg gtctgtgcca tgtcccgctc ctatggtggt tgaggagaaa ggcggggaag 1918
cttctcagc cttgcagata tgtgtggcat ttactagcca gagctctgaa aggcagtgtc 1978
gtctgtttct tgtactggga ccaaagtaaa aatccaagca cattccccct gcagttaggg 2038
gaggccctac tgccttctca aagcagagag gcagcttatc aaactcagcc caaaactctg 2098
tttcatgagg tggggagatg gagcaggga gtacagagtg ggatgggtcag gacctgggcc 2158
attgcaacca aaatggggac ttctgggta gggagggtcac tccctctact cactgagcta 2218
ggattagga gggttattgc cccaaccatt gcaatgggag gtggaggga aggctcagcc 2278
tctcattgt ctaaagagg cctaaatgtg tgaagtgcga tttctgctt ttgtgtacccc 2338
accaccccat taccacagct gcctttgtgt gtttgtgtca ataaaaagcc aaaccctg 2396

<210> 47
<211> 138
<212> PRT
<213> Homo sapiens

<400> 47
Met Ile Ser Leu Thr Asp Thr Gln Lys Ile Gly Met Gly Leu Thr Gly
1 5 10 15
Phe Gly Val Phe Phe Leu Phe Phe Gly Met Ile Leu Phe Phe Asp Lys
20 25 30
Ala Leu Leu Ala Ile Gly Asn Val Leu Phe Val Ala Gly Leu Ala Phe
35 40 45

Val	Ile	Gly	Leu	Glu	Arg	Thr	Phe	Arg	Phe	Phe	Phe	Gln	Lys	His	Lys
50						55					60				
Met	Lys	Ala	Thr	Gly	Phe	Phe	Leu	Gly	Gly	Val	Phe	Val	Val	Leu	Ile
65					70					75					80
Gly	Trp	Pro	Leu	Ile	Gly	Met	Ile	Phe	Glu	Ile	Tyr	Gly	Phe	Phe	Leu
				85					90					95	
Leu	Phe	Arg	Gly	Phe	Phe	Pro	Val	Val	Val	Gly	Phe	Ile	Arg	Arg	Val
			100					105					110		
Pro	Val	Leu	Gly	Ser	Leu	Leu	Asn	Leu	Pro	Gly	Ile	Arg	Ser	Phe	Val
		115					120					125			
Asp	Lys	Val	Gly	Glu	Ser	Asn	Asn	Met	Val						
	130					135									

<210> 48
 <211> 2976
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (110)..(523)

<400> 48
 agacgtggcg gctctgcgct gggctgtttc ccggttcat ttctcccgac tcagcttccc 60
 accctgggct ttccgaggtg ctgtgcgcgc tgtccccacc actgcagcc atg atc tcc 118
 Met Ile Ser
 1

tta	acg	gac	acg	cag	aaa	att	gga	atg	gga	tta	aca	gga	ttt	gga	gtg	166
Leu	Thr	Asp	Thr	Gln	Lys	Ile	Gly	Met	Gly	Leu	Thr	Gly	Phe	Gly	Val	
	5					10					15					
ttt	ttc	ctg	ttc	ttt	gga	atg	att	ctc	ttt	ttt	gac	aaa	gca	cta	ctg	214
Phe	Phe	Leu	Phe	Phe	Gly	Met	Ile	Leu	Phe	Phe	Asp	Lys	Ala	Leu	Leu	
	20				25					30					35	
gct	att	gga	aat	gtt	tta	ttt	gta	gcc	ggc	ttg	gct	ttt	gta	att	ggc	262
Ala	Ile	Gly	Asn	Val	Leu	Phe	Val	Ala	Gly	Leu	Ala	Phe	Val	Ile	Gly	
			40					45						50		
tta	gaa	aga	aca	ttc	aga	ttc	ttc	ttc	caa	aaa	cat	aaa	atg	aaa	gct	310
Leu	Glu	Arg	Thr	Phe	Arg	Phe	Phe	Phe	Gln	Lys	His	Lys	Met	Lys	Ala	
			55					60					65			
aca	ggt	ttt	ttt	ctg	ggt	ggt	gta	ttt	gta	gtc	ctt	att	ggt	tgg	cct	358
Thr	Gly	Phe	Phe	Leu	Gly	Gly	Val	Phe	Val	Val	Leu	Ile	Gly	Trp	Pro	
	70						75					80				
ttg	ata	ggc	atg	atc	ttc	gaa	att	tat	gga	ttt	ttt	ctc	ttg	ttc	agg	406

Leu_Ile Gly Met Ile Phe Glu Ile Tyr Gly Phe Phe Leu Leu Phe Arg
85 90 95

ggc ttc ttt cct gtc gtt gtt ggc ttt att aga aga gtg cca gtc ctt 454
Gly Phe Phe Pro Val Val Val Gly Phe Ile Arg Arg Val Pro Val Leu
100 105 110 115

gga tcc ctc cta aat tta cct gga att aga tca ttt gta gat aaa gtt 502
Gly Ser Leu Leu Asn Leu Pro Gly Ile Arg Ser Phe Val Asp Lys Val
120 125 130

gga gaa agc aac aat atg gta taacaacaag tgaatttgaa gactcattta 553
Gly Glu Ser Asn Asn Met Val
135

aaatattgtg ttattttataa agtcatttga agaattattca gcacaaaatt aaattacatg 613
aaatagcttg taatgttctt tacaggagtt taaaacgtat agcctacaaa gtaccagcag 673
caaattagca aagaagcagt gaaaacaggc ttctactcaa gtgaactaag aagaagtcag 733
caagcaaact gagagaggtg aaatccatgt taatgatgct taagaaactc ttgaaggcta 793
tttgtgttgt ttttccacaa tgtgcgaaac tcagccatcc ttagagaact gtggtgcctg 853
tttcttttct ttttattttg aaggctcagg agcatccata ggcatttgct ttttagaaat 913
gtccactgca atggcaaaaa tatttccagt tgcactgtat ctctggaagt gatgcatgaa 973
ttcgattgga ttgtgtcatt ttaaagtatt aaaaccaagg aaaccccaat tttgatgtat 1033
ggattacttt tttttgtaaa catgggttaaa ataaaacttc tgtgggttctt ctgaatctta 1093
atatttcaaa gccagggtgaa aatctgaact agatattctt tgttggaata tgcaaaggtc 1153
attctttact aacttttagt tactaaatta tagctaagtt ttgtcagcag catactccgg 1213
aaagtctcat acttcttggg agtctgcct cctaagtatc tgtctatata attcattaag 1273
tgtaagtatt taacaaaaaa gcattcttga ccatgaatga agtagtttgt ttcatagctt 1333
gtctcattga atagtattat tgaagatact aaatgatgca aaccaaattg attttttcca 1393
tgtcatgatg taatttttct ttcttcttct ttttttttaa attttagcag tggcttatta 1453
tttgtttttc ataaattaaa ataacttttg ataatgttta ctttaagaca tgtaacatgt 1513
taaaaggtta aacttatggc tgttttttaa gggctattca tttaatctga gttttccctt 1573
attttcagct ttttctagc atataatagt cattaagcat gacatatcct tcatatgata 1633
actcatcttg agttaattag aaaatacctg agttcacgtg ctaaagtcatt ttcactgtaa 1693
taaactgact atggtttctt aagaacatga cactaaaaaa aaagtgggtt ttttccaccg 1753
ttgctgatta ttagacagta ggaaatagct gttttcttta gttttacaag atgtgacagc 1813

tttagtggta gatgtagggga aacatttcaa cagccatagt actatttggt ttaccactga 1873
 ttgcactggt ttgttttttt aacagttgca aagcttttta atgcataaaa gtataattga 1933
 aatctgtggt atttatttac aaacatgtct acaaaaatag attacagctt attttatttt 1993
 tagttaaatc tcttaataca cagagaactc ccaatcttgc tcatctaaat aaggaaagac 2053
 ttggtgtata gtgtgatggt ttagtcttaa ggattaagac atttttggta cttgcatttg 2113
 acttacgatg tatctgtgaa aatgggatga tattgacaaa tggagactcc tacctcaata 2173
 gttaatggaa taataagagg ctactgttgt gtctaattgt cttcaaaaaa gtaatatcct 2233
 cacttggaga gtgtcaaata catactttga ggattgactt tatataaggt gccctgtaga 2293
 actctgttac acatattttt gacccatatt atttacaatg tcttgataat tctacctttt 2353
 tagagcaaga atagtatctg ctaatgtaag ggacatctgt atttaactcc tttgtagaca 2413
 tgaatttcta tcaaaatggt ctttgcactg taacagagat tccttttttc aataatctta 2473
 attcaaaagc attattagac ttgaaagggg ttgataatct ccagtcctt agtaaagatt 2533
 gagagagggt ggagcagttt tcagttttta atgagtctgc agttaatatc aaatgtgagt 2593
 ttgggactgc ctggcaacat ttatatttct tattcagaac ccttgatgag actattttta 2653
 aacatactag tctgctgata gaaagcacta tacatcctat tgtttctttc tttccaaaat 2713
 cagccttctg tctgtaacaa aaatgtactt tatagagatg gaggaaaagg tctaatacta 2773
 catagcctta agtgtttctg tcattgttca agtgattttt ctgtaacaga aacatatttg 2833
 gaatgttttt cttttccctt tataaattgt aattcctgaa atactgctgc tttaaaaagt 2893
 cccactgtca gattatatta tctaacaatt gaatattgta aatatacttg tcttacctct 2953
 caataaaagg gtacttttct att 2976

<210> 49

<211> 359

<212> PRT

<213> Homo sapiens

<400> 49

Met	Ser	Lys	Glu	Thr	Ile	Ile	Lys	Cys	Glu	Lys	Gln	Lys	Pro	Arg	Phe
1				5					10					15	

His	Ala	Phe	Leu	Lys	Ile	Asn	Gln	Ala	Lys	Pro	Glu	Cys	Gly	Arg	Gln
			20					25					30		

Ser	Leu	Val	Glu	Leu	Leu	Ile	Arg	Pro	Val	Gln	Arg	Leu	Pro	Ser	Val
		35					40					45			

Ala	Leu	Leu	Leu	Asn	Asp	Leu	Lys	Lys	His	Thr	Ala	Asp	Glu	Asn	Pro
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50 55 60
 Asp Lys Ser Thr Leu Glu Lys Ala Ile Gly Ser Leu Lys Glu Val Met
 65 70 75 80
 Thr His Ile Asn Glu Asp Lys Arg Lys Thr Glu Ala Gln Lys Gln Ile
 85 90 95
 Phe Asp Val Val Tyr Glu Val Asp Gly Cys Pro Ala Asn Leu Leu Ser
 100 105 110
 Ser His Arg Ser Leu Val Gln Arg Val Glu Thr Ile Ser Leu Gly Glu
 115 120 125
 His Pro Cys Asp Arg Gly Glu Gln Val Thr Leu Phe Leu Phe Asn Asp
 130 135 140
 Cys Leu Glu Ile Ala Arg Lys Arg His Lys Val Ile Gly Thr Phe Arg
 145 150 155 160
 Ser Pro His Gly Gln Thr Arg Pro Pro Ala Ser Leu Lys His Ile His
 165 170 175
 Leu Met Pro Leu Ser Gln Ile Lys Lys Val Leu Asp Ile Arg Glu Thr
 180 185 190
 Glu Asp Cys His Asn Ala Phe Ala Leu Leu Val Arg Pro Pro Thr Glu
 195 200 205
 Gln Ala Asn Val Leu Leu Ser Phe Gln Met Thr Ser Asp Glu Leu Pro
 210 215 220
 Lys Glu Asn Trp Leu Lys Met Leu Cys Arg His Val Ala Asn Thr Ile
 225 230 235 240
 Cys Lys Ala Asp Ala Glu Asn Leu Ile Tyr Thr Ala Asp Pro Glu Ser
 245 250 255
 Phe Glu Val Asn Thr Lys Asp Met Asp Ser Thr Leu Ser Arg Ala Ser
 260 265 270
 Arg Ala Ile Lys Lys Thr Ser Lys Lys Val Thr Arg Ala Phe Ser Phe
 275 280 285
 Ser Lys Thr Pro Lys Arg Ala Leu Arg Arg Ala Leu Met Thr Ser His
 290 295 300
 Gly Ser Val Glu Gly Arg Ser Pro Ser Ser Asn Asp Lys His Val Met
 305 310 315 320
 Ser Arg Leu Ser Ser Thr Ser Ser Leu Ala Gly Ile Pro Ser Pro Ser
 325 330 335
 Leu Val Ser Leu Pro Ser Phe Phe Glu Arg Arg Ser His Thr Leu Ser
 340 345 350
 Arg Ser Thr Thr His Leu Ile

```
<210> 50
<211> 2636
<212> DNA
<213> Homo sapiens
```

```
<220>  
<221> CDS  
<222> (327) .. (1403)
```

<400>	50																	
cttcaaagca	gtcagcaagg	tggaagttg	caaaagagct	ttatcaaact	gaaagtaatt	60												
atgttaatat	attggcaaca	attattcagt	tattttcaagt	accattggaa	gaggaaggac	120												
aacgtggtgg	acctatcctt	gcaccagagg	agattaagac	tatttttggg	agcatcccag	180												
atatctttga	tgtacacact	aagataaagg	atgatcttga	agaccttata	gttaattggg	240												
atgagagcaa	aagcattggg	gacatttttc	tgaaatattc	aaaagatttg	gtaaaaacct	300												
accctccctt	tgtaaaacttc	tttgaa	atg	agc	aag	gaa	aca	att	att	aaa	tgt	353						
			Met	Ser	Lys	Glu	Thr	Ile	Ile	Lys	Cys							
			1				5											
gaa	aaa	cag	aaa	cca	aga	ttt	cat	gct	ttt	ctc	aag	ata	aac	caa	gca	401		
Glu	Lys	Gln	Lys	Pro	Arg	Phe	His	Ala	Phe	Leu	Lys	Ile	Asn	Gln	Ala			
10					15					20					25			
aaa	cca	gaa	tgt	gga	cgg	cag	agc	ctt	gtt	gaa	ctt	ctt	atc	cga	cca	449		
Lys	Pro	Glu	Cys	Gly	Arg	Gln	Ser	Leu	Val	Glu	Leu	Leu	Ile	Arg	Pro			
				30					35					40				
gta	cag	agg	tta	ccc	agt	gtt	gca	tta	ctt	tta	aat	gat	ctt	aag	aag	497		
Val	Gln	Arg	Leu	Pro	Ser	Val	Ala	Leu	Leu	Leu	Asn	Asp	Leu	Lys	Lys			
			45					50					55					
cat	aca	gct	gat	gaa	aat	cca	gac	aaa	agc	act	tta	gaa	aaa	gct	att	545		
His	Thr	Ala	Asp	Glu	Asn	Pro	Asp	Lys	Ser	Thr	Leu	Glu	Lys	Ala	Ile			
		60					65				70							
gga	tca	ctg	aag	gaa	gta	atg	acg	cat	att	aat	gag	gat	aag	aga	aaa	593		
Gly	Ser	Leu	Lys	Glu	Val	Met	Thr	His	Ile	Asn	Glu	Asp	Lys	Arg	Lys			
	75					80					85							
aca	gaa	gct	caa	aag	caa	att	ttt	gat	gtt	gtt	tat	gaa	gta	gat	gga	641		
Thr	Glu	Ala	Gln	Lys	Gln	Ile	Phe	Asp	Val	Val	Tyr	Glu	Val	Asp	Gly			
90					95					100					105			
tgc	cca	gct	aat	ctt	tta	tct	tct	cac	cga	agc	tta	gta	cag	cgg	gtt	689		
Cys	Pro	Ala	Asn	Leu	Leu	Ser	Ser	His	Arg	Ser	Leu	Val	Gln	Arg	Val			
				110					115					120				
gaa	aca	att	tct	cta	ggt	gag	cac	ccc	tgt	gac	aga	gga	gaa	caa	gta	737		
Glu	Thr	Ile	Ser	Leu	Gly	Glu	His	Pro	Cys	Asp	Arg	Gly	Glu	Gln	Val			

- - - - - 125 - - - - - 130 - - - - - 135 - - - - -	
act ctc ttc ctc ttc aat gat tgc cta gag ata gca aga aaa cgg cac	785
Thr Leu Phe Leu Phe Asn Asp Cys Leu Glu Ile Ala Arg Lys Arg His	
140 145 150	
aag gtt att ggc act ttt agg agt cct cat ggc caa acc cga ccc cca	833
Lys Val Ile Gly Thr Phe Arg Ser Pro His Gly Gln Thr Arg Pro Pro	
155 160 165	
gct tct ctt aag cat att cac cta atg cct ctt tct cag att aag aag	881
Ala Ser Leu Lys His Ile His Leu Met Pro Leu Ser Gln Ile Lys Lys	
170 175 180 185	
gta ttg gac ata aga gag aca gaa gat tgc cat aat gct ttt gcc ttg	929
Val Leu Asp Ile Arg Glu Thr Glu Asp Cys His Asn Ala Phe Ala Leu	
190 195 200	
ctt gtg agg cca cca aca gag cag gca aat gtg cta ctc agt ttc cag	977
Leu Val Arg Pro Pro Thr Glu Gln Ala Asn Val Leu Leu Ser Phe Gln	
205 210 215	
atg aca tca gat gaa ctt cca aaa gaa aac tgg cta aag atg ctg tgt	1025
Met Thr Ser Asp Glu Leu Pro Lys Glu Asn Trp Leu Lys Met Leu Cys	
220 225 230	
cga cat gta gct aac acc att tgt aaa gca gat gct gag aat ctt att	1073
Arg His Val Ala Asn Thr Ile Cys Lys Ala Asp Ala Glu Asn Leu Ile	
235 240 245	
tat act gct gat cca gaa tcc ttt gaa gta aat aca aaa gat atg gac	1121
Tyr Thr Ala Asp Pro Glu Ser Phe Glu Val Asn Thr Lys Asp Met Asp	
250 255 260 265	
agt aca ttg agt aga gca tca aga gca ata aaa aag act tca aaa aag	1169
Ser Thr Leu Ser Arg Ala Ser Arg Ala Ile Lys Lys Thr Ser Lys Lys	
270 275 280	
gtt aca aga gca ttc tct ttc tcc aaa act cca aaa aga gct ctt cga	1217
Val Thr Arg Ala Phe Ser Phe Ser Lys Thr Pro Lys Arg Ala Leu Arg	
285 290 295	
agg gct ctt atg aca tcc cac ggc tca gtg gag gga aga agt cct tcc	1265
Arg Ala Leu Met Thr Ser His Gly Ser Val Glu Gly Arg Ser Pro Ser	
300 305 310	
agc aat gat aag cat gta atg agt cgt ctt tct agc aca tca tca tta	1313
Ser Asn Asp Lys His Val Met Ser Arg Leu Ser Ser Thr Ser Ser Leu	
315 320 325	
gca ggt atc cct tct ccc tcc ctt gtc agc ctt cct tcc ttc ttt gaa	1361
Ala Gly Ile Pro Ser Pro Ser Leu Val Ser Leu Pro Ser Phe Phe Glu	
330 335 340 345	
agg aga agt cat acg tta agt aga tct aca act cat ttg ata	1403
Arg Arg Ser His Thr Leu Ser Arg Ser Thr Thr His Leu Ile	
350 355	

tgaagcgtta ccaaaatctt aaattataga aatgtataga cacctcatac tcaaataaga 1463
 aactgactta aatggtactt gtaattagca cttggtgaaa gctggaagga agataaataa 1523
 cactaaacta tgctatttga tttttcttct tgaaagagta aggtttacct gttacatttt 1583
 caagttaatt catgtaaaaa atgatatgta ttttgatgta atttatctct tgtttgaatc 1643
 tgtcattcaa aggccaaataa tttaagttgc tatcagctga tattagtagc tttgcaaccc 1703
 tgatagagta aataaatttt atgggcgggt gccaaatact gctgtgaatc tatttgtata 1763
 gtatccatga atgaatttat ggaaatagat atttgtgcag ctcaatttat gcagagatta 1823
 aatgacatca taatactgga tgaaaacttg catagaattc tgattaaata gtgggtctgt 1883
 ttcacatgtg cagtttgaag tatttaaata accactcctt tcacagttta ttttcttctc 1943
 aagcgttttc aagatctagc atgtggattt taaaagattt gccctcatta acaagaataa 2003
 catttaaagg agattgtttc aaaatatttt tgcaaattga gataaggaca gaaagattga 2063
 gaaacattgt atattttgca aaaacaagat gtttgtagct gtttcagaga gagtacggta 2123
 tatttatggg aattttatcc actagcaaat cttgatttag tttgatagtg tgtggaattt 2183
 tattttgaag gataagacca tgggaaaatt gtggtaaaga ctgtttgtac ccttcatgaa 2243
 ataattctga agttgccatc agttttacta atcttctgtg aaatgcatag atatgcgcac 2303
 gttcaacttt ttattgtggg cttataatta aatgtaaaat tgaaaattca tttgctgttt 2363
 caaagtgtga tatctttcac aatagccttt ttatagtcag taattcagaa taatcaagtt 2423
 catatggata aatgcatttt tatttcctat ttctttaggg agtgctacaa atgtttgtca 2483
 cttaaatttc aagtttctgt tttaatagtt aactgactat agattgtttt ctatgccatg 2543
 tatgtgccac ttctgagagt agtaaagac tctttgctac attttaaaag caattgtatt 2603
 agtaagaact ttgtaaataa atacctaaaa ccc 2636

<210> 51
 <211> 883
 <212> PRT
 <213> Homo sapiens

<400> 51
 Met Ala Glu Asn Ser Val Leu Thr Ser Thr Thr Gly Arg Thr Ser Leu
 1 5 10 15
 Ala Asp Ser Ser Ile Phe Asp Ser Lys Val Thr Glu Ile Ser Lys Glu
 20 25 30
 Asn Leu Leu Ile Gly Ser Thr Ser Tyr Val Glu Glu Glu Met Pro Gln

35 40 45
 Ile Glu Thr Arg Val Ile Leu Val Gln Glu Ala Gly Lys Gln Glu Glu
 50 55 60
 Leu Thr Lys Ala Leu Lys Asp Ile Lys Val Gly Phe Val Lys Met Glu
 65 70 75 80
 Ser Val Glu Glu Phe Glu Gly Leu Asp Ser Pro Glu Phe Glu Asn Val
 85 90 95
 Phe Val Val Thr Asp Phe Gln Asp Ser Val Phe Asn Asp Leu Tyr Lys
 100 105 110
 Ala Asp Cys Arg Val Ile Gly Pro Pro Val Val Leu Asn Cys Ser Gln
 115 120 125
 Lys Gly Glu Pro Leu Pro Phe Ser Cys Arg Pro Leu Tyr Cys Thr Ser
 130 135 140
 Met Met Asn Leu Val Leu Cys Phe Thr Gly Phe Arg Lys Lys Glu Glu
 145 150 155 160
 Leu Val Arg Leu Val Thr Leu Val His His Met Gly Gly Val Ile Arg
 165 170 175
 Lys Asp Phe Asn Ser Lys Val Thr His Leu Val Ala Asn Cys Thr Gln
 180 185 190
 Gly Glu Lys Phe Arg Val Ala Val Ser Leu Gly Thr Pro Ile Met Lys
 195 200 205
 Pro Glu Trp Ile Tyr Lys Ala Trp Glu Arg Arg Asn Glu Gln Asp Phe
 210 215 220
 Tyr Ala Ala Val Asp Asp Phe Arg Asn Glu Phe Lys Val Pro Pro Phe
 225 230 235 240
 Gln Asp Cys Ile Phe Ser Phe Leu Gly Phe Ser Asp Glu Glu Lys Thr
 245 250 255
 Asn Met Glu Glu Met Thr Glu Met Gln Gly Gly Lys Tyr Leu Pro Leu
 260 265 270
 Gly Asp Glu Arg Cys Thr His Leu Val Val Glu Glu Asn Ile Val Lys
 275 280 285
 Asp Leu Pro Phe Glu Pro Ser Lys Lys Leu Tyr Val Val Lys Gln Glu
 290 295 300
 Trp Phe Trp Gly Ser Ile Gln Met Asp Ala Arg Ala Gly Glu Thr Met
 305 310 315 320
 Tyr Leu Tyr Glu Lys Ala Asn Thr Pro Glu Leu Lys Lys Ser Val Ser
 325 330 335
 Met Leu Ser Leu Asn Thr Pro Asn Ser Asn Arg Lys Arg Arg Arg Leu

340	345	350
Lys Glu Thr Leu Ala Gln Leu Ser Arg Asp Thr Asp Val Ser Pro Phe 355 360 365		
Pro Pro Arg Lys Arg Pro Ser Ala Glu His Ser Leu Ser Ile Gly Ser 370 375 380		
Leu Leu Asp Ile Ser Asn Thr Pro Glu Ser Ser Ile Asn Tyr Gly Asp 385 390 395 400		
Thr Pro Lys Ser Cys Thr Lys Ser Ser Lys Ser Ser Thr Pro Val Pro 405 410 415		
Ser Lys Gln Ser Ala Arg Trp Gln Val Ala Lys Glu Leu Tyr Gln Thr 420 425 430		
Glu Ser Asn Tyr Val Asn Ile Leu Ala Thr Ile Ile Gln Leu Phe Gln 435 440 445		
Val Pro Leu Glu Glu Glu Gly Gln Arg Gly Gly Pro Ile Leu Ala Pro 450 455 460		
Glu Glu Ile Lys Thr Ile Phe Gly Ser Ile Pro Asp Ile Phe Asp Val 465 470 475 480		
His Thr Lys Ile Lys Asp Asp Leu Glu Asp Leu Ile Val Asn Trp Asp 485 490 495		
Glu Ser Lys Ser Ile Gly Asp Ile Phe Leu Lys Tyr Ser Lys Asp Leu 500 505 510		
Val Lys Thr Tyr Pro Pro Phe Val Asn Phe Phe Glu Met Ser Lys Glu 515 520 525		
Thr Ile Ile Lys Cys Glu Lys Gln Lys Pro Arg Phe His Ala Phe Leu 530 535 540		
Lys Ile Asn Gln Ala Lys Pro Glu Cys Gly Arg Gln Ser Leu Val Glu 545 550 555 560		
Leu Leu Ile Arg Pro Val Gln Arg Leu Pro Ser Val Ala Leu Leu Leu 565 570 575		
Asn Asp Leu Lys Lys His Thr Ala Asp Glu Asn Pro Asp Lys Ser Thr 580 585 590		
Leu Glu Lys Ala Ile Gly Ser Leu Lys Glu Val Met Thr His Ile Asn 595 600 605		
Glu Asp Lys Arg Lys Thr Glu Ala Gln Lys Gln Ile Phe Asp Val Val 610 615 620		
Tyr Glu Val Asp Gly Cys Pro Ala Asn Leu Leu Ser Ser His Arg Ser 625 630 635 640		
Leu Val Gln Arg Val Glu Thr Ile Ser Leu Gly Glu His Pro Cys Asp		

<400> 52

```

agagtgtctga tttagaagaa tacaaatc atg gct gaa aat agt gta tta aca 52
                        Met Ala Glu Asn Ser Val Leu Thr
                        1                      5

tcc act act ggg agg act agc ttg gca gac tct tcc att ttt gat tct 100
Ser Thr Thr Gly Arg Thr Ser Leu Ala Asp Ser Ser Ile Phe Asp Ser
      10                      15                      20

aaa gtt act gag att tcc aag gaa aac tta ctt att gga tct act tca 148
Lys Val Thr Glu Ile Ser Lys Glu Asn Leu Leu Ile Gly Ser Thr Ser
      25                      30                      35                      40

tat gta gaa gaa gag atg cct cag att gaa aca aga gtg ata ttg gtt 196
Tyr Val Glu Glu Glu Met Pro Gln Ile Glu Thr Arg Val Ile Leu Val
                        45                      50                      55

caa gaa gct gga aaa caa gaa gaa ctt aca aaa gcc tta aag gac att 244
Gln Glu Ala Gly Lys Gln Glu Glu Leu Thr Lys Ala Leu Lys Asp Ile
                        60                      65                      70

aaa gtg ggc ttt gta aag atg gag tca gtg gaa gaa ttt gaa ggt ttg 292
Lys Val Gly Phe Val Lys Met Glu Ser Val Glu Glu Phe Glu Gly Leu
      75                      80                      85

gat tct ccg gaa ttt gaa aat gta ttt gta gtc acg gac ttt cag gat 340
Asp Ser Pro Glu Phe Glu Asn Val Phe Val Val Thr Asp Phe Gln Asp
      90                      95                      100

tct gtc ttt aat gac ctc tac aag gct gat tgt aga gtt att gga cca 388
Ser Val Phe Asn Asp Leu Tyr Lys Ala Asp Cys Arg Val Ile Gly Pro
    105                      110                      115                      120

cca gtt gta tta aat tgt tca caa aaa gga gag cct ttg cca ttt tca 436
Pro Val Val Leu Asn Cys Ser Gln Lys Gly Glu Pro Leu Pro Phe Ser
                        125                      130                      135

tgt cgc ccg ttg tat tgt aca agt atg atg aat cta gta cta tgc ttt 484
Cys Arg Pro Leu Tyr Cys Thr Ser Met Met Asn Leu Val Leu Cys Phe
                        140                      145                      150

act gga ttt agg aaa aaa gaa gaa cta gtc agg ttg gtg aca ttg gtc 532
Thr Gly Phe Arg Lys Lys Glu Glu Leu Val Arg Leu Val Thr Leu Val
      155                      160                      165

cat cac atg ggt gga gtt att cga aaa gac ttt aat tca aaa gtt aca 580
His His Met Gly Gly Val Ile Arg Lys Asp Phe Asn Ser Lys Val Thr
      170                      175                      180

cat ttg gtg gca aat tgt aca caa gga gaa aaa ttc agg gtt gct gtg 628
His Leu Val Ala Asn Cys Thr Gln Gly Glu Lys Phe Arg Val Ala Val
    185                      190                      195                      200

agt cta ggt act cca att atg aag cca gaa tgg att tat aaa gct tgg 676
Ser Leu Gly Thr Pro Ile Met Lys Pro Glu Trp Ile Tyr Lys Ala Trp
                        205                      210                      215

```

gaa agg cgg aat gaa cag gat ttc tat gca gca gtt gat gac ttt aga	724
Glu Arg Arg Asn Glu Gln Asp Phe Tyr Ala Ala Val Asp Asp Phe Arg	
220 225 230	
aat gaa ttt aaa gtt cct cca ttt caa gat tgt att ttt agt ttc ctg	772
Asn Glu Phe Lys Val Pro Pro Phe Gln Asp Cys Ile Phe Ser Phe Leu	
235 240 245	
gga ttt tca gat gaa gag aaa acc aat atg gaa gaa atg act gaa atg	820
Gly Phe Ser Asp Glu Glu Lys Thr Asn Met Glu Glu Met Thr Glu Met	
250 255 260	
caa gga ggt aaa tat tta ccg ctt gga gat gaa aga tgc act cac ctt	868
Gln Gly Gly Lys Tyr Leu Pro Leu Gly Asp Glu Arg Cys Thr His Leu	
265 270 275 280	
gta gtt gaa gag aat ata gta aaa gat ctt ccc ttt gaa cct tca aag	916
Val Val Glu Glu Asn Ile Val Lys Asp Leu Pro Phe Glu Pro Ser Lys	
285 290 295	
aaa ctt tat gtt gtc aag caa gag tgg ttc tgg gga agc att caa atg	964
Lys Leu Tyr Val Val Lys Gln Glu Trp Phe Trp Gly Ser Ile Gln Met	
300 305 310	
gat gcc cga gct gga gaa act atg tat tta tat gaa aag gca aat act	1012
Asp Ala Arg Ala Gly Glu Thr Met Tyr Leu Tyr Glu Lys Ala Asn Thr	
315 320 325	
cct gag ctc aag aaa tca gtg tca atg ctt tct cta aat acc cct aac	1060
Pro Glu Leu Lys Lys Ser Val Ser Met Leu Ser Leu Asn Thr Pro Asn	
330 335 340	
agc aat cgc aaa cga cgt cgt tta aaa gaa aca ctt gct cag ctt tca	1108
Ser Asn Arg Lys Arg Arg Arg Leu Lys Glu Thr Leu Ala Gln Leu Ser	
345 350 355 360	
aga gat aca gac gtg tca cca ttt cca ccc cgt aag cgc cca tca gct	1156
Arg Asp Thr Asp Val Ser Pro Phe Pro Pro Arg Lys Arg Pro Ser Ala	
365 370 375	
gag cat tcc ctt tcc ata ggg tca ctc cta gat atc tcc aac aca cca	1204
Glu His Ser Leu Ser Ile Gly Ser Leu Leu Asp Ile Ser Asn Thr Pro	
380 385 390	
gag tct agc att aac tat gga gac acc cca aag tct tgt act aag tct	1252
Glu Ser Ser Ile Asn Tyr Gly Asp Thr Pro Lys Ser Cys Thr Lys Ser	
395 400 405	
tct aaa agc tcc act cca gtt cct tca aag cag tca gca agg tgg caa	1300
Ser Lys Ser Ser Thr Pro Val Pro Ser Lys Gln Ser Ala Arg Trp Gln	
410 415 420	
gtt gca aaa gag ctt tat caa act gaa agt aat tat gtt aat ata ttg	1348
Val Ala Lys Glu Leu Tyr Gln Thr Glu Ser Asn Tyr Val Asn Ile Leu	
425 430 435 440	
gca aca att att cag tta ttt caa gta cca ttg gaa gag gaa gga caa	1396

Ala Thr Ile Ile Gln Leu Phe Gln Val Pro Leu Glu Glu Glu Gly Gln	445	450	455	
cgt ggt gga cct atc ctt gca cca gag gag att aag act att ttt ggt	1444			
Arg Gly Gly Pro Ile Leu Ala Pro Glu Glu Ile Lys Thr Ile Phe Gly	460	465	470	
agc atc cca gat atc ttt gat gta cac act aag ata aag gat gat ctt	1492			
Ser Ile Pro Asp Ile Phe Asp Val His Thr Lys Ile Lys Asp Asp Leu	475	480	485	
gaa gac ctt ata gtt aat tgg gat gag agc aaa agc att ggt gac att	1540			
Glu Asp Leu Ile Val Asn Trp Asp Glu Ser Lys Ser Ile Gly Asp Ile	490	495	500	
ttt ctg aaa tat tca aaa gat ttg gta aaa acc tac cct ccc ttt gta	1588			
Phe Leu Lys Tyr Ser Lys Asp Leu Val Lys Thr Tyr Pro Pro Phe Val	505	510	515	520
aac ttc ttt gaa atg agc aag gaa aca att att aaa tgt gaa aaa cag	1636			
Asn Phe Phe Glu Met Ser Lys Glu Thr Ile Ile Lys Cys Glu Lys Gln	525	530	535	
aaa cca aga ttt cat gct ttt ctc aag ata aac caa gca aaa cca gaa	1684			
Lys Pro Arg Phe His Ala Phe Leu Lys Ile Asn Gln Ala Lys Pro Glu	540	545	550	
tgt gga cgg cag agc ctt gtt gaa ctt ctt atc cga cca gta cag agg	1732			
Cys Gly Arg Gln Ser Leu Val Glu Leu Leu Ile Arg Pro Val Gln Arg	555	560	565	
tta ccc agt gtt gca tta ctt tta aat gat ctt aag aag cat aca gct	1780			
Leu Pro Ser Val Ala Leu Leu Leu Asn Asp Leu Lys Lys His Thr Ala	570	575	580	
gat gaa aat cca gac aaa agc act tta gaa aaa gct att gga tca ctg	1828			
Asp Glu Asn Pro Asp Lys Ser Thr Leu Glu Lys Ala Ile Gly Ser Leu	585	590	595	600
aag gaa gta atg acg cat att aat gag gat aag aga aaa aca gaa gct	1876			
Lys Glu Val Met Thr His Ile Asn Glu Asp Lys Arg Lys Thr Glu Ala	605	610	615	
caa aag caa att ttt gat gtt gtt tat gaa gta gat gga tgc cca gct	1924			
Gln Lys Gln Ile Phe Asp Val Val Tyr Glu Val Asp Gly Cys Pro Ala	620	625	630	
aat ctt tta tct tct cac cga agc tta gta cag cgg gtt gaa aca att	1972			
Asn Leu Leu Ser Ser His Arg Ser Leu Val Gln Arg Val Glu Thr Ile	635	640	645	
tct cta ggt gag cac ccc tgt gac aga gga gaa caa gta act ctc ttc	2020			
Ser Leu Gly Glu His Pro Cys Asp Arg Gly Glu Gln Val Thr Leu Phe	650	655	660	
ctc ttc aat gat tgc cta gag ata gca aga aaa cgg cac aag gtt att	2068			
Leu Phe Asn Asp Cys Leu Glu Ile Ala Arg Lys Arg His Lys Val Ile				

665	670	675	680	
ggc act ttt agg agt cct cat ggc caa acc cga ccc cca gct tct ctt	2116			
Gly Thr Phe Arg Ser Pro His Gly Gln Thr Arg Pro Pro Ala Ser Leu				
685 690 695				
aag cat att cac cta atg cct ctt tct cag att aag aag gta ttg gac	2164			
Lys His Ile His Leu Met Pro Leu Ser Gln Ile Lys Lys Val Leu Asp				
700 705 710				
ata aga gag aca gaa gat tgc cat aat gct ttt gcc ttg ctt gtg agg	2212			
Ile Arg Glu Thr Glu Asp Cys His Asn Ala Phe Ala Leu Leu Val Arg				
715 720 725				
cca cca aca gag cag gca aat gtg cta ctc agt ttc cag atg aca tca	2260			
Pro Pro Thr Glu Gln Ala Asn Val Leu Leu Ser Phe Gln Met Thr Ser				
730 735 740				
gat gaa ctt cca aaa gaa aac tgg cta aag atg ctg tgt cga cat gta	2308			
Asp Glu Leu Pro Lys Glu Asn Trp Leu Lys Met Leu Cys Arg His Val				
745 750 755 760				
gct aac acc att tgt aaa gca gat gct gag aat ctt att tat act gct	2356			
Ala Asn Thr Ile Cys Lys Ala Asp Ala Glu Asn Leu Ile Tyr Thr Ala				
765 770 775				
gat cca gaa tcc ttt gaa gta aat aca aaa gat atg gac agt aca ttg	2404			
Asp Pro Glu Ser Phe Glu Val Asn Thr Lys Asp Met Asp Ser Thr Leu				
780 785 790				
agt aga gca tca aga gca ata aaa aag act tca aaa aag gtt aca aga	2452			
Ser Arg Ala Ser Arg Ala Ile Lys Lys Thr Ser Lys Lys Val Thr Arg				
795 800 805				
gca ttc tct ttc tcc aaa act cca aaa aga gct ctt cga agg gct ctt	2500			
Ala Phe Ser Phe Ser Lys Thr Pro Lys Arg Ala Leu Arg Arg Ala Leu				
810 815 820				
atg aca tcc cac ggc tca gtg gag gga aga agt cct tcc agc aat gat	2548			
Met Thr Ser His Gly Ser Val Glu Gly Arg Ser Pro Ser Ser Asn Asp				
825 830 835 840				
aag cat gta atg agt cgt ctt tct agc aca tca tca tta gca ggt atc	2596			
Lys His Val Met Ser Arg Leu Ser Ser Thr Ser Ser Leu Ala Gly Ile				
845 850 855				
cct tct ccc tcc ctt gtc agc ctt cct tcc ttc ttt gaa agg aga agt	2644			
Pro Ser Pro Ser Leu Val Ser Leu Pro Ser Phe Phe Glu Arg Arg Ser				
860 865 870				
cat acg tta agt aga tct aca act cat ttg ata tgaagcgtta ccaaaatctt	2697			
His Thr Leu Ser Arg Ser Thr Thr His Leu Ile				
875 880				
aaattataga aatgtataga cacctcatatc tcaaataaga aactgactta aatggtactt	2757			
gtaattagca cttggtgaaa gctggaagga agataaataa cactaaacta tgctatttga	2817			

tttttcttct tgaaagagta aggtttacct gttacatttt caagttaatt catgtaaaaa 2877
 atgatatgta ttttgatgta atttatctct tgtttgaatc tgtcattcaa aggccaataa 2937
 ttttaagttgc tatcagctga tattagtagc tttgcaaccc tgatagagta aataaatttt 2997
 atgggcgggg gccaaatact gctgtgaatc tatttgtata gtatccatga atgaatttat 3057
 ggaaatagat atttgtgcag ctcaatttat gcagagatta aatgacatca taatactgga 3117
 tgaaaacttg catagaattc tgattaaata gtgggtctgt ttcacatgtg cagtttgaag 3177
 tatttaaata accactcctt tcacagttta ttttcttctc aagcgttttc aagatctagc 3237
 atgtggattt taaaagattt gccctcatta acaagaataa catttaaagg agattgtttc 3297
 aaaatatttt tgcaattga gataaggaca gaaagattga gaaacattgt atattttgca 3357
 aaaacaagat gtttgtagct gtttcagaga gagtacggta ttttatggg aattttatcc 3417
 actagcaaat cttgatttag tttgatagtg tgtggaattt tttttgaag gataagacca 3477
 tgggaaaatt gtggtaaaga ctgtttgtac ccttcatgaa ataattctga agttgccatc 3537
 agttttacta atcttctgtg aaatgcatag atatgcgc atgttcaacttt ttattgtggt 3597
 cttataatta aatgtaaaat tgaaaattca tttgctgttt caaagtgtga tatctttcac 3657
 aatagccttt ttatagtcag taattcagaa taatcaagtt catatggata aatgcatttt 3717
 tatttcttat ttctttaggg agtgctacaa atgtttgtca cttaaatttc aagtttctgt 3777
 tttaatagtt aactgactat agattgtttt ctatgccatg tatgtgccac ttctgagagt 3837
 agtaaagac tctttgctac attttaaaag caattgtatt agtaagaact ttgtaaataa 3897
 atacctaaaa ccc 3910

<210> 53
 <211> 622
 <212> PRT
 <213> Homo sapiens

<400> 53
 Met Glu Gly Pro Gly Leu Gly Ser Gln Cys Arg Asn His Ser His Gly
 1 5 10 15
 Pro His Pro Pro Gly Phe Gly Arg Tyr Gly Ile Cys Ala His Glu Asn
 20 25 30
 Lys Glu Leu Ala Asn Ala Arg Glu Ala Leu Pro Leu Ile Glu Asp Ser
 35 40 45
 Ser Asn Cys Asp Ile Val Lys Ala Thr Gln Tyr Gly Ile Phe Glu Arg
 50 55 60

Cys	Lys	Glu	Leu	Val	Glu	Ala	Gly	Tyr	Asp	Val	Arg	Gln	Pro	Asp	Lys	
65					70					75					80	
Glu	Asn	Val	Ser	Leu	Leu	His	Trp	Ala	Ala	Ile	Asn	Asn	Arg	Leu	Asp	
				85					90					95		
Leu	Val	Lys	Phe	Tyr	Ile	Ser	Lys	Gly	Ala	Val	Val	Asp	Gln	Leu	Gly	
			100					105					110			
Gly	Asp	Leu	Asn	Ser	Thr	Pro	Leu	His	Trp	Ala	Ile	Arg	Gln	Gly	His	
		115					120					125				
Leu	Pro	Met	Val	Ile	Leu	Leu	Leu	Gln	His	Gly	Ala	Asp	Pro	Thr	Leu	
	130					135					140					
Ile	Asp	Gly	Glu	Gly	Phe	Ser	Ser	Ile	His	Leu	Ala	Val	Leu	Phe	Gln	
145					150					155					160	
His	Met	Pro	Ile	Ile	Ala	Tyr	Leu	Ile	Ser	Lys	Gly	Gln	Ser	Val	Asn	
			165					170						175		
Met	Thr	Asp	Val	Asn	Gly	Gln	Thr	Pro	Leu	Met	Leu	Ser	Ala	His	Lys	
			180					185					190			
Val	Ile	Gly	Pro	Glu	Pro	Thr	Gly	Phe	Leu	Leu	Lys	Phe	Asn	Pro	Ser	
		195					200					205				
Leu	Asn	Val	Val	Asp	Lys	Ile	His	Gln	Asn	Thr	Pro	Leu	His	Trp	Ala	
	210					215					220					
Val	Ala	Ala	Gly	Asn	Val	Asn	Ala	Val	Asp	Lys	Leu	Leu	Glu	Ala	Gly	
225				230					235					240		
Ser	Ser	Leu	Asp	Ile	Gln	Asn	Val	Lys	Gly	Glu	Thr	Pro	Leu	Asp	Met	
			245					250					255			
Ala	Leu	Gln	Asn	Lys	Asn	Gln	Leu	Ile	Ile	His	Met	Leu	Lys	Thr	Glu	
		260					265					270				
Ala	Lys	Met	Arg	Ala	Asn	Gln	Lys	Phe	Arg	Leu	Trp	Arg	Trp	Leu	Gln	
	275					280					285					
Lys	Cys	Glu	Leu	Phe	Leu	Leu	Leu	Met	Leu	Ser	Val	Ile	Thr	Met	Trp	
	290				295						300					
Ala	Ile	Gly	Tyr	Ile	Leu	Asp	Phe	Asn	Ser	Asp	Ser	Trp	Leu	Leu	Lys	
305				310					315						320	
Gly	Cys	Leu	Leu	Val	Thr	Leu	Phe	Phe	Leu	Thr	Ser	Leu	Phe	Pro	Arg	
			325					330					335			
Phe	Leu	Val	Gly	Tyr	Lys	Asn	Leu	Val	Tyr	Leu	Pro	Thr	Ala	Phe	Leu	
			340				345					350				
Leu	Ser	Ser	Val	Phe	Trp	Ile	Phe	Met	Thr	Trp	Phe	Ile	Leu	Phe	Phe	
	355					360					365					

<221> CDS

<222> (104)..(1969)

<400> 54

gcgccagcag gaagtgggag aagaggcgac ccaaggcggg ctggcgggct ggcggcagtc 60

gctacttgcc tagtagcctc agccgctgtg ggctcctggg gag atg gag ggg ccg 115
Met Glu Gly Pro
1

ggg ctg ggc tcg cag tgc agg aat cac agc cat ggc ccc cac cct cca 163
Gly Leu Gly Ser Gln Cys Arg Asn His Ser His Gly Pro His Pro Pro
5 10 15 20

gga ttt ggt cga tat ggc atc tgt gca cat gaa aac aaa gaa ctt gcc 211
Gly Phe Gly Arg Tyr Gly Ile Cys Ala His Glu Asn Lys Glu Leu Ala
25 30 35

aat gca aga gaa gct ctt cct ctt ata gag gac tct agt aac tgt gac 259
Asn Ala Arg Glu Ala Leu Pro Leu Ile Glu Asp Ser Ser Asn Cys Asp
40 45 50

att gtc aaa gct act caa tac gga att ttt gaa cga tgt aaa gag ttg 307
Ile Val Lys Ala Thr Gln Tyr Gly Ile Phe Glu Arg Cys Lys Glu Leu
55 60 65

gta gaa gca gga tat gat gtc agg caa cca gat aaa gaa aat gtg tcg 355
Val Glu Ala Gly Tyr Asp Val Arg Gln Pro Asp Lys Glu Asn Val Ser
70 75 80

ctt ctt cat tgg gct gct att aac aac aga ctg gat ctt gta aag ttt 403
Leu Leu His Trp Ala Ala Ile Asn Asn Arg Leu Asp Leu Val Lys Phe
85 90 95 100

tat att tca aaa ggt gct gtt gta gat cag ttg ggt gga gat tta aat 451
Tyr Ile Ser Lys Gly Ala Val Val Asp Gln Leu Gly Gly Asp Leu Asn
105 110 115

tca act cct ctt cac tgg gcc atc cga caa gga cat tta cct atg gtc 499
Ser Thr Pro Leu His Trp Ala Ile Arg Gln Gly His Leu Pro Met Val
120 125 130

ata tta tta ctc cag cat ggt gca gac ccc act ctt att gat gga gag 547
Ile Leu Leu Leu Gln His Gly Ala Asp Pro Thr Leu Ile Asp Gly Glu
135 140 145

gga ttc agc agc atc cac ctg gca gta ttg ttt caa cac atg cct att 595
Gly Phe Ser Ser Ile His Leu Ala Val Leu Phe Gln His Met Pro Ile
150 155 160

ata gca tat ctc atc tca aag gga cag agt gtg aat atg aca gat gta 643
Ile Ala Tyr Leu Ile Ser Lys Gly Gln Ser Val Asn Met Thr Asp Val
165 170 175 180

aat ggg cag aca cct ctc atg tta tca gct cac aaa gta att ggg cca 691
Asn Gly Gln Thr Pro Leu Met Leu Ser Ala His Lys Val Ile Gly Pro
185 190 195

gaa cca act gga ttt ctt tta aag ttt aat cct tct ctc aat gtg gtt	739
Glu Pro Thr Gly Phe Leu Leu Lys Phe Asn Pro Ser Leu Asn Val Val	
200 205 210	
gat aaa ata cac caa aac act cca ctt cac tgg gca gtt gca gca gga	787
Asp Lys Ile His Gln Asn Thr Pro Leu His Trp Ala Val Ala Ala Gly	
215 220 225	
aat gtt aat gca gtt gat aag ctt ttg gaa gct ggt tct agc ctg gat	835
Asn Val Asn Ala Val Asp Lys Leu Leu Glu Ala Gly Ser Ser Leu Asp	
230 235 240	
atc cag aat gtt aag gga gaa aca cct ctt gat atg gct cta caa aac	883
Ile Gln Asn Val Lys Gly Glu Thr Pro Leu Asp Met Ala Leu Gln Asn	
245 250 255 260	
aaa aat cag ctc att att cat atg cta aaa aca gaa gcc aaa atg aga	931
Lys Asn Gln Leu Ile Ile His Met Leu Lys Thr Glu Ala Lys Met Arg	
265 270 275	
gcc aac caa aag ttc aga ctt tgg agg tgg ctg cag aaa tgc gag ctc	979
Ala Asn Gln Lys Phe Arg Leu Trp Arg Trp Leu Gln Lys Cys Glu Leu	
280 285 290	
ttc ctg ctg ctg atg ctt tct gtg att acc atg tgg gct att gga tac	1027
Phe Leu Leu Leu Met Leu Ser Val Ile Thr Met Trp Ala Ile Gly Tyr	
295 300 305	
ata ttg gac ttc aat tca gat tct tgg ctt tta aaa gga tgt ctt cta	1075
Ile Leu Asp Phe Asn Ser Asp Ser Trp Leu Leu Lys Gly Cys Leu Leu	
310 315 320	
gta aca ctg ttt ttt ctg aca tct ttg ttt cca agg ttc ttg gtt ggg	1123
Val Thr Leu Phe Phe Leu Thr Ser Leu Phe Pro Arg Phe Leu Val Gly	
325 330 335 340	
tat aag aac ctt gta tac tta cca aca gcc ttt ctg cta agt tct gtt	1171
Tyr Lys Asn Leu Val Tyr Leu Pro Thr Ala Phe Leu Leu Ser Ser Val	
345 350 355	
ttt tgg ata ttt atg act tgg ttc atc tta ttt ttt cct gat tta gca	1219
Phe Trp Ile Phe Met Thr Trp Phe Ile Leu Phe Phe Pro Asp Leu Ala	
360 365 370	
gga gcc cct ttc tat ttc agt ttc att ttc agc ata gta gcc ttt cta	1267
Gly Ala Pro Phe Tyr Phe Ser Phe Ile Phe Ser Ile Val Ala Phe Leu	
375 380 385	
tac ttt ttc tat aag act tgg gca act gat cca ggc ttc act aag gct	1315
Tyr Phe Phe Tyr Lys Thr Trp Ala Thr Asp Pro Gly Phe Thr Lys Ala	
390 395 400	
tct gaa gaa gaa aag aaa gtg aat atc atc acc ctt gca gaa act ggc	1363
Ser Glu Glu Glu Lys Lys Val Asn Ile Ile Thr Leu Ala Glu Thr Gly	
405 410 415 420	

tct ctg gac ttc aga aca ttt tgt aca tca tgt ctt ata agg aag cca 1411
Ser Leu Asp Phe Arg Thr Phe Cys Thr Ser Cys Leu Ile Arg Lys Pro
425 430 435
tta agg tca ctc cac tgc cat gta tgc aac tgc tgt gtg gct cga tat 1459
Leu Arg Ser Leu His Cys His Val Cys Asn Cys Cys Val Ala Arg Tyr
440 445 450
gat caa cac tgc ctg tgg act gga cgg tgc ata ggt ttt ggc aac cat 1507
Asp Gln His Cys Leu Trp Thr Gly Arg Cys Ile Gly Phe Gly Asn His
455 460 465
cac tat tac ata ttc ttc ttg ttt ttc ctt tcc atg gta tgt ggc tgg 1555
His Tyr Tyr Ile Phe Phe Leu Phe Phe Leu Ser Met Val Cys Gly Trp
470 475 480
att ata tat gga tct ttc atc tat ttg tcc agt cat tgt gcc aca aca 1603
Ile Ile Tyr Gly Ser Phe Ile Tyr Leu Ser Ser His Cys Ala Thr Thr
485 490 495 500
ttc aaa gaa gat gga tta tgg act tac ctc aat cag att gtg gcc tgt 1651
Phe Lys Glu Asp Gly Leu Trp Thr Tyr Leu Asn Gln Ile Val Ala Cys
505 510 515
tcc cct tgg gtt tta tat atc ttg atg cta gca act ttc cat ttc tca 1699
Ser Pro Trp Val Leu Tyr Ile Leu Met Leu Ala Thr Phe His Phe Ser
520 525 530
tgg tca aca ttt tta tta tta aat caa ctc ttt cag att gcc ttt ctg 1747
Trp Ser Thr Phe Leu Leu Leu Asn Gln Leu Phe Gln Ile Ala Phe Leu
535 540 545
ggc ctg acc tcc cat gag aga atc agc ctg cag aag cag agc aag cat 1795
Gly Leu Thr Ser His Glu Arg Ile Ser Leu Gln Lys Gln Ser Lys His
550 555 560
atg aaa cag acg ttg tcc ctc agg aag aca cca tac aat ctt gga ttc 1843
Met Lys Gln Thr Leu Ser Leu Arg Lys Thr Pro Tyr Asn Leu Gly Phe
565 570 575 580
atg cag aac ctg gca gat ttc ttt cag tgt ggc tgc ttt ggc ttg gtg 1891
Met Gln Asn Leu Ala Asp Phe Phe Gln Cys Gly Cys Phe Gly Leu Val
585 590 595
aag ccc tgt gtg gta gat tgg aca tca cag tac acc atg gtc ttt cac 1939
Lys Pro Cys Val Val Asp Trp Thr Ser Gln Tyr Thr Met Val Phe His
600 605 610
cca gcc agg gag aag gtt ctt cgc tca gta tgaagaaaag caacccaaaa 1989
Pro Ala Arg Glu Lys Val Leu Arg Ser Val
615 620
ctctcaatct gatttgtttt tgtttatgtc gatgcctgt agtttgaaag tgaagtaaag 2049
atttagaatt cacctaagtc caaaggaaaa cacgtggttt ttaaagccat taggtaaaaa 2109
aagttctcaa taaaggcatt acaatttttt aggttttagaa agatggactt ttctgataaa 2169

tcttggcaga catctaaaaa aaaaaccata tttttcacaa gaaaatgcaa gttacttttt 2229
 ttggaaataa tactcaactga ttatggataa aatggaatat tttcagatac tatattggct 2289
 gtttcaaaat agtactattc tttaaacttg taatttttgc taagttattt gtctttgttg 2349
 tatctataaa tatgtaaaaa atatttaa atagatgtacct gttttgcttt cacactta at 2409
 aaaaaatttt tttttgt 2426

<210> 55
 <211> 257
 <212> PRT
 <213> Homo sapiens

<400> 55
 Met Ala Ser Lys Ile Gly Ser Arg Arg Trp Met Leu Gln Leu Ile Met
 1 5 10 15
 Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp Gly Cys Phe
 20 25 30
 Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg Lys Pro
 35 40 45
 Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala Ala Val Leu
 50 55 60
 Cys Ala Ser Phe Met Ser Phe Gly Val Lys Arg Arg Trp Phe Ala Leu
 65 70 75 80
 Gly Ala Ala Leu Gln Leu Ala Ile Ser Thr Tyr Ala Ala Tyr Ile Gly
 85 90 95
 Gly Tyr Val His Tyr Gly Asp Trp Leu Lys Val Arg Met Tyr Ser Arg
 100 105 110
 Thr Val Ala Ile Ile Gly Gly Phe Leu Val Leu Ala Ser Gly Ala Gly
 115 120 125
 Glu Leu Tyr Arg Arg Lys Pro Arg Ser Arg Ser Leu Gln Ser Thr Gly
 130 135 140
 Gln Val Phe Leu Gly Ile Tyr Leu Ile Cys Val Ala Tyr Ser Leu Gln
 145 150 155 160
 His Ser Lys Glu Asp Arg Leu Ala Tyr Leu Asn His Leu Pro Gly Gly
 165 170 175
 Glu Leu Met Ile Gln Leu Phe Phe Val Leu Tyr Gly Ile Leu Ala Leu
 180 185 190
 Ala Phe Leu Ser Gly Tyr Tyr Val Thr Leu Ala Ala Gln Ile Leu Ala
 195 200 205

Val	Leu	Leu	Pro	Pro	Val	Met	Leu	Leu	Ile	Asp	Gly	Asn	Val	Ala	Tyr
210						215					220				
Trp	His	Asn	Thr	Arg	Arg	Val	Glu	Phe	Trp	Asn	Gln	Met	Lys	Leu	Leu
225					230					235				240	
Gly	Glu	Ser	Val	Gly	Ile	Phe	Gly	Thr	Ala	Val	Ile	Leu	Ala	Thr	Asp
				245					250					255	

Gly

<210> 56
 <211> 1520
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (10)..(780)

<400> 56
 tttcccaag atg gcg tcg aag ata ggt tcg aga cgg tgg atg ttg cag ctg 51
 Met Ala Ser Lys Ile Gly Ser Arg Arg Trp Met Leu Gln Leu
 1 5 10

atc atg cag ttg ggt tcg gtg ctg ctc aca cgc tgc ccc ttt tgg ggc 99
 Ile Met Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp Gly
 15 20 25 30

tgc ttc agc cag ctc atg ctg tac gct gag agg gct gag gca cgc cgg 147
 Cys Phe Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg
 35 40 45

aag ccc gac atc cca gtg cct tac ctg tat ttc gac atg ggg gca gcc 195
 Lys Pro Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala Ala
 50 55 60

gtg ctg tgc gct agt ttc atg tcc ttt ggc gtg aag cgg cgc tgg ttc 243
 Val Leu Cys Ala Ser Phe Met Ser Phe Gly Val Lys Arg Arg Trp Phe
 65 70 75

gcg ctg ggg gcc gca ctc caa ttg gcc att agc acc tac gcc gcc tac 291
 Ala Leu Gly Ala Ala Leu Gln Leu Ala Ile Ser Thr Tyr Ala Ala Tyr
 80 85 90

atc ggg ggc tac gtc cac tac ggg gac tgg ctg aag gtc cgt atg tac 339
 Ile Gly Gly Tyr Val His Tyr Gly Asp Trp Leu Lys Val Arg Met Tyr
 95 100 105 110

tcg cgc aca gtt gcc atc atc ggc ggc ttt ctt gtg ttg gcc agc ggt 387
 Ser Arg Thr Val Ala Ile Ile Gly Gly Phe Leu Val Leu Ala Ser Gly
 115 120 125

gct ggg gag ctg tac cgc cgg aaa cct cgc agc cgc tcc ctg cag tcc 435
 Ala Gly Glu Leu Tyr Arg Arg Lys Pro Arg Ser Arg Ser Leu Gln Ser

	130	135	140	
acc ggc cag gtg ttc ctg ggt atc tac ctc atc tgt gtg gcc tac tca				483
Thr Gly Gln Val Phe Leu Gly Ile Tyr Leu Ile Cys Val Ala Tyr Ser				
	145	150	155	
ctg cag cac agc aag gag gac cgg ctg gcg tat ctg aac cat ctc cca				531
Leu Gln His Ser Lys Glu Asp Arg Leu Ala Tyr Leu Asn His Leu Pro				
	160	165	170	
gga ggg gag ctg atg atc cag ctg ttc ttc gtg ctg tat ggc atc ctg				579
Gly Gly Glu Leu Met Ile Gln Leu Phe Phe Val Leu Tyr Gly Ile Leu				
	175	180	185	190
gcc ctg gcc ttt ctg tca ggc tac tac gtg acc ctc gct gcc cag atc				627
Ala Leu Ala Phe Leu Ser Gly Tyr Tyr Val Thr Leu Ala Ala Gln Ile				
	195	200	205	
ctg gct gta ctg ctg ccc cct gtc atg ctg ctc att gat ggc aat gtt				675
Leu Ala Val Leu Leu Pro Pro Val Met Leu Leu Ile Asp Gly Asn Val				
	210	215	220	
gct tac tgg cac aac acg cgg cgt gtt gag ttc tgg aac cag atg aag				723
Ala Tyr Trp His Asn Thr Arg Arg Val Glu Phe Trp Asn Gln Met Lys				
	225	230	235	
ctc ctt gga gag agt gtg ggc atc ttc gga act gct gtc atc ctg gcc				771
Leu Leu Gly Glu Ser Val Gly Ile Phe Gly Thr Ala Val Ile Leu Ala				
	240	245	250	
act gat ggc tgagttttat ggcaagaggc tgagatgggc acagggagcc				820
Thr Asp Gly				
	255			
actgaggggtc accctgcctt cctccttgct ggcccagctg ctgtttatatt atgctttttg				880
gtctgtttgt ttgatctttt gcttttttaa aattgttttt tgcagttaag aggcagctca				940
tttgtccaaa tttctgggct cagcgcttgg gagggcagga gccctggcac taatgctgta				1000
caggtttttt tctgtttagg agagctgagg ccagctgccc actgagtctc ctgtccctga				1060
gaagggagta tggcagggct gggatgcggc tactgagagt gggagagtgg gagacagagg				1120
aaggaagatg gagattggaa gtgagcaaat gtgaaaaatt cctctttgaa cctggcagat				1180
gcagctagggc tctgcagtgc tgtttggaga ctgtgagagg gagtgtgtgt gttgacacat				1240
gtggatcagg cccaggaagg gcacaggggc tgagcactac agaagtcaca tgggttctca				1300
gggtatgcc aagggcagaaa cagtaccggc tctctgtcac tcacctgag agtagagcag				1360
accctgttct gctctgggct gtgaaggggt ggagcaggca gtggccagct ttgcccttcc				1420
tgctgtctct gtttctagct ccatggttgg cctgggtggg gtggagttcc ctcccaaaca				1480
ccagaccaca cagtctcca aaaataaaca ttttatatag				1520

<210> 57
 <211> 107
 <212> PRT
 <213> Homo sapiens

<400> 57
 Met Ala Leu Phe Ala Gly Gly Lys Leu Arg Val His Leu Asp Ile Gln
 1 5 10 15
 Val Gly Glu His Ala Asn Asn Tyr Pro Glu Ile Ala Ala Lys Asp Lys
 20 25 30
 Leu Thr Glu Leu Gln Leu Arg Ala Arg Gln Leu Leu Asp Gln Val Glu
 35 40 45
 Gln Ile Gln Lys Glu Gln Asp Tyr Gln Arg Tyr Arg Glu Glu Arg Phe
 50 55 60
 Arg Leu Thr Ser Glu Ser Thr Asn Gln Arg Val Leu Trp Trp Ser Ile
 65 70 75 80
 Ala Gln Thr Val Ile Leu Ile Leu Thr Gly Ile Trp Gln Met Arg His
 85 90 95
 Leu Lys Ser Phe Phe Glu Ala Lys Lys Leu Val
 100 105

<210> 58
 <211> 1496
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (9)..(329)

<400> 58
 ctaccagg atg gct ctc ttc gct ggt ggc aaa ctg cgt gtg cat ctc gac 50
 Met Ala Leu Phe Ala Gly Gly Lys Leu Arg Val His Leu Asp
 1 5 10
 atc cag gtt ggg gag cat gcc aac aac tac cct gag att gct gca aaa 98
 Ile Gln Val Gly Glu His Ala Asn Asn Tyr Pro Glu Ile Ala Ala Lys
 15 20 25 30
 gat aag ctg acg gag cta cag ctc cgc gcc cgc cag ttg ctt gat cag 146
 Asp Lys Leu Thr Glu Leu Gln Leu Arg Ala Arg Gln Leu Leu Asp Gln
 35 40 45
 gtg gaa cag att cag aag gag cag gat tac caa agg tat cgt gaa gag 194
 Val Glu Gln Ile Gln Lys Glu Gln Asp Tyr Gln Arg Tyr Arg Glu Glu
 50 55 60
 cgc ttc cga ctg acg agc gag agc acc aac cag agg gtc cta tgg tgg 242

<400> 59

Met	Met	Ile	His	Gly	Phe	Gln	Ser	Ser	His	Arg	Asp	Phe	Cys	Phe	Gly
1				5					10					15	
Pro	Trp	Lys	Leu	Thr	Ala	Ser	Lys	Thr	His	Ile	Met	Lys	Ser	Ala	Asp
			20					25					30		
Val	Glu	Lys	Leu	Ala	Asp	Glu	Leu	His	Met	Pro	Ser	Leu	Pro	Glu	Met
		35					40					45			
Met	Phe	Gly	Asp	Asn	Val	Leu	Arg	Ile	Gln	His	Gly	Ser	Gly	Phe	Gly
	50					55					60				
Ile	Glu	Phe	Asn	Ala	Thr	Asp	Ala	Leu	Arg	Cys	Val	Asn	Asn	Tyr	Gln
65					70					75					80
Gly	Met	Leu	Lys	Val	Ala	Cys	Ala	Glu	Glu	Trp	Gln	Glu	Ser	Arg	Thr
				85					90					95	
Glu	Gly	Glu	His	Ser	Lys	Glu	Val	Ile	Lys	Pro	Tyr	Asp	Trp	Thr	Tyr
			100					105					110		
Thr	Thr	Asp	Tyr	Lys	Gly	Thr	Leu	Leu	Gly	Glu	Ser	Leu	Lys	Leu	Lys
		115					120					125			
Val	Val	Pro	Thr	Thr	Asp	His	Ile	Asp	Thr	Glu	Lys	Leu	Lys	Ala	Arg
		130				135					140				
Glu	Gln	Ile	Lys	Phe	Phe	Glu	Glu	Val	Leu	Leu	Phe	Glu	Asp	Glu	Leu
145					150					155					160
His	Asp	His	Gly	Val	Ser	Ser	Leu	Ser	Val	Lys	Ile	Arg	Val	Met	Pro
			165						170					175	
Ser	Ser	Phe	Phe	Leu	Leu	Leu	Arg	Phe	Phe	Leu	Arg	Ile	Asp	Gly	Val
			180					185					190		
Leu	Ile	Arg	Met	Asn	Asp	Thr	Arg	Leu	Tyr	His	Glu	Ala	Asp	Lys	Thr
		195					200					205			
Tyr	Met	Leu	Arg	Glu	Tyr	Thr	Ser	Arg	Glu	Ser	Lys	Ile	Ser	Ser	Leu
	210					215					220				
Met	His	Val	Pro	Pro	Ser	Leu	Phe	Thr	Glu	Pro	Asn	Glu	Ile	Ser	Gln
225					230					235					240
Tyr	Leu	Pro	Ile	Lys	Glu	Ala	Val	Cys	Glu	Lys	Leu	Ile	Phe	Pro	Glu
			245						250					255	
Arg	Ile	Asp	Pro	Asn	Pro	Ala	Asp	Ser	Gln	Lys	Ser	Thr	Gln	Val	Glu
			260					265					270		

<210> 60

<211> 1916

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (117)..(932)

<400> 60

atggtaacgg ctcggaagcc taggaggctg ggccggaggg aggcggagga accggtgttc 60

gccgccgcgc ctgcttcagc ttattccttg tggcctctgc gggtcctgcc tcagcc atg 119
Met
1

atg atc cac ggc ttc cag agc agc cac cgg gat ttc tgc ttc ggg ccc 167
Met Ile His Gly Phe Gln Ser Ser His Arg Asp Phe Cys Phe Gly Pro
5 10 15

tgg aag ctg acg gcg tcc aag acc cac atc atg aag tcg gcg gat gtg 215
Trp Lys Leu Thr Ala Ser Lys Thr His Ile Met Lys Ser Ala Asp Val
20 25 30

gag aaa tta gcc gat gaa tta cat atg cca tct ctc cct gaa atg atg 263
Glu Lys Leu Ala Asp Glu Leu His Met Pro Ser Leu Pro Glu Met Met
35 40 45

ttt gga gac aac gtt tta aga atc cag cat ggg tct ggc ttt gga att 311
Phe Gly Asp Asn Val Leu Arg Ile Gln His Gly Ser Gly Phe Gly Ile
50 55 60 65

gag ttc aat gct aca gat gcg tta aga tgt gta aac aac tac caa gga 359
Glu Phe Asn Ala Thr Asp Ala Leu Arg Cys Val Asn Asn Tyr Gln Gly
70 75 80

atg ctt aaa gtg gcc tgt gct gaa gag tgg caa gaa agc agg acg gag 407
Met Leu Lys Val Ala Cys Ala Glu Glu Trp Gln Glu Ser Arg Thr Glu
85 90 95

ggc gaa cac tcc aaa gag gtt att aaa cca tat gat tgg acc tat aca 455
Gly Glu His Ser Lys Glu Val Ile Lys Pro Tyr Asp Trp Thr Tyr Thr
100 105 110

aca gat tat aag gga acc tta ctt gga gaa tct ctt aag tta aag gtt 503
Thr Asp Tyr Lys Gly Thr Leu Leu Gly Glu Ser Leu Lys Leu Lys Val
115 120 125

gta cct aca aca gat cat ata gat aca gaa aaa ttg aaa gcc aga gaa 551
Val Pro Thr Thr Asp His Ile Asp Thr Glu Lys Leu Lys Ala Arg Glu
130 135 140 145

cag att aag ttt ttt gaa gaa gtt ctc ctt ttt gag gat gaa ctt cat 599
Gln Ile Lys Phe Phe Glu Glu Val Leu Leu Phe Glu Asp Glu Leu His
150 155 160

gat cat gga gtt tca agc ctg agt gtg aag att aga gta atg cct tct 647
Asp His Gly Val Ser Ser Leu Ser Val Lys Ile Arg Val Met Pro Ser
165 170 175

agc ttt ttc ctg ctg ttg cgg ttt ttc ttg aga att gat ggg gtg ctt 695

Ser	Phe	Phe	Leu	Leu	Leu	Arg	Phe	Phe	Leu	Arg	Ile	Asp	Gly	Val	Leu		
		180					185					190					
atc	aga	atg	aat	gac	acg	aga	ctt	tac	cat	gag	gct	gac	aag	acc	tac	743	
Ile	Arg	Met	Asn	Asp	Thr	Arg	Leu	Tyr	His	Glu	Ala	Asp	Lys	Thr	Tyr		
		195				200					205						
atg	tta	cga	gaa	tat	acg	tca	cga	gaa	agc	aaa	att	tct	agt	ttg	atg	791	
Met	Leu	Arg	Glu	Tyr	Thr	Ser	Arg	Glu	Ser	Lys	Ile	Ser	Ser	Leu	Met		
		210				215				220					225		
cat	gtt	cca	cct	tcc	ctc	ttc	acg	gaa	cct	aat	gaa	ata	tcc	cag	tat	839	
His	Val	Pro	Pro	Ser	Leu	Phe	Thr	Glu	Pro	Asn	Glu	Ile	Ser	Gln	Tyr		
				230					235					240			
tta	cca	ata	aag	gaa	gca	gtt	tgt	gag	aag	cta	ata	ttt	cca	gaa	aga	887	
Leu	Pro	Ile	Lys	Glu	Ala	Val	Cys	Glu	Lys	Leu	Ile	Phe	Pro	Glu	Arg		
			245					250					255				
att	gat	cct	aac	cca	gca	gac	tca	caa	aaa	agt	aca	caa	gtg	gaa		932	
Ile	Asp	Pro	Asn	Pro	Ala	Asp	Ser	Gln	Lys	Ser	Thr	Gln	Val	Glu			
		260					265					270					
taaaatgtga	tacaacatat	actcactatg	gaatctgact	ggacaccttg	gctatgtgta	992											
aggggttatt	tttattatga	gaattaattg	ccttggttat	gtacagattt	tctgtagcct	1052											
taaaggaaaa	aaaaataaag	atcggttacag	gcagggttca	ctcaactgct	atttgtactg	1112											
tctgtcttca	cattcatatt	ccagatttat	atcttctgga	gttaaatttg	gatgatttct	1172											
aaattatcac	aaagtgggac	ctcagcagta	gtgatgtgtg	tgtctcatga	gcagtgagca	1232											
cagtctgcat	tcatcatgaa	acactatctt	ctaccaggag	gagggttaatg	taaatcacca	1292											
aatcccaatg	ccttggtgact	ttcataggat	tcctgatcat	gcatgttgat	gtactggctc	1352											
ttcaactttgg	gctttctgat	gtttattcac	acctttggag	agttgcaact	tgccacatac	1412											
gaaattagtc	tcatagtgtg	gtgaacttca	accccaaaat	tttaaaaatg	tatttcccc	1472											
cagttttaaa	ttgcctttga	aatttaaaaa	aaaaaattta	gacttagtac	cagaaccaa	1532											
aatacctaga	tttttgagga	acttattaca	tacatagaaa	catgaatatg	gtttaccwct	1592											
gtgtgtgtgt	gtgtgtgtgt	gtgtatacag	actttttttt	ttaacttggt	gattcagatg	1652											
tcttggtccc	tgaatagtcc	tagattaact	atcttgagaa	ttgattgtta	aaaattacag	1712											
ggaattaaaa	taattgcctt	ttttttttta	gagggttaaga	gatgggtaga	agagtatgcc	1772											
tctgaaaatt	ttattagttt	attcttgtgg	agaataccaa	gaaaatgtgt	atttgcccat	1832											
tgctaaatat	gatatatgcc	atcttgtatt	tatttgtccc	aagtgtcttt	ttttaagagg	1892											
agaataaaca	ataaggaatt	actg				1916											

<210> 61
 <211> 219
 <212> PRT
 <213> Homo sapiens

 <400> 61
 Met Asn Arg Leu Phe Gly Lys Ala Lys Pro Lys Ala Pro Pro Pro Ser
 1 5 10 15
 Leu Thr Asp Cys Ile Gly Thr Val Asp Ser Arg Ala Glu Ser Ile Asp
 20 25 30
 Lys Lys Ile Ser Arg Leu Asp Ala Glu Leu Val Lys Tyr Lys Asp Gln
 35 40 45
 Ile Lys Lys Met Arg Glu Gly Pro Ala Lys Asn Met Val Lys Gln Lys
 50 55 60
 Ala Leu Arg Val Leu Lys Gln Lys Arg Met Tyr Glu Gln Gln Arg Asp
 65 70 75 80
 Asn Leu Ala Gln Gln Ser Phe Asn Met Glu Gln Ala Asn Tyr Thr Ile
 85 90 95
 Gln Ser Leu Lys Asp Thr Lys Thr Thr Val Asp Ala Met Lys Leu Gly
 100 105 110
 Val Lys Glu Met Lys Lys Ala Tyr Lys Gln Val Lys Ile Asp Gln Ile
 115 120 125
 Glu Asp Leu Gln Asp Gln Leu Glu Asp Met Met Glu Asp Ala Asn Glu
 130 135 140
 Ile Gln Glu Ala Leu Ser Arg Ser Tyr Gly Thr Pro Glu Leu Asp Glu
 145 150 155 160
 Asp Asp Leu Glu Ala Glu Leu Asp Ala Leu Gly Asp Glu Leu Leu Ala
 165 170 175
 Asp Glu Asp Ser Ser Tyr Leu Asp Glu Ala Ala Ser Ala Pro Ala Ile
 180 185 190
 Pro Glu Gly Val Pro Thr Asp Thr Lys Asn Lys Asp Gly Val Leu Val
 195 200 205
 Asp Glu Phe Gly Leu Pro Gln Ile Pro Ala Ser
 210 215

<210> 62
 <211> 1362
 <212> DNA
 <213> Homo sapiens

<220>

--<221> CDS--

<222> (49)..(705)

<400> 62

```
gttttctggt tttgctctag tgtttgggtt tcttcgcggc tgctcaag atg aac cga 57
                                         Met Asn Arg
                                         1

ctc ttc ggg aaa gcg aaa ccc aag gct ccg ccg ccc agc ctg act gac 105
Leu Phe Gly Lys Ala Lys Pro Lys Ala Pro Pro Pro Ser Leu Thr Asp
      5                               10                               15

tgc att ggc acg gtg gac agt aga gca gaa tcc att gac aag aag att 153
Cys Ile Gly Thr Val Asp Ser Arg Ala Glu Ser Ile Asp Lys Lys Ile
      20                               25                               30                               35

tct cga ttg gat gct gag cta gtg aag tat aag gat cag atc aag aag 201
Ser Arg Leu Asp Ala Glu Leu Val Lys Tyr Lys Asp Gln Ile Lys Lys
                               40                               45                               50

atg aga gag ggt cct gca aag aat atg gtc aag cag aaa gcc ttg cga 249
Met Arg Glu Gly Pro Ala Lys Asn Met Val Lys Gln Lys Ala Leu Arg
                               55                               60                               65

gtt tta aag caa aag agg atg tat gag cag cag cgg gac aat ctt gcc 297
Val Leu Lys Gln Lys Arg Met Tyr Glu Gln Gln Arg Asp Asn Leu Ala
      70                               75                               80

caa cag tca ttc aac atg gaa caa gcc aat tat acc atc cag tct ttg 345
Gln Gln Ser Phe Asn Met Glu Gln Ala Asn Tyr Thr Ile Gln Ser Leu
      85                               90                               95

aag gac acc aag acc acg gtt gat gct atg aaa ctg gga gta aag gaa 393
Lys Asp Thr Lys Thr Thr Val Asp Ala Met Lys Leu Gly Val Lys Glu
100                               105                               110                               115

atg aag aag gca tac aag caa gtg aag atc gac cag att gag gat tta 441
Met Lys Lys Ala Tyr Lys Gln Val Lys Ile Asp Gln Ile Glu Asp Leu
                               120                               125                               130

caa gac cag cta gag gat atg atg gaa gat gca aat gaa atc caa gaa 489
Gln Asp Gln Leu Glu Asp Met Met Glu Asp Ala Asn Glu Ile Gln Glu
                               135                               140                               145

gca ctg agt cgc agt tat ggc acc cca gaa ctg gat gaa gat gat tta 537
Ala Leu Ser Arg Ser Tyr Gly Thr Pro Glu Leu Asp Glu Asp Asp Leu
      150                               155                               160

gaa gca gag ttg gat gca cta ggt gat gag ctt ctg gct gat gaa gac 585
Glu Ala Glu Leu Asp Ala Leu Gly Asp Glu Leu Leu Ala Asp Glu Asp
      165                               170                               175

agt tct tat ttg gat gag gca gca tct gca cct gca att cca gaa ggt 633
Ser Ser Tyr Leu Asp Glu Ala Ala Ser Ala Pro Ala Ile Pro Glu Gly
180                               185                               190                               195

gtt ccc act gat aca aaa aac aag gat gga gtt ctg gtg gat gaa ttt 681
```

Val Pro Thr Asp Thr Lys Asn Lys Asp Gly Val Leu Val Asp Glu Phe
200 205 210

gga ttg cca cag atc cct gct tca tagatttgca tcattcaagc atatcttgta 735
Gly Leu Pro Gln Ile Pro Ala Ser
215

aaacaaacac atattatggg actaggaaat atttatcttt ccaaatttgc cataacagat 795
ttaggtttct ttcctttctt tgaaggaaag ttttaattaca ttgctctttt attttttcca 855
ttaagagact cattgcttgg gaaatgcttt ctctgtacta aaatttgatt cctttttttt 915
cttatgaaaa acgaactcag tttaaaagta tttttagctc gtatgacttg ttttcattca 975
ttaataataa tttgaaataa aactaaggaa atggaatctt aaaagtctat gacagtgtaa 1035
ctctacagtc tcaaatgac ctgataaatt gataagacaa agatgagatt attggggctg 1095
ttcatattat gattcagaat cattttctat tgtggtatta taggttggtt aaagtgatgg 1155
cctttttgat gggttttggt gtgtcttggt aacaagtcgt tactgtgtcc attattggaa 1215
tggaattatc actactgtat catgagtggg tattttgatt ctatgggtcc ctcagtatta 1275
catcttgact tgtaatcaat tatgaatatt tcttgatatt taatgtatag gacatttatt 1335
tatactcaat aaatattttt caaaagg 1362

<210> 63
<211> 622
<212> PRT
<213> Homo sapiens

<400> 63
Met Ala Asp Gly Pro Asp Glu Tyr Asp Thr Glu Ala Gly Cys Val Pro
1 5 10 15
Leu Leu His Pro Glu Glu Ile Lys Pro Gln Ser His Tyr Asn His Gly
20 25 30
Tyr Gly Glu Pro Leu Gly Arg Lys Thr His Ile Asp Asp Tyr Ser Thr
35 40 45
Trp Asp Ile Val Lys Ala Thr Gln Tyr Gly Ile Tyr Glu Arg Cys Arg
50 55 60
Glu Leu Val Glu Ala Gly Tyr Asp Val Arg Gln Pro Asp Lys Glu Asn
65 70 75 80
Val Thr Leu Leu His Trp Ala Ala Ile Asn Asn Arg Ile Asp Leu Val
85 90 95
Lys Tyr Tyr Ile Ser Lys Gly Ala Ile Val Asp Gln Leu Gly Gly Asp
100 105 110

Leu Ala-Glu-Thr-Gly Ser Leu Asp Leu Ser Ile Phe Cys Ser Thr Cys
 420 425 430
 Leu Ile Arg Lys Pro Val Arg Ser Lys His Cys Gly Val Cys Asn Arg
 435 440 445
 Cys Ile Ala Lys Phe Asp His His Cys Pro Trp Val Gly Asn Cys Val
 450 455 460
 Gly Ala Gly Asn His Arg Tyr Phe Met Gly Tyr Leu Phe Phe Leu Leu
 465 470 475 480
 Phe Met Ile Cys Trp Met Ile Tyr Gly Cys Ile Ser Tyr Trp Gly Leu
 485 490 495
 His Cys Glu Thr Thr Tyr Thr Lys Asp Gly Phe Trp Thr Tyr Ile Thr
 500 505 510
 Gln Ile Ala Thr Cys Ser Pro Trp Met Phe Trp Met Phe Leu Asn Ser
 515 520 525
 Val Phe His Phe Met Trp Val Ala Val Leu Leu Met Cys Gln Met Tyr
 530 535 540
 Gln Ile Ser Cys Leu Gly Ile Thr Thr Asn Glu Arg Met Asn Ala Arg
 545 550 555 560
 Arg Tyr Lys His Phe Lys Val Thr Thr Thr Ser Ile Glu Ser Pro Phe
 565 570 575
 Asn His Gly Cys Val Arg Asn Ile Ile Asp Phe Phe Glu Phe Arg Cys
 580 585 590
 Cys Gly Leu Phe Arg Pro Val Ile Val Asp Trp Thr Arg Gln Tyr Thr
 595 600 605
 Ile Glu Tyr Asp Gln Ile Ser Gly Ser Gly Tyr Gln Leu Val
 610 615 620

<210> 64
 <211> 2948
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (14)..(1879)

<400> 64
 atttaacacc aag atg gcg gac ggc ccg gat gag tac gat acc gaa gcg 49
 Met Ala Asp Gly Pro Asp Glu Tyr Asp Thr Glu Ala
 1 5 10
 ggc tgt gtg ccc ctt ctc cac cca gag gaa atc aaa ccc caa agc cat 97
 Gly Cys Val Pro Leu Leu His Pro Glu Glu Ile Lys Pro Gln Ser His
 15 20 25

tat aac cat gga tat ggt gaa cct ctt gga cgg aaa act cat att gat	145
Tyr Asn His Gly Tyr Gly Glu Pro Leu Gly Arg Lys Thr His Ile Asp	
30 35 40	
gat tac agc aca tgg gac ata gtc aag gct aca caa tat gga ata tat	193
Asp Tyr Ser Thr Trp Asp Ile Val Lys Ala Thr Gln Tyr Gly Ile Tyr	
45 50 55 60	
gaa cgc tgt cga gaa ttg gtg gaa gca ggt tat gat gta cgg caa ccg	241
Glu Arg Cys Arg Glu Leu Val Glu Ala Gly Tyr Asp Val Arg Gln Pro	
65 70 75	
gac aaa gaa aat gtt acc ctc ctc cat tgg gct gcc atc aat aac aga	289
Asp Lys Glu Asn Val Thr Leu Leu His Trp Ala Ala Ile Asn Asn Arg	
80 85 90	
ata gat tta gtc aaa tac tat att tcg 'aaa ggt gct att gtg gat caa	337
Ile Asp Leu Val Lys Tyr Tyr Ile Ser Lys Gly Ala Ile Val Asp Gln	
95 100 105	
ctt gga ggg gac ctg aat tca act cca ttg cac tgg gcc aca aga caa	385
Leu Gly Gly Asp Leu Asn Ser Thr Pro Leu His Trp Ala Thr Arg Gln	
110 115 120	
ggc cat cta tcc atg gtt gtg caa cta atg aaa tat ggt gca gat cct	433
Gly His Leu Ser Met Val Val Gln Leu Met Lys Tyr Gly Ala Asp Pro	
125 130 135 140	
tca tta att gat gga gaa gga tgt agc tgt att cat ctg gct gct cag	481
Ser Leu Ile Asp Gly Glu Gly Cys Ser Cys Ile His Leu Ala Ala Gln	
145 150 155	
ttc gga cat acc tca att gtt gct tat ctc ata gca aaa gga cag gat	529
Phe Gly His Thr Ser Ile Val Ala Tyr Leu Ile Ala Lys Gly Gln Asp	
160 165 170	
gta gat atg atg gat cag aat gga atg acg cct tta atg tgg gca gca	577
Val Asp Met Met Asp Gln Asn Gly Met Thr Pro Leu Met Trp Ala Ala	
175 180 185	
tat aga aca cat agt gtg gat cca act aga ttg ctt tta aca ttc aat	625
Tyr Arg Thr His Ser Val Asp Pro Thr Arg Leu Leu Leu Thr Phe Asn	
190 195 200	
gtt tca gtt aac ctt ggt gac aag tat cac aaa aac act gct ctg cat	673
Val Ser Val Asn Leu Gly Asp Lys Tyr His Lys Asn Thr Ala Leu His	
205 210 215 220	
tgg gca gtg cta gca ggg aat acc aca gtc att agc ctt ctt ctg gaa	721
Trp Ala Val Leu Ala Gly Asn Thr Thr Val Ile Ser Leu Leu Leu Glu	
225 230 235	
gct gga gct aat gtt gat gcc cag aat atc aag ggc gaa tca gcg ctt	769
Ala Gly Ala Asn Val Asp Ala Gln Asn Ile Lys Gly Glu Ser Ala Leu	
240 245 250	

gat ttg gca aaa cag aga aaa aat gtg tgg atg atc aac cac tta caa	817
Asp Leu Ala Lys Gln Arg Lys Asn Val Trp Met Ile Asn His Leu Gln	
255 260 265	
gag gca agg caa gca aaa gga tat gac aat ccg tcc ttc ctt aga aag	865
Glu Ala Arg Gln Ala Lys Gly Tyr Asp Asn Pro Ser Phe Leu Arg Lys	
270 275 280	
ctg aaa gct gat aag gaa ttt cgg cag aaa gta atg tta gga act cct	913
Leu Lys Ala Asp Lys Glu Phe Arg Gln Lys Val Met Leu Gly Thr Pro	
285 290 295 300	
ttc cta gtt att tgg ctg gtt ggg ttt ata gca gac cta aat att gat	961
Phe Leu Val Ile Trp Leu Val Gly Phe Ile Ala Asp Leu Asn Ile Asp	
305 310 315	
tct tgg ctc att aaa ggg cta atg tat ggt ggt gtt tgg gct aca gta	1009
Ser Trp Leu Ile Lys Gly Leu Met Tyr Gly Gly Val Trp Ala Thr Val	
320 325 330	
cag ttt ctt tca aaa tcc ttt ttc gat cat tca atg cat agt gca ttg	1057
Gln Phe Leu Ser Lys Ser Phe Phe Asp His Ser Met His Ser Ala Leu	
335 340 345	
ccc ctt ggg ata tat ttg gca acc aaa ttc tgg atg tat gtg acg tgg	1105
Pro Leu Gly Ile Tyr Leu Ala Thr Lys Phe Trp Met Tyr Val Thr Trp	
350 355 360	
ttc ttc tgg ttt tgg aat gat ctc aac ttt tta ttt atc cat ctt cca	1153
Phe Phe Trp Phe Trp Asn Asp Leu Asn Phe Leu Phe Ile His Leu Pro	
365 370 375 380	
ttc ctt gcc aat agt gtt gca ctt ttc tac aat ttt gga aaa tct tgg	1201
Phe Leu Ala Asn Ser Val Ala Leu Phe Tyr Asn Phe Gly Lys Ser Trp	
385 390 395	
aaa tca gat cca ggg att att aaa gca aca gaa gag caa aag aaa aag	1249
Lys Ser Asp Pro Gly Ile Ile Lys Ala Thr Glu Glu Gln Lys Lys Lys	
400 405 410	
aca ata gtt gaa ctt gca gag aca gga agt ctg gac ctc agt ata ttc	1297
Thr Ile Val Glu Leu Ala Glu Thr Gly Ser Leu Asp Leu Ser Ile Phe	
415 420 425	
tgc agt acc tgt ttg ata cga aaa ccg gtg agg tcc aaa cat tgt ggt	1345
Cys Ser Thr Cys Leu Ile Arg Lys Pro Val Arg Ser Lys His Cys Gly	
430 435 440	
gtg tgc aac cgc tgt ata gca aaa ttt gat cat cat tgc cca tgg gtg	1393
Val Cys Asn Arg Cys Ile Ala Lys Phe Asp His His Cys Pro Trp Val	
445 450 455 460	
ggg aac tgt gta ggt gca ggc aac cat aga tat ttt atg ggc tac cta	1441
Gly Asn Cys Val Gly Ala Gly Asn His Arg Tyr Phe Met Gly Tyr Leu	
465 470 475	
ttc ttc ttg ctt ttt atg atc tgc tgg atg att tat ggt tgt ata tct	1489

[illegible]

tactctgagg ttttacggtc tgataatgaa gcacttgcac gagtatagta agtcatgttt 2589
 ttttgttcaa atttaaaagc cctgctaatt gcatgacaca ccacatagaa tgtatactag 2649
 cagatactat ccagtgaagc ataaattaga atttaatttg atgttcaaaa acagttccat 2709
 ttttaagggg taaggtggta ttttcaagaa aaggcagaac aaataatgca aaattctcag 2769
 taatagtgat acatggatat acttcctttt aaattctcag ctgcaaaata attgtagaca 2829
 aaataatggc atttaactaa agatggagca tgatctgtgt acatagcaca tgtgaataaa 2889
 agaaaagctg acagtatatt ctgggtttcaa taaaatgacc tatcagaaag tagaatttc 2948

<210> 65
 <211> 632
 <212> PRT
 <213> Homo sapiens

<400> 65
 Met Gln Arg Glu Glu Gly Phe Asn Thr Lys Met Ala Asp Gly Pro Asp
 1 5 10 15
 Glu Tyr Asp Thr Glu Ala Gly Cys Val Pro Leu Leu His Pro Glu Glu
 20 25 30
 Ile Lys Pro Gln Ser His Tyr Asn His Gly Tyr Gly Glu Pro Leu Gly
 35 40 45
 Arg Lys Thr His Ile Asp Asp Tyr Ser Thr Trp Asp Ile Val Lys Ala
 50 55 60
 Thr Gln Tyr Gly Ile Tyr Glu Arg Cys Arg Glu Leu Val Glu Ala Gly
 65 70 75 80
 Tyr Asp Val Arg Gln Pro Asp Lys Glu Asn Val Thr Leu Leu His Trp
 85 90 95
 Ala Ala Ile Asn Asn Arg Ile Asp Leu Val Lys Tyr Tyr Ile Ser Lys
 100 105 110
 Gly Ala Ile Val Asp Gln Leu Gly Gly Asp Leu Asn Ser Thr Pro Leu
 115 120 125
 His Trp Ala Thr Arg Gln Gly His Leu Ser Met Val Val Gln Leu Met
 130 135 140
 Lys Tyr Gly Ala Asp Pro Ser Leu Ile Asp Gly Glu Gly Cys Ser Cys
 145 150 155 160
 Ile His Leu Ala Ala Gln Phe Gly His Thr Ser Ile Val Ala Tyr Leu
 165 170 175
 Ile Ala Lys Gly Gln Asp Val Asp Met Met Asp Gln Asn Gly Met Thr
 180 185 190

Pro	Leu	Met	Trp	Ala	Ala	Tyr	Arg	Thr	His	Ser	Val	Asp	Pro	Thr	Arg	195	200	205
Leu	Leu	Leu	Thr	Phe	Asn	Val	Ser	Val	Asn	Leu	Gly	Asp	Lys	Tyr	His	210	215	220
Lys	Asn	Thr	Ala	Leu	His	Trp	Ala	Val	Leu	Ala	Gly	Asn	Thr	Thr	Val	225	230	235
Ile	Ser	Leu	Leu	Leu	Glu	Ala	Gly	Ala	Asn	Val	Asp	Ala	Gln	Asn	Ile	245	250	255
Lys	Gly	Glu	Ser	Ala	Leu	Asp	Leu	Ala	Lys	Gln	Arg	Lys	Asn	Val	Trp	260	265	270
Met	Ile	Asn	His	Leu	Gln	Glu	Ala	Arg	Gln	Ala	Lys	Gly	Tyr	Asp	Asn	275	280	285
Pro	Ser	Phe	Leu	Arg	Lys	Leu	Lys	Ala	Asp	Lys	Glu	Phe	Arg	Gln	Lys	290	295	300
Val	Met	Leu	Gly	Thr	Pro	Phe	Leu	Val	Ile	Trp	Leu	Val	Gly	Phe	Ile	305	310	315
Ala	Asp	Leu	Asn	Ile	Asp	Ser	Trp	Leu	Ile	Lys	Gly	Leu	Met	Tyr	Gly	325	330	335
Gly	Val	Trp	Ala	Thr	Val	Gln	Phe	Leu	Ser	Lys	Ser	Phe	Phe	Asp	His	340	345	350
Ser	Met	His	Ser	Ala	Leu	Pro	Leu	Gly	Ile	Tyr	Leu	Ala	Thr	Lys	Phe	355	360	365
Trp	Met	Tyr	Val	Thr	Trp	Phe	Phe	Trp	Phe	Trp	Asn	Asp	Leu	Asn	Phe	370	375	380
Leu	Phe	Ile	His	Leu	Pro	Phe	Leu	Ala	Asn	Ser	Val	Ala	Leu	Phe	Tyr	385	390	395
Asn	Phe	Gly	Lys	Ser	Trp	Lys	Ser	Asp	Pro	Gly	Ile	Ile	Lys	Ala	Thr	405	410	415
Glu	Glu	Gln	Lys	Lys	Lys	Thr	Ile	Val	Glu	Leu	Ala	Glu	Thr	Gly	Ser	420	425	430
Leu	Asp	Leu	Ser	Ile	Phe	Cys	Ser	Thr	Cys	Leu	Ile	Arg	Lys	Pro	Val	435	440	445
Arg	Ser	Lys	His	Cys	Gly	Val	Cys	Asn	Arg	Cys	Ile	Ala	Lys	Phe	Asp	450	455	460
His	His	Cys	Pro	Trp	Val	Gly	Asn	Cys	Val	Gly	Ala	Gly	Asn	His	Arg	465	470	475
Tyr	Phe	Met	Gly	Tyr	Leu	Phe	Phe	Leu	Leu	Phe	Met	Ile	Cys	Trp	Met	485	490	495

Ile Tyr Gly Cys Ile Ser Tyr Trp Gly Leu His Cys Glu Thr Thr Tyr
 500 505 510
 Thr Lys Asp Gly Phe Trp Thr Tyr Ile Thr Gln Ile Ala Thr Cys Ser
 515 520 525
 Pro Trp Met Phe Trp Met Phe Leu Asn Ser Val Phe His Phe Met Trp
 530 535 540
 Val Ala Val Leu Leu Met Cys Gln Met Tyr Gln Ile Ser Cys Leu Gly
 545 550 555 560
 Ile Thr Thr Asn Glu Arg Met Asn Ala Arg Arg Tyr Lys His Phe Lys
 565 570 575
 Val Thr Thr Thr Ser Ile Glu Ser Pro Phe Asn His Gly Cys Val Arg
 580 585 590
 Asn Ile Ile Asp Phe Phe Glu Phe Arg Cys Cys Gly Leu Phe Arg Pro
 595 600 605
 Val Ile Val Asp Trp Thr Arg Gln Tyr Thr Ile Glu Tyr Asp Gln Ile
 610 615 620
 Ser Gly Ser Gly Tyr Gln Leu Val
 625 630

<210> 66
 <211> 4715
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (108)..(2003)

<400> 66
 gaagaaggag gaggaggccc gcgtgcctc cggcggggct cgcgctcgcc ccgcgctcgc 60

cctccgcctc gcccgagccc cgggaggggtg aaacgctttc tcccagc atg cag cgg 116
 Met Gln Arg
 1

gag gag gga ttt aac acc aag atg gcg gac ggc ccg gat gag tac gat 164
 Glu Glu Gly Phe Asn Thr Lys Met Ala Asp Gly Pro Asp Glu Tyr Asp
 5 10 15

acc gaa gcg ggc tgt gtg ccc ctt ctc cac cca gag gaa atc aaa ccc 212
 Thr Glu Ala Gly Cys Val Pro Leu Leu His Pro Glu Glu Ile Lys Pro
 20 25 30 35

caa agc cat tat aac cat gga tat ggt gaa cct ctt gga cgg aaa act 260
 Gln Ser His Tyr Asn His Gly Tyr Gly Glu Pro Leu Gly Arg Lys Thr
 40 45 50

- cat -att gat gat-tac agc aca tgg-gac ata gtc aag-gct aca caa tat	308
His Ile Asp Asp Tyr Ser Thr Trp Asp Ile Val Lys Ala Thr Gln Tyr	
55 60 65	
gga ata tat gaa cgc tgt cga gaa ttg gtg gaa gca ggt tat gat gta	356
Gly Ile Tyr Glu Arg Cys Arg Glu Leu Val Glu Ala Gly Tyr Asp Val	
70 75 80	
cgg caa ccg gac aaa gaa aat gtt acc ctc ctc cat tgg gct gcc atc	404
Arg Gln Pro Asp Lys Glu Asn Val Thr Leu Leu His Trp Ala Ala Ile	
85 90 95	
aat aac aga ata gat tta gtc aaa tac tat att tcg aaa ggt gct att	452
Asn Asn Arg Ile Asp Leu Val Lys Tyr Tyr Ile Ser Lys Gly Ala Ile	
100 105 110 115	
gtg gat caa ctt gga ggg gac ctg aat tca act cca ttg cac tgg gcc	500
Val Asp Gln Leu Gly Gly Asp Leu Asn Ser Thr Pro Leu His Trp Ala	
120 125 130	
aca aga caa ggc cat cta tcc atg gtt gtg caa cta atg aaa tat ggt	548
Thr Arg Gln Gly His Leu Ser Met Val Val Gln Leu Met Lys Tyr Gly	
135 140 145	
gca gat cct tca tta att gat gga gaa gga tgt agc tgt att cat ctg	596
Ala Asp Pro Ser Leu Ile Asp Gly Glu Gly Cys Ser Cys Ile His Leu	
150 155 160	
gct gct cag ttc gga cat acc tca att gtt gct tat ctc ata gca aaa	644
Ala Ala Gln Phe Gly His Thr Ser Ile Val Ala Tyr Leu Ile Ala Lys	
165 170 175	
gga cag gat gta gat atg atg gat cag aat gga atg acg cct tta atg	692
Gly Gln Asp Val Asp Met Met Asp Gln Asn Gly Met Thr Pro Leu Met	
180 185 190 195	
tgg gca gca tat aga aca cat agt gtg gat cca act aga ttg ctt tta	740
Trp Ala Ala Tyr Arg Thr His Ser Val Asp Pro Thr Arg Leu Leu Leu	
200 205 210	
aca ttc aat gtt tca gtt aac ctt ggt gac aag tat cac aaa aac act	788
Thr Phe Asn Val Ser Val Asn Leu Gly Asp Lys Tyr His Lys Asn Thr	
215 220 225	
gct ctg cat tgg gca gtg cta gca ggg aat acc aca gtc att agc ctt	836
Ala Leu His Trp Ala Val Leu Ala Gly Asn Thr Thr Val Ile Ser Leu	
230 235 240	
ctt ctg gaa gct gga gct aat gtt gat gcc cag aat atc aag ggc gaa	884
Leu Leu Glu Ala Gly Ala Asn Val Asp Ala Gln Asn Ile Lys Gly Glu	
245 250 255	
tca gcg ctt gat ttg gca aaa cag aga aaa aat gtg tgg atg atc aac	932
Ser Ala Leu Asp Leu Ala Lys Gln Arg Lys Asn Val Trp Met Ile Asn	
260 265 270 275	
cac tta caa gag gca agg caa gca aaa gga tat gac aat ccg tcc ttc	980

His-Leu	Gln	Glu	Ala	Arg	Gln	Ala	Lys	Gly	Tyr	Asp	Asn	Pro	Ser	Phe			
			280					285					290				
ctt aga aag ctg aaa gct gat aag gaa ttt cgg cag aaa gta atg tta	1028																
Leu Arg Lys Leu Lys Ala Asp Lys Glu Phe Arg Gln Lys Val Met Leu			295				300					305					
gga act cct ttc cta gtt att tgg ctg gtt ggg ttt ata gca gac cta	1076																
Gly Thr Pro Phe Leu Val Ile Trp Leu Val Gly Phe Ile Ala Asp Leu			310				315				320						
aat att gat tct tgg ctc att aaa ggg cta atg tat ggt ggt gtt tgg	1124																
Asn Ile Asp Ser Trp Leu Ile Lys Gly Leu Met Tyr Gly Gly Val Trp			325			330				335							
gct aca gta cag ttt ctt tca aaa tcc ttt ttc gat cat tca atg cat	1172																
Ala Thr Val Gln Phe Leu Ser Lys Ser Phe Phe Asp His Ser Met His			340		345			350								355	
agt gca ttg ccc ctt ggg ata tat ttg gca acc aaa ttc tgg atg tat	1220																
Ser Ala Leu Pro Leu Gly Ile Tyr Leu Ala Thr Lys Phe Trp Met Tyr			360				365						370				
gtg acg tgg ttc ttc tgg ttt tgg aat gat ctc aac ttt tta ttt atc	1268																
Val Thr Trp Phe Phe Trp Phe Trp Asn Asp Leu Asn Phe Leu Phe Ile			375				380					385					
cat ctt cca ttc ctt gcc aat agt gtt gca ctt ttc tac aat ttt gga	1316																
His Leu Pro Phe Leu Ala Asn Ser Val Ala Leu Phe Tyr Asn Phe Gly			390				395				400						
aaa tct tgg aaa tca gat cca ggg att att aaa gca aca gaa gag caa	1364																
Lys Ser Trp Lys Ser Asp Pro Gly Ile Ile Lys Ala Thr Glu Glu Gln			405			410			415								
aag aaa aag aca ata gtt gaa ctt gca gag aca gga agt ctg gac ctc	1412																
Lys Lys Lys Thr Ile Val Glu Leu Ala Glu Thr Gly Ser Leu Asp Leu			420		425			430					435				
agt ata ttc tgc agt acc tgt ttg ata cga aaa ccg gtg agg tcc aaa	1460																
Ser Ile Phe Cys Ser Thr Cys Leu Ile Arg Lys Pro Val Arg Ser Lys			440				445					450					
cat tgt ggt gtg tgc aac cgc tgt ata gca aaa ttt gat cat cat tgc	1508																
His Cys Gly Val Cys Asn Arg Cys Ile Ala Lys Phe Asp His His Cys			455				460					465					
cca tgg gtg ggt aac tgt gta ggt gca ggc aac cat aga tat ttt atg	1556																
Pro Trp Val Gly Asn Cys Val Gly Ala Gly Asn His Arg Tyr Phe Met			470			475						480					
ggc tac cta ttc ttc ttg ctt ttt atg atc tgc tgg atg att tat ggt	1604																
Gly Tyr Leu Phe Phe Leu Leu Phe Met Ile Cys Trp Met Ile Tyr Gly			485			490				495							
tgt ata tct tac tgg gga ctc cac tgt gag acc act tac acc aag gat	1652																
Cys Ile Ser Tyr Trp Gly Leu His Cys Glu Thr Thr Tyr Thr Lys Asp																	

500	505	510	515	
gga ttt tgg aca tac att act cag att gcc acg tgt tca cct tgg atg				1700
Gly Phe Trp Thr Tyr Ile Thr Gln Ile Ala Thr Cys Ser Pro Trp Met				
	520	525	530	
ttt tgg atg ttc ctg aac agt gtt ttc cac ttc atg tgg gtg gct gta				1748
Phe Trp Met Phe Leu Asn Ser Val Phe His Phe Met Trp Val Ala Val				
	535	540	545	
tta ctc atg tgt cag atg tac cag ata tca tgt tta ggt att act aca				1796
Leu Leu Met Cys Gln Met Tyr Gln Ile Ser Cys Leu Gly Ile Thr Thr				
	550	555	560	
aat gaa aga atg aat gcc agg aga tac aag cac ttt aaa gtc aca aca				1844
Asn Glu Arg Met Asn Ala Arg Arg Tyr Lys His Phe Lys Val Thr Thr				
	565	570	575	
acg tct att gaa agc cca ttc aac cat gga tgt gta aga aat att ata				1892
Thr Ser Ile Glu Ser Pro Phe Asn His Gly Cys Val Arg Asn Ile Ile				
	580	585	590	595
gac ttc ttt gaa ttt cga tgc tgt ggc ctc ttt cgt cct gtt atc gtg				1940
Asp Phe Phe Glu Phe Arg Cys Cys Gly Leu Phe Arg Pro Val Ile Val				
	600	605	610	
gac tgg acc agg cag tat aca ata gaa tat gac caa ata tca gga tct				1988
Asp Trp Thr Arg Gln Tyr Thr Ile Glu Tyr Asp Gln Ile Ser Gly Ser				
	615	620	625	
ggg tac cag ctg gtg tagcgacatc ttatcctatg aagcatattg ctgagtgggtg				2043
Gly Tyr Gln Leu Val				
	630			
cctgaaaatt gtgtctgtcc gtgtctttct cacactogaa tccacatcct ttgaacaaga				2103
gcatgctatg tgtagggcta atgggtgaatt ttacagtctt tttttcaaca cttttattaa				2163
caaaagtaaa catggacaga acacactgcc atttctggga agagtaaaga tgataaaaaa				2223
taattttaat gggtcttaat gtggaaattc acaacatact caacttttgg gttttgttct				2283
cacagtattt ttcacaaaaa aagggtaaac ttattctatt gacagacatg gtgtactgat				2343
cagaaatggt cagttttaac taaaactaaa tttatgttat ttggctaaat gttatgatgc				2403
agtctagtac gagtattgca tctaattcca ggagcattgt tttaagttga ttgactagtt				2463
attatgtaca tttcagaatg tacacataaa tactgtgatg aaaatcatgt gattgggatc				2523
tactgtgatg ttgtcttcaa aggcaggaga aaataatggt cacaataaaa tgtgctaaca				2583
atgttttgtt tctatcagct gttgcaatgc tgatatattt ctagttcagt gaaataattt				2643
gtagtaacct tactctgagg ttttacggtc tgataatgaa gcacttgcac gagtatagta				2703
agtcatgttt ttttgttcaa atttaaaagc cctgctaatt gcatgacaca ccacatagaa				2763

tgtatactag cagatactat ccagtgaagc ataaattaga atttaatttg atgttcaaaa 2823
 acagttccat ttttaagggt taagggtgga ttttcaagaa aaggcagaac aaataatgca 2883
 aaattctcag taatagtgat acatggatat acttcctttt aaattctcag ctgcaaaaata 2943
 attgtagaca aaataatggc atttaactaa agatggagca tgatctaagt acatagcaca 3003
 tgtgaataaa agaaaagctg acagtatatt ctggtttcaa taaaatgacc tatcagaaaag 3063
 tagaatttca tccccagag tatttcagtt tatccaatat tgagtaagtt ctgaaacagt 3123
 tttagaaaaa attttctttt tgttaaagt gatgcactga tcaatttttg tcacagcatt 3183
 ttcatacctt catggtggac tactagtcac tgcttccata aatattgttt acagggtgag 3243
 atttggttta ttcattctaa gtgctgtagc aaactgtggt tcgagcaacc tgtgggaaat 3303
 ctgtgagagg gaatggggtg ggagatgtgg gggaatggtg gtcagactga tgacagatcc 3363
 tagaccaatg taaagaatgt gtatctgtat ataaataatt tatcaaatag ttttctcttt 3423
 gtgtctgtgt tagtggtttt aaagctgctc atttcatttt gtccaacca aaagaaaagg 3483
 gagataacta atgagcttct agtgatgttc aaaattgctg ttaataggca ttataccctg 3543
 caagttcact gcatgtctga tgcttggtaa aactagtctt ccctgtaaaa tgcagattac 3603
 aggtattaaa gcaatctagt ggtatacccg ccccttgctt tagtaagagg agcagtgaaa 3663
 tgtatatagt tgatgttcag tatttccaag taccattttt atatagtagc ttatttgacc 3723
 ataagtcaca catcaaaaaa agattaccct tagtgatatgt gttttaatat tagaaaattg 3783
 gcatatgtac tttatttttg aaaaggggaag agatgggtgt ggggtggcaa tagcattgtg 3843
 ccattttgtc atagaatgta aaaattgggt aactttacaa atgtcagcta gttttgacta 3903
 ctaattgggg gaaatttttag ataattttta aattcaaagt tatttataaa atgctagaat 3963
 ttgttttaat tttttgtatt ttgagccact tcacatgaag actcagttgc atttttatcg 4023
 aatacatttt tatcaacagt taaagactat ggtgggtttt tcagagtttg gctaagaatg 4083
 ttgttaccat cttctttgtt tgtggtacaa tattttcagt gcaaaagaga tgtcattcag 4143
 ttaaaaagac aaacctctag atgtgtaatt acatggaaaa tactagcaat gtgaatgctt 4203
 ttgtagtaac catcttgtag tacctgtgaa atctataact cagaaatggc cagatgggtca 4263
 ggagccagct atgcagcagt ataccatctg ttttaattatt ttgtaggtcc tgtgtgtgga 4323
 accaactata aaccagttc taaagtgtg tatgatggtg aacctttggg aatagttctt 4383
 atcaacttaa ttggatactt ttagcaaata ggaacttaat tctcagcact gaacatgaat 4443

-tacttcocttg gagttttttt tcattcatat ttttgttgtt tccäggaatt tatttgatāt 4503
 taatgggCGT aaaacagcat cattgtactt aagctatgga tgtttttatt ttatatatttc 4563
 tttatttata actgtgccaa gtattatttt gctacttacc gtgttattct gtggaaagaa 4623
 aaacctgtaa agtgtttaat aaattagccc tccttacata aattaaatgt caaaattttg 4683
 taaaatatta atcagaataa atactgactc tt 4715

<210> 67
 <211> 498
 <212> PRT
 <213> Homo sapiens

<400> 67
 Met Ala Arg Leu Glu Val Ile Glu Leu Pro His Ser Pro Gln Asn Leu
 1 5 10 15
 Leu Val Ser Pro Asn Ser Ser His Ser His Ala Val Val Leu Ser Trp
 20 25 30
 Val Arg Pro Phe Asp Gly Asn Ser Pro Ile Leu Tyr Tyr Ile Val Glu
 35 40 45
 Leu Ser Glu Asn Asn Ser Pro Trp Lys Val His Leu Ser Asn Val Gly
 50 55 60
 Pro Glu Met Thr Gly Val Thr Val Ser Gly Leu Thr Pro Ala Arg Thr
 65 70 75 80
 Tyr Gln Phe Arg Val Cys Ala Val Asn Glu Val Gly Arg Gly Gln Tyr
 85 90 95
 Ser Ala Glu Thr Ser Arg Leu Met Leu Pro Glu Glu Pro Pro Ser Ala
 100 105 110
 Pro Pro Lys Asn Ile Val Ala Ser Gly Arg Thr Asn Gln Ser Ile Met
 115 120 125
 Val Gln Trp Gln Pro Pro Pro Glu Thr Glu His Asn Gly Val Leu Arg
 130 135 140
 Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly Leu Pro Gly Glu Tyr Gln
 145 150 155 160
 Gln Arg Asn Ile Thr Ser Pro Glu Val Asn Tyr Cys Leu Val Thr Asp
 165 170 175
 Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln Val Ala Ala Tyr Asn Gly
 180 185 190
 Ala Gly Leu Gly Val Phe Ser Arg Ala Val Thr Glu Tyr Thr Leu Gln
 195 200 205
 Gly Val Pro Thr Ala Pro Pro Gln Asn Val Gln Thr Glu Ala Val Asn

--210 -- --215 -- --220 --
 Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro Pro Pro Gln Gln Phe Ile
 225 230 235 240
 Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu Ala Trp Pro Ala Asp Ala
 245 250 255
 Pro Glu Ala Val Thr Val Val Thr Ile Ala Pro Asp Phe His Gly Val
 260 265 270
 His His Gly His Ile Thr Asn Leu Lys Lys Phe Thr Ala Tyr Phe Thr
 275 280 285
 Ser Val Leu Cys Phe Thr Thr Pro Gly Asp Gly Pro Pro Ser Thr Pro
 290 295 300
 Gln Leu Val Trp Thr Gln Glu Asp Lys Pro Gly Ala Val Gly His Leu
 305 310 315 320
 Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu Lys Val Ser Trp Gln Glu
 325 330 335
 Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly Tyr Gln Ile Ser Trp Glu
 340 345 350
 Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr His Thr Leu Asn Ser Thr
 355 360 365
 Met His Glu Tyr Lys Ile Gln Gly Leu Ser Ser Leu Thr Thr Tyr Thr
 370 375 380
 Ile Asp Val Ala Ala Val Thr Ala Val Gly Thr Gly Leu Val Thr Ser
 385 390 395 400
 Ser Thr Ile Ser Ser Gly Val Pro Pro Asp Leu Pro Gly Ala Pro Ser
 405 410 415
 Asn Leu Val Ile Ser Asn Ile Ser Pro Arg Ser Ala Thr Leu Gln Phe
 420 425 430
 Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile Ser Arg Trp Ile Val Glu
 435 440 445
 Gly Gln Met Arg Pro Glu Gly Val Gly Leu Pro Ala Glu Val Thr Gln
 450 455 460
 Pro Ser His Glu Ala Gly Leu Glu Pro Ala Asn Leu Gly Ser Leu Trp
 465 470 475 480
 Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser Gln Lys Leu Trp Glu Phe
 485 490 495
 Ser Cys

<210> 68
 <211> 1902
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (22)..(1515)

<400> 68

```

gaaggaggga atgactccag g atg gcc cgg ctg gaa gtg att gaa ctg cct 51
                        Met Ala Arg Leu Glu Val Ile Glu Leu Pro
                          1                      5              10

cat tca cct cag aac ctc ctg gtc agc cct aat tct tcc cac agc cac 99
His Ser Pro Gln Asn Leu Leu Val Ser Pro Asn Ser Ser His Ser His
                        15                      20              25

gcc gtg gtg ctc tct tgg gtc cgg ccc ttt gat gga aac agt cct att 147
Ala Val Val Leu Ser Trp Val Arg Pro Phe Asp Gly Asn Ser Pro Ile
                        30                      35              40

ctt tat tac atc gtg gag ctg tct gaa aac aac tct cca tgg aag gtg 195
Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn Ser Pro Trp Lys Val
                        45                      50              55

cat ctg tca aac gtt ggc cct gag atg aca ggc gtc acc gtg agt ggc 243
His Leu Ser Asn Val Gly Pro Glu Met Thr Gly Val Thr Val Ser Gly
                        60                      65              70

ctg act ccg gct cgt acc tat caa ttc cgg gtg tgc gcg gtg aat gaa 291
Leu Thr Pro Ala Arg Thr Tyr Gln Phe Arg Val Cys Ala Val Asn Glu
                        75                      80              85

gtg ggc agg ggc cag tac agt gcc gag aca agc agg ttg atg cta cct 339
Val Gly Arg Gly Gln Tyr Ser Ala Glu Thr Ser Arg Leu Met Leu Pro
                        95                      100             105

gaa gaa cca ccc agt gct ccc ccg aaa aat ata gtg gcc agt ggg cgg 387
Glu Glu Pro Pro Ser Ala Pro Pro Lys Asn Ile Val Ala Ser Gly Arg
                        110                      115             120

act aat cag tcc att atg gtc cag tgg cag cca ccc cca gaa aca gag 435
Thr Asn Gln Ser Ile Met Val Gln Trp Gln Pro Pro Pro Glu Thr Glu
                        125                      130             135

cac aac ggg gtg ttg cgt gga tac atc ctc agg tac cgc ctg gct ggc 483
His Asn Gly Val Leu Arg Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly
                        140                      145             150

ctt ccc gga gag tac cag cag cgg aac atc acc agc ccg gag gtg aac 531
Leu Pro Gly Glu Tyr Gln Gln Arg Asn Ile Thr Ser Pro Glu Val Asn
                        155                      160             165             170

tac tgc ctg gtg aca gac ctg atc atc tgg aca cag tat gag ata cag 579
Tyr Cys Leu Val Thr Asp Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln

```

175										180										185										
gtg	gcg	gcg	tac	aac	ggg	gcc	ggt	ctg	ggc	gtc	ttc	agc	agg	gca	gtg	627														
Val	Ala	Ala	Tyr	Asn	Gly	Ala	Gly	Leu	Gly	Val	Phe	Ser	Arg	Ala	Val															
			190					195					200																	
acc	gag	tac	acc	ttg	cag	gga	gtg	ccc	acc	gcg	ccc	ccg	cag	aac	gtg	675														
Thr	Glu	Tyr	Thr	Leu	Gln	Gly	Val	Pro	Thr	Ala	Pro	Pro	Gln	Asn	Val															
			205				210					215																		
cag	acg	gaa	gcc	gtg	aac	tcc	acc	acc	att	cag	ttc	ctg	tg	aac	cct	723														
Gln	Thr	Glu	Ala	Val	Asn	Ser	Thr	Thr	Ile	Gln	Phe	Leu	Trp	Asn	Pro															
			220				225				230																			
ccg	cct	cag	cag	ttt	atc	aat	ggc	atc	aac	cag	gga	tac	aag	ctt	ctg	771														
Pro	Pro	Gln	Gln	Phe	Ile	Asn	Gly	Ile	Asn	Gln	Gly	Tyr	Lys	Leu	Leu															
235					240					245					250															
gca	tg	ccg	gca	gat	gcc	ccc	gag	gct	gtc	act	gtg	gtc	act	att	gcc	819														
Ala	Trp	Pro	Ala	Asp	Ala	Pro	Glu	Ala	Val	Thr	Val	Val	Thr	Ile	Ala															
				255					260					265																
cca	gat	ttc	cac	gga	gtc	cac	cat	gga	cac	ata	acg	aac	ctg	aag	aag	867														
Pro	Asp	Phe	His	Gly	Val	His	His	Gly	His	Ile	Thr	Asn	Leu	Lys	Lys															
			270					275					280																	
ttt	acc	gcc	tac	ttc	act	tcc	gtt	ctg	tgc	ttc	acc	acc	cct	ggg	gac	915														
Phe	Thr	Ala	Tyr	Phe	Thr	Ser	Val	Leu	Cys	Phe	Thr	Thr	Pro	Gly	Asp															
			285				290					295																		
ggg	cct	ccc	agc	aca	cct	cag	ctg	gtc	tg	act	cag	gaa	gac	aaa	cca	963														
Gly	Pro	Pro	Ser	Thr	Pro	Gln	Leu	Val	Trp	Thr	Gln	Glu	Asp	Lys	Pro															
	300					305					310																			
gga	gct	gtg	gga	cat	ctg	agt	ttc	aca	gag	atc	ttg	gac	aca	tct	ctc	1011														
Gly	Ala	Val	Gly	His	Leu	Ser	Phe	Thr	Glu	Ile	Leu	Asp	Thr	Ser	Leu															
315					320					325					330															
aag	gtc	agc	tg	cag	gag	ccc	ctg	gag	aaa	aat	ggc	atc	att	act	ggc	1059														
Lys	Val	Ser	Trp	Gln	Glu	Pro	Leu	Glu	Lys	Asn	Gly	Ile	Ile	Thr	Gly															
				335					340				345																	
tat	cag	atc	tct	tg	gaa	gtg	tac	ggc	agg	aac	gac	tct	cgt	ctc	acg	1107														
Tyr	Gln	Ile	Ser	Trp	Glu	Val	Tyr	Gly	Arg	Asn	Asp	Ser	Arg	Leu	Thr															
			350					355					360																	
cac	acc	ctg	aac	agc	acg	atg	cac	gag	tac	aag	atc	caa	ggc	ctc	tca	1155														
His	Thr	Leu	Asn	Ser	Thr	Met	His	Glu	Tyr	Lys	Ile	Gln	Gly	Leu	Ser															
			365				370					375																		
tct	ctc	acc	acc	tac	acc	atc	gac	gtg	gcc	gct	gtg	act	gcc	gtg	ggc	1203														
Ser	Leu	Thr	Thr	Tyr	Thr	Ile	Asp	Val	Ala	Ala	Val	Thr	Ala	Val	Gly															
	380					385					390																			
act	ggc	ctg	gtg	act	tca	tcc	acc	att	tct	tct	gga	gtg	ccc	cca	gac	1251														
Thr	Gly	Leu	Val	Thr	Ser	Ser	Thr	Ile	Ser	Ser	Gly	Val	Pro	Pro	Asp															
395					400					405					410															

ctt cct ggt gcc cca tcc aac ctg gtc att tcc aac atc agc cct cgc 1299
 Leu Pro Gly Ala Pro Ser Asn Leu Val Ile Ser Asn Ile Ser Pro Arg
 415 420 425

tcc gcc acc ctt cag ttc cgg cca ggc tat gac ggg aaa acg tcc atc 1347
 Ser Ala Thr Leu Gln Phe Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile
 430 435 440

tcc agg tgg att gtt gag ggg cag atg aga cct gaa ggt gtt gga tta 1395
 Ser Arg Trp Ile Val Glu Gly Gln Met Arg Pro Glu Gly Val Gly Leu
 445 450 455

cct gcc gag gtc aca cag cca agc cat gaa gcc gga ttg gag cct gca 1443
 Pro Ala Glu Val Thr Gln Pro Ser His Glu Ala Gly Leu Glu Pro Ala
 460 465 470

aac ctc gga agt ctg tgg ctg ctc agc ctg gtg tat tgg tgt tac agc 1491
 Asn Leu Gly Ser Leu Trp Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser
 475 480 485 490

cag aaa ctt tgg gaa ttc tct tgt tagttgggta gttttactgt aattttctat 1545
 Gln Lys Leu Trp Glu Phe Ser Cys
 495

aaagaattca tatcatctgt taatggcgac agtttttggt tcttcctttg aattttttat 1605

attctttctt tctctttttt gtttcttctt ctttgagtat tttgtaatct tactgggagg 1665

gctaaagcgt cttctatcat atcgaattgg gacaatgata gaagacaatc tttgttttgt 1725

cactctaaag aaattattgt aagattttat catcagggtat gacatttaca ccattgatgt 1785

aggcttttta aaaaatatat ccagcctgta ttggggttaag atgattcttt tctgatcctg 1845

atttcctagg agttgggttt ttttttttta aagcataaat aaatttaatt gcatcag 1902

<210> 69

<211> 498

<212> PRT

<213> Homo sapiens

<400> 69

Met Ala Arg Leu Glu Val Ile Glu Leu Pro His Ser Pro Gln Asn Leu
 1 5 10 15

Leu Val Ser Pro Asn Ser Ser His Ser His Ala Val Val Leu Ser Trp
 20 25 30

Val Arg Pro Phe Asp Gly Asn Ser Pro Ile Leu Tyr Tyr Ile Val Glu
 35 40 45

Leu Ser Glu Asn Asn Ser Pro Trp Lys Val His Leu Ser Asn Val Gly
 50 55 60

Pro Glu Met Thr Gly Val Thr Val Ser Gly Leu Thr Pro Ala Arg Thr

65					70					75					80
Tyr	Gln	Phe	Arg	Val	Cys	Ala	Val	Asn	Glu	Val	Gly	Arg	Gly	Gln	Tyr
				85					90					95	
Ser	Ala	Glu	Thr	Ser	Arg	Leu	Met	Leu	Pro	Glu	Glu	Pro	Pro	Ser	Ala
			100					105					110		
Pro	Pro	Lys	Asn	Ile	Val	Ala	Ser	Gly	Arg	Thr	Asn	Gln	Ser	Ile	Met
		115					120					125			
Val	Gln	Trp	Gln	Pro	Pro	Pro	Glu	Thr	Glu	His	Asn	Gly	Val	Leu	Arg
	130					135					140				
Gly	Tyr	Ile	Leu	Arg	Tyr	Arg	Leu	Ala	Gly	Leu	Pro	Gly	Glu	Tyr	Gln
145					150					155					160
Gln	Arg	Asn	Ile	Thr	Ser	Pro	Glu	Val	Asn	Tyr	Cys	Leu	Val	Thr	Asp
			165						170					175	
Leu	Ile	Ile	Trp	Thr	Gln	Tyr	Glu	Ile	Gln	Val	Ala	Ala	Tyr	Asn	Gly
			180					185					190		
Ala	Gly	Leu	Gly	Val	Phe	Ser	Arg	Ala	Val	Thr	Glu	Tyr	Thr	Leu	Gln
		195					200					205			
Gly	Val	Pro	Thr	Ala	Pro	Pro	Gln	Asn	Val	Gln	Thr	Glu	Ala	Val	Asn
	210					215					220				
Ser	Thr	Thr	Ile	Gln	Phe	Leu	Trp	Asn	Pro	Pro	Pro	Gln	Gln	Phe	Ile
225				230						235					240
Asn	Gly	Ile	Asn	Gln	Gly	Tyr	Lys	Leu	Leu	Ala	Trp	Pro	Ala	Asp	Ala
			245					250						255	
Pro	Glu	Ala	Val	Thr	Val	Val	Thr	Ile	Ala	Pro	Asp	Phe	His	Gly	Val
			260					265					270		
His	His	Gly	His	Ile	Thr	Asn	Leu	Lys	Lys	Phe	Thr	Ala	Tyr	Phe	Thr
		275					280					285			
Ser	Val	Leu	Cys	Phe	Thr	Thr	Pro	Gly	Asp	Gly	Pro	Pro	Ser	Thr	Pro
	290					295					300				
Gln	Leu	Val	Trp	Thr	Gln	Glu	Asp	Lys	Pro	Gly	Ala	Val	Gly	His	Leu
305					310					315					320
Ser	Phe	Thr	Glu	Ile	Leu	Asp	Thr	Ser	Leu	Lys	Val	Ser	Trp	Gln	Glu
			325						330					335	
Pro	Leu	Glu	Lys	Asn	Gly	Ile	Ile	Thr	Gly	Tyr	Gln	Ile	Ser	Trp	Glu
			340					345					350		
Val	Tyr	Gly	Arg	Asn	Asp	Ser	Arg	Leu	Thr	His	Thr	Leu	Asn	Ser	Thr
		355					360					365			
Thr	His	Glu	Tyr	Lys	Ile	Gln	Gly	Leu	Ser	Ser	Leu	Thr	Thr	Tyr	Thr

370	375	380
Ile Asp Val Ala Ala Val Thr Ala Val Gly Thr Gly Leu Val Thr Ser		
385	390	395 400
Ser Thr Ile Ser Ser Gly Val Pro Pro Asp Leu Pro Gly Ala Pro Ser		
	405	410 415
Asn Leu Val Ile Ser Asn Ile Ser Pro Arg Ser Ala Thr Leu Gln Phe		
	420	425 430
Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile Ser Arg Trp Ile Val Glu		
	435	440 445
Gly Gln Met Arg His Gln Gly Val Gly Leu Pro Ala Glu Val Thr Gln		
	450	455 460
Pro Ser His Glu Ala Gly Leu Glu Pro Ala Asn Leu Gly Ser Leu Trp		
465	470	475 480
Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser Gln Lys Leu Trp Glu Phe		
	485	490 495

Ser Cys

<210> 70
 <211> 1902
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (22)..(1515)

<400> 70	
gaaggaggga atgactccag g atg gcc cgg ctg gaa gtg att gaa ctg cct	51
Met Ala Arg Leu Glu Val Ile Glu Leu Pro	
1 5 10	
cat tca cct cag aac ctc ctg gtc agc cct aat tct tcc cac agc cac	99
His Ser Pro Gln Asn Leu Leu Val Ser Pro Asn Ser Ser His Ser His	
15 20 25	
gcc gtg gtg ctc tct tgg gtc cgg ccc ttt gat gga aac agt cct att	147
Ala Val Val Leu Ser Trp Val Arg Pro Phe Asp Gly Asn Ser Pro Ile	
30 35 40	
ctt tat tac atc gtg gag ctg tct gaa aac aac tct cca tgg aag gtg	195
Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn Ser Pro Trp Lys Val	
45 50 55	
cat ctg tca aac gtt ggc cct gag atg aca ggc gtc acc gtg agt ggc	243
His Leu Ser Asn Val Gly Pro Glu Met Thr Gly Val Thr Val Ser Gly	
60 65 70	

ctg act ccg gct cgt acc tat caa ttc cgg gtg tgc gcg gtg aat gaa	291
Leu Thr Pro Ala Arg Thr Tyr Gln Phe Arg Val Cys Ala Val Asn Glu	
75 80 85 90	
gtg ggc agg ggc cag tac agt gcc gag aca agc agg ttg atg cta cct	339
Val Gly Arg Gly Gln Tyr Ser Ala Glu Thr Ser Arg Leu Met Leu Pro	
95 100 105	
gaa gaa cca ccc agt gct ccc ccg aaa aat ata gtg gcc agt ggg cgg	387
Glu Glu Pro Pro Ser Ala Pro Pro Lys Asn Ile Val Ala Ser Gly Arg	
110 115 120	
act aat cag tcc att atg gtc cag tgg cag cca ccc cca gaa aca gag	435
Thr Asn Gln Ser Ile Met Val Gln Trp Gln Pro Pro Pro Glu Thr Glu	
125 130 135	
cac aac ggg gtg ttg cgt gga tac atc ctc agg tac cgc ctg gct ggc	483
His Asn Gly Val Leu Arg Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly	
140 145 150	
ctt ccc gga gag tac cag cag cgg aac atc acc agc ccg gag gtg aac	531
Leu Pro Gly Glu Tyr Gln Gln Arg Asn Ile Thr Ser Pro Glu Val Asn	
155 160 165 170	
tac tgc ctg gtg aca gac ctg atc atc tgg aca cag tat gag ata cag	579
Tyr Cys Leu Val Thr Asp Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln	
175 180 185	
gtg gcg gcg tac aac ggg gcc ggt ctg ggc gtc ttc agc agg gca gtg	627
Val Ala Ala Tyr Asn Gly Ala Gly Leu Gly Val Phe Ser Arg Ala Val	
190 195 200	
acc gag tac acc ttg cag gga gtg ccc acc gcg ccc ccg cag aac gtg	675
Thr Glu Tyr Thr Leu Gln Gly Val Pro Thr Ala Pro Pro Gln Asn Val	
205 210 215	
cag acg gaa gcc gtg aac tcc acc acc att cag ttc ctg tgg aac cct	723
Gln Thr Glu Ala Val Asn Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro	
220 225 230	
ccg cct cag cag ttt atc aat ggc atc aac cag gga tac aag ctt ctg	771
Pro Pro Gln Gln Phe Ile Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu	
235 240 245 250	
gca tgg ccg gca gat gcc ccc gag gct gtc act gtg gtc act att gcc	819
Ala Trp Pro Ala Asp Ala Pro Glu Ala Val Thr Val Val Thr Ile Ala	
255 260 265	
cca gat ttc cac gga gtc cac cat gga cac ata acg aac ctg aag aag	867
Pro Asp Phe His Gly Val His His Gly His Ile Thr Asn Leu Lys Lys	
270 275 280	
ttt acc gcc tac ttc act tcc gtt ctg tgc ttc acc acc cct ggg gac	915
Phe Thr Ala Tyr Phe Thr Ser Val Leu Cys Phe Thr Thr Pro Gly Asp	
285 290 295	
ggg cct ccc agc aca cct cag ctg gtc tgg act cag gaa gac aaa cca	963

Gly	Pro	Pro	Ser	Thr	Pro	Gln	Leu	Val	Trp	Thr	Gln	Glu	Asp	Lys	Pro		
300						305					310						
gga gct gtg gga cat ctg agt ttc aca gag atc ttg gac aca tct ctc 1011																	
Gly	Ala	Val	Gly	His	Leu	Ser	Phe	Thr	Glu	Ile	Leu	Asp	Thr	Ser	Leu		
315					320					325					330		
aag gtc agc tgg cag gag ccc ctg gag aaa aat ggc atc att act ggc 1059																	
Lys	Val	Ser	Trp	Gln	Glu	Pro	Leu	Glu	Lys	Asn	Gly	Ile	Ile	Thr	Gly		
				335					340					345			
tat cag atc tct tgg gaa gtg tac ggc agg aac gac tct cgt ctc acg 1107																	
Tyr	Gln	Ile	Ser	Trp	Glu	Val	Tyr	Gly	Arg	Asn	Asp	Ser	Arg	Leu	Thr		
			350					355					360				
cac acc ctg aac agc acg acg cac gag tac aag atc caa ggc ctc tca 1155																	
His	Thr	Leu	Asn	Ser	Thr	Thr	His	Glu	Tyr	Lys	Ile	Gln	Gly	Leu	Ser		
		365					370					375					
tct ctc acc acc tac acc atc gac gtg gcc gct gtg act gcc gtg ggc 1203																	
Ser	Leu	Thr	Thr	Tyr	Thr	Ile	Asp	Val	Ala	Ala	Val	Thr	Ala	Val	Gly		
	380					385					390						
act ggc ctg gtg act tca tcc acc att tct tct gga gtg ccc cca gac 1251																	
Thr	Gly	Leu	Val	Thr	Ser	Ser	Thr	Ile	Ser	Ser	Gly	Val	Pro	Pro	Asp		
395					400					405					410		
ctt cct ggt gcc cca tcc aac ctg gtc att tcc aac atc agc cct cgc 1299																	
Leu	Pro	Gly	Ala	Pro	Ser	Asn	Leu	Val	Ile	Ser	Asn	Ile	Ser	Pro	Arg		
				415					420					425			
tcc gcc acc ctt cag ttc cgg cca ggc tat gac ggg aaa acg tcc atc 1347																	
Ser	Ala	Thr	Leu	Gln	Phe	Arg	Pro	Gly	Tyr	Asp	Gly	Lys	Thr	Ser	Ile		
			430					435					440				
tcc agg tgg att gtt gag ggg cag atg aga cat caa ggt gtt gga tta 1395																	
Ser	Arg	Trp	Ile	Val	Glu	Gly	Gln	Met	Arg	His	Gln	Gly	Val	Gly	Leu		
		445					450					455					
cct gcc gag gtc aca cag cca agc cat gaa gcc gga ttg gag cct gca 1443																	
Pro	Ala	Glu	Val	Thr	Gln	Pro	Ser	His	Glu	Ala	Gly	Leu	Glu	Pro	Ala		
	460					465					470						
aac ctc gga agt ctg tgg ctg ctc agc ctg gtg tat tgg tgt tac agc 1491																	
Asn	Leu	Gly	Ser	Leu	Trp	Leu	Leu	Ser	Leu	Val	Tyr	Trp	Cys	Tyr	Ser		
475					480					485				490			
cag aaa ctt tgg gaa ttc tct tgt tagttggtta gttttactgt aattttctat 1545																	
Gln	Lys	Leu	Trp	Glu	Phe	Ser	Cys										
				495													
aaagaattca tatcatctgt taatggcgac agtttttggt tcttcctttg aattttttat 1605																	
attcttttctt tctctttttt gtttcttctt ctttgagtat tttgtaatat tactgggagg 1665																	
gctaaagcgt cttctatcat atcgaattgg gacaatgata gaagacaatc tttgttttgt 1725																	

cactctaaag aaattattgt aagattttat catcaggtat gacatttaca ccattgatgt 1785

aggcttttta aaaaatatat ccagcctgta ttgggttaag atgattcttt tctgatcctg 1845

atttcctagg agttgggtttt ttttttttta aagcataaat aaatttaatt gcatcag 1902

<210> 71

<211> 245

<212> PRT

<213> Homo sapiens

<400> 71

Met Pro Val Gln Leu Ser Glu His Pro Glu Trp Asn Glu Ser Met His
1 5 10 15

Ser Leu Arg Ile Ser Val Gly Gly Leu Pro Val Leu Ala Ser Met Thr
20 25 30

Lys Ala Ala Asp Pro Arg Phe Arg Pro Arg Trp Lys Val Ile Leu Thr
35 40 45

Phe Phe Val Gly Ala Ala Ile Leu Trp Leu Leu Cys Ser His Arg Pro
50 55 60

Ala Pro Gly Arg Pro Pro Thr His Asn Ala His Asn Trp Arg Leu Gly
65 70 75 80

Gln Ala Pro Ala Asn Trp Tyr Asn Asp Thr Tyr Pro Leu Ser Pro Pro
85 90 95

Gln Arg Thr Pro Ala Gly Ile Arg Tyr Arg Ile Ala Val Ile Ala Asp
100 105 110

Leu Asp Thr Glu Ser Arg Ala Gln Glu Glu Asn Thr Trp Phe Ser Tyr
115 120 125

Leu Lys Lys Gly Tyr Leu Thr Leu Ser Asp Ser Gly Asp Lys Val Ala
130 135 140

Val Glu Trp Asp Lys Asp His Gly Val Leu Glu Ser His Leu Ala Glu
145 150 155 160

Lys Gly Arg Gly Met Glu Leu Ser Asp Leu Ile Val Phe Asn Gly Lys
165 170 175

Leu Tyr Ser Val Asp Asp Arg Thr Gly Val Val Tyr Gln Ile Glu Gly
180 185 190

Ser Lys Ala Val Pro Trp Val Ile Leu Ser Asp Gly Asp Gly Thr Val
195 200 205

Glu Lys Gly Phe Lys Ala Glu Trp Leu Ala Val Arg Glu Ile Val Arg
210 215 220

Lys Arg Trp Arg Leu Val Lys Gln Val Ser His Val Gly Val Leu Gly
225 230 235 240

Gln Trp Ile Gln Arg
245

<210> 72
<211> 1551
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (127)..(861)

<400> 72
ggaagtcggc caccttcctc cgtcccggcc gttagcccag ccaagcccag ccaagcccag 60
ccaagcccgc cggatcgagg gcaccggagc cagccccgca gcgggtcccg cctgtctgtc 120
acgctg atg ccc gtg cag ctg tct gag cac ccg gaa tgg aat gag tct 168
Met Pro Val Gln Leu Ser Glu His Pro Glu Trp Asn Glu Ser
1 5 10
atg cac tcc ctc cgg atc agt gtg ggg ggc ctt cct gtg ctg gcg tcc 216
Met His Ser Leu Arg Ile Ser Val Gly Gly Leu Pro Val Leu Ala Ser
15 20 25 30
atg acc aag gcc gcg gac ccc cgc ttc cgc ccc cgc tgg aag gtg atc 264
Met Thr Lys Ala Ala Asp Pro Arg Phe Arg Pro Arg Trp Lys Val Ile
35 40 45
ctg acg ttc ttt gtg ggt gct gcc atc ctc tgg ctg ctc tgc tcc cac 312
Leu Thr Phe Phe Val Gly Ala Ala Ile Leu Trp Leu Leu Cys Ser His
50 55 60
cgc ccg gcc ccc ggc agg ccc ccc acc cac aat gca cac aac tgg agg 360
Arg Pro Ala Pro Gly Arg Pro Pro Thr His Asn Ala His Asn Trp Arg
65 70 75
ctc ggc cag gcg ccc gcc aac tgg tac aat gac acc tac ccc ctg tct 408
Leu Gly Gln Ala Pro Ala Asn Trp Tyr Asn Asp Thr Tyr Pro Leu Ser
80 85 90
ccc cca caa agg aca ccg gct ggg att cgg tat cga atc gca gtt atc 456
Pro Pro Gln Arg Thr Pro Ala Gly Ile Arg Tyr Arg Ile Ala Val Ile
95 100 105 110
gca gac ctg gac aca gag tca agg gcc caa gag gaa aac acc tgg ttc 504
Ala Asp Leu Asp Thr Glu Ser Arg Ala Gln Glu Glu Asn Thr Trp Phe
115 120 125
agt tac ctg aaa aag ggc tac ctg acc ctg tca gac agt ggg gac aag 552
Ser Tyr Leu Lys Lys Gly Tyr Leu Thr Leu Ser Asp Ser Gly Asp Lys
130 135 140
gtg gcc gtg gaa tgg gac aaa gac cat ggg gtc ctg gag tcc cac ctg 600
Val Ala Val Glu Trp Asp Lys Asp His Gly Val Leu Glu Ser His Leu

```

      145      150      155
gcg gag aag ggg aga ggc atg gag cta tcc gac ctg att gtt ttc aat 648
Ala Glu Lys Gly Arg Gly Met Glu Leu Ser Asp Leu Ile Val Phe Asn
      160      165      170

ggg aaa ctc tac tcc gtg gat gac cgg acg ggg gtc gtc tac cag atc 696
Gly Lys Leu Tyr Ser Val Asp Asp Arg Thr Gly Val Val Tyr Gln Ile
      175      180      185      190

gaa ggc agc aaa gcc gtg ccc tgg gtg att ctg tcc gac ggc gac ggc 744
Glu Gly Ser Lys Ala Val Pro Trp Val Ile Leu Ser Asp Gly Asp Gly
      195      200      205

acc gtg gag aaa ggc ttc aag gcc gaa tgg ctg gca gtg cgg gag att 792
Thr Val Glu Lys Gly Phe Lys Ala Glu Trp Leu Ala Val Arg Glu Ile
      210      215      220

gta agg aag cgg tgg cgg ctg gtg aag caa gtc tca cat gtc ggc gtt 840
Val Arg Lys Arg Trp Arg Leu Val Lys Gln Val Ser His Val Gly Val
      225      230      235

ctt ggc caa tgg ata caa aga taaagaaaat gttgcctttt tctaggaact 891
Leu Gly Gln Trp Ile Gln Arg
      240      245

gtcagaaatc ctcatgcctt tcaagacttc tgtgaatgac ttgaattttt tattccctgc 951
ctaggggtctg tgaacgaggc ctgtctcttc cctgggggttt ctttccatgg cctttatttc 1011
tctctttcca gtgggagttt tgcaggctct tctctgtgga aacttcacga gcgttggtcg 1071
ggcctcggct tcgctggagt gtactccagg gtgaaggcag agtgggattt gagaccacag 1131
tagtgaggga agcgaaggaa gtgaacgctg aatgtgacgc atttctgaag agctcagctg 1191
tcaccgggca tagcctggaa gccccaagtc tgttctgact ttgcctggct gtctccttga 1251
ccgcctcct agatcattgt ccttgatgtc caggctgggt catttaaaat agagatgcaa 1311
tcaggaaggt tgggggactt gggactgtgg ctgaattgag accttgctga tgtattcatg 1371
tcagcacctg agtcacagcc caggtgcccg gaagcagcct cttcgcatag gcagtgattt 1431
gcgattactt taaagctcac cttttttctt cccctctctg ttcgctgctg tcagcataat 1491
gattgtgttc cttccctatg ggatccatct gttttgtaaa caataaagcg tctgaggggag 1551

<210> 73
<211> 352
<212> PRT
<213> Homo sapiens

<400> 73
Met Glu Ser Gly Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly
  1           5           10           15

```


Thr	Thr	Ser	Val	Val	Thr	Ala	Ala	Leu	Tyr	Ser	Val	Tyr	Arg	Gln	Lys		
			20					25					30				
Ala	Arg	Val	Ser	Gln	Glu	Leu	Lys	Gly	Ala	Lys	Lys	Val	His	Leu	Gly		
		35					40					45					
Glu	Asp	Leu	Lys	Ser	Ile	Leu	Ser	Glu	Ala	Pro	Gly	Lys	Cys	Val	Pro		
	50					55					60						
Tyr	Ala	Val	Ile	Glu	Gly	Ala	Val	Arg	Ser	Val	Lys	Glu	Thr	Leu	Asn		
	65			70						75					80		
Ser	Gln	Phe	Val	Glu	Asn	Cys	Lys	Gly	Val	Ile	Gln	Arg	Leu	Thr	Leu		
				85					90					95			
Gln	Glu	His	Lys	Met	Val	Trp	Asn	Arg	Thr	Thr	His	Leu	Trp	Asn	Asp		
			100					105					110				
Cys	Ser	Lys	Ile	Ile	His	Gln	Arg	Thr	Asn	Thr	Val	Pro	Phe	Asp	Leu		
		115					120					125					
Val	Pro	His	Glu	Asp	Gly	Val	Asp	Val	Ala	Val	Arg	Val	Leu	Lys	Pro		
	130					135					140						
Leu	Asp	Ser	Val	Asp	Leu	Gly	Leu	Glu	Thr	Val	Tyr	Glu	Lys	Phe	His		
	145				150					155					160		
Pro	Ser	Ile	Gln	Ser	Phe	Thr	Asp	Val	Ile	Gly	His	Tyr	Ile	Ser	Gly		
				165					170						175		
Glu	Arg	Pro	Lys	Gly	Ile	Gln	Glu	Thr	Glu	Glu	Met	Leu	Lys	Val	Gly		
			180					185					190				
Ala	Thr	Leu	Thr	Gly	Val	Gly	Glu	Leu	Val	Leu	Asp	Asn	Asn	Ser	Val		
		195					200					205					
Arg	Leu	Gln	Pro	Pro	Lys	Gln	Gly	Met	Gln	Tyr	Tyr	Leu	Ser	Ser	Gln		
	210					215					220						
Asp	Phe	Asp	Ser	Leu	Leu	Gln	Arg	Gln	Glu	Ser	Ser	Val	Arg	Leu	Trp		
	225				230					235					240		
Lys	Val	Leu	Ala	Leu	Val	Phe	Gly	Phe	Ala	Thr	Cys	Ala	Thr	Leu	Phe		
				245					250					255			
Phe	Ile	Leu	Arg	Lys	Gln	Tyr	Leu	Gln	Arg	Gln	Glu	Arg	Leu	Arg	Leu		
			260					265					270				
Lys	Gln	Met	Gln	Glu	Glu	Phe	Gln	Glu	His	Glu	Ala	Gln	Leu	Leu	Ser		
		275					280					285					
Arg	Ala	Lys	Pro	Glu	Asp	Arg	Glu	Ser	Leu	Lys	Ser	Ala	Cys	Val	Val		
	290					295					300						
Cys	Leu	Ser	Ser	Phe	Lys	Ser	Cys	Val	Phe	Leu	Glu	Cys	Gly	His	Val		
	305				310					315					320		

Cys Ser Cys Thr Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys
 325 330 335

Pro Ile Cys Arg Gln Ala Ile Thr Arg Val Ile Pro Pro Tyr Asn Ser
 340 345 350

<210> 74

<211> 2401

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (103)..(1158)

<400> 74

ttaggccggg ggggtgcggt cctggtcgga aggaggtgga gagtcggggg tcaccaggcc 60

tatccttggc gccacagtcg gccacggggg ctgcgcgcg tc atg gag agc gga 114
 Met Glu Ser Gly
 1

ggg cgg ccc tcg ctg tgc cag ttc atc ctc ctg ggc acc acc tct gtg 162
 Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly Thr Thr Ser Val
 5 10 15 20

gtc acc gcc gcc ctg tac tcc gtg tac cgg cag aag gcc cgg gtc tcc 210
 Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys Ala Arg Val Ser
 25 30 35

caa gag ctc aag gga gct aaa aaa gtt cat ttg ggt gaa gat tta aag 258
 Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly Glu Asp Leu Lys
 40 45 50

agt att ctt tca gaa gct cca gga aaa tgc gtg cct tat gct gtt ata 306
 Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro Tyr Ala Val Ile
 55 60 65

gaa gga gct gtg cgg tct gtt aaa gaa acg ctt aac agc cag ttt gtg 354
 Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn Ser Gln Phe Val
 70 75 80

gaa aac tgc aag ggg gta att cag cgg ctg aca ctt cag gag cac aag 402
 Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu Gln Glu His Lys
 85 90 95 100

atg gtg tgg aat cga acc acc cac ctt tgg aat gat tgc tca aag atc 450
 Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp Cys Ser Lys Ile
 105 110 115

att cat cag agg acc aac aca gtg ccc ttt gac ctg gtg ccc cac gag 498
 Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu Val Pro His Glu
 120 125 130

gat ggc gtg gat gtg gct gtg cga gtg ctg aag ccc ctg gac tca gtg 546

Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro Leu Asp Ser Val	-
135 140 145	
gat ctg ggt cta gag act gtg tat gag aag ttc cac ccc tcg att cag	594
Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His Pro Ser Ile Gln	
150 155 160	
tcc ttc acc gat gtc atc ggc cac tac atc agc ggt gag cgg ccc aaa	642
Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly Glu Arg Pro Lys	
165 170 175 180	
ggc atc caa gag acc gag gag atg ctg aag gtg ggg gcc acc ctc aca	690
Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly Ala Thr Leu Thr	
185 190 195	
ggg gtt ggc gaa ctg gtc ctg gac aac aac tct gtc cgc ctg cag ccg	738
Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val Arg Leu Gln Pro	
200 205 210	
ccc aaa caa ggc atg cag tac tat cta agc agc cag gac ttc gac agc	786
Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln Asp Phe Asp Ser	
215 220 225	
ctg ctg cag agg cag gag tcg agc gtc agg ctc tgg aag gtg ctg gcg	834
Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp Lys Val Leu Ala	
230 235 240	
ctg gtt ttt ggc ttt gcc aca tgt gcc acc ctc ttc ttc att ctc cgg	882
Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe Phe Ile Leu Arg	
245 250 255 260	
aag cag tat ctg cag cgg cag gag cgc ctg cgc ctc aag cag atg cag	930
Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu Lys Gln Met Gln	
265 270 275	
gag gag ttc cag gag cat gag gcc cag ctg ctg agc cga gcc aag cct	978
Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser Arg Ala Lys Pro	
280 285 290	
gag gac agg gag agt ctg aag agc gcc tgt gta gtg tgt ctg agc agc	1026
Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val Cys Leu Ser Ser	
295 300 305	
ttc aag tcc tgc gtc ttt ctg gag tgt ggg cac gtt tgt tcc tgc acc	1074
Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val Cys Ser Cys Thr	
310 315 320	
gag tgc tac cgc gcc ttg cca gag ccc aag aag tgc cct atc tgc aga	1122
Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys Pro Ile Cys Arg	
325 330 335 340	
cag gcg atc acc cgg gtg ata ccc ccg tac aac agc taatagtttg	1168
Gln Ala Ile Thr Arg Val Ile Pro Pro Tyr Asn Ser	
345 350	
gaagccgcac agcttgacct ggaagcaccc ctgccccctt ttcagggatt tttatctcga	1228

```

_ggcctttgga ggagcagtgg tgggggtagc tgtcacctcc aggtatgatt gagggaggaa 1288
tcgggtagaa actctccaga cccatgcctc caatggcagg atgctgcctt tcccacctga 1348
gaggggaccc tgtccatgtg cagcctcatc agagcctcac cctgggagga tgccgtggcg 1408
tctcctccca ggagccagat cagtgcgagt gtgactgaaa atgcctcatc acttaagcac 1468
caaagccagt gatcagcagc tcttctgttc ctgtgtcttc tgtttttttc tgggtgaatcg 1528
ttgcttgctg tggacttggg ggaggactca gaggggagga aaggctgggc cccgagtaca 1588
acggatgcct tgggtgctgc ctccgaagag actctgccgc agcttttctt ctttttcctc 1648
atgccccggg aaacagtctt tcttcagaat tgtcaggctg ggcagggtcaa cttgtgttcc 1708
tttccctca cctgcttgcc tccttaacgc ctgcacgtgt gtgtagagga caaaagaaag 1768
tgaagtcagc acatccgctt ctgccagat ggtcggggcc ccgggcaaca gattgaagag 1828
agatcatgtg aagggcagtt ggtcaggcag gcctcctggg ttccgcaactg gccctgattt 1888
gaactcctgc cacttgggag agctcggggg ggccctggg tttccctcct ggagaatgag 1948
gcgagaggc ctgcctcct gaaggacgca gtgtggatgc cactggccta gtgtcctggc 2008
ctcacagctt ccttgcaagg ctgtcacaag gaaaagcagc cggctggcac cctgagcata 2068
tgccctcttg gggctccctc atccagcccg tcgcagcttt gacatcttgg tgtactcatg 2128
tcgcttctcc ttgtgttacc cctcccagt attaccattt gccctcacc tgcccttggg 2188
gagcctttta gtgcaagaca gatggggctg ttttcccca cctctgagta gttggaggtc 2248
acatacacag ctcttttttt attgcccttt tctgcctctg aatgttcatc tctcgtcctc 2308
ctttgtgcag gcgaggaagg ggtgcctca ggggcccaca ctagtgtgat gcagtgtcca 2368
gtgtgaacag cagaaattaa acatgttgca acc 2401

```

<210> 75

<211> 352

<212> PRT

<213> Homo sapiens

<400> 75

```

Met Glu Ser Gly Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly
  1             5             10             15

```

```

Thr Thr Ser Val Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys
      20             25             30

```

```

Ala Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly
      35             40             45

```

```

Glu Asp Leu Lys Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro

```

50	55	60
Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn		
65	70	75 80
Ser Gln Phe Val Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu		
	85	90 95
Gln Glu His Lys Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp		
	100	105 110
Cys Ser Lys Ile Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu		
	115	120 125
Val Pro His Glu Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro		
	130	135 140
Leu Asp Ser Val Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His		
145	150	155 160
Pro Ser Ile Gln Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly		
	165	170 175
Glu Arg Pro Lys Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly		
	180	185 190
Ala Thr Leu Thr Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val		
	195	200 205
Arg Leu Gln Pro Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln		
	210	215 220
Asp Phe Asp Ser Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp		
225	230	235 240
Lys Val Leu Ala Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe		
	245	250 255
Phe Ile Leu Arg Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu		
	260	265 270
Lys Gln Met Gln Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser		
	275	280 285
Arg Ala Lys Pro Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val		
	290	295 300
Cys Leu Ser Ser Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val		
305	310	315 320
Cys Ser Cys Thr Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys		
	325	330 335
Pro Ile Cys Arg Gln Ala Ile Thr Arg Val Ile Pro Leu Tyr Asn Ser		
	340	345 350

```

<210> 76
<211> 2401
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (103)..(1158)

<400> 76
ttaggcgagg ggggtgcggt cctggtcgga aggaggtgga gagtcggggg tcaccaggcc 60

tatccttggc gccacagtcg gccaccgggg ctcgcgcgcg tc atg gag agc gga      114
                                   Met Glu Ser Gly
                                   1

ggg cgg ccc tcg ctg tgc cag ttc atc ctc ctg ggc acc acc tct gtg      162
Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly Thr Thr Ser Val
  5                      10                      15                      20

gtc acc gcc gcc ctg tac tcc gtg tac cgg cag aag gcc cgg gtc tcc      210
Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys Ala Arg Val Ser
                25                      30                      35

caa gag ctc aag gga gct aaa aaa gtt cat ttg ggt gaa gat tta aag      258
Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly Glu Asp Leu Lys
                40                      45                      50

agt att ctt tca gaa gct cca gga aaa tgc gtg cct tat gct gtt ata      306
Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro Tyr Ala Val Ile
                55                      60                      65

gaa gga gct gtg cgg tct gtt aaa gaa acg ctt aac agc cag ttt gtg      354
Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn Ser Gln Phe Val
                70                      75                      80

gaa aac tgc aag ggg gta att cag cgg ctg aca ctt cag gag cac aag      402
Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu Gln Glu His Lys
                85                      90                      95

atg gtg tgg aat cga acc acc cac ctt tgg aat gat tgc tca aag atc      450
Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp Cys Ser Lys Ile
                105                      110                      115

att cat cag agg acc aac aca gtg ccc ttt gac ctg gtg ccc cac gag      498
Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu Val Pro His Glu
                120                      125                      130

gat ggc gtg gat gtg gct gtg cga gtg ctg aag ccc ctg gac tca gtg      546
Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro Leu Asp Ser Val
                135                      140                      145

gat ctg ggt cta gag act gtg tat gag aag ttc cac ccc tcg att cag      594
Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His Pro Ser Ile Gln
                150                      155                      160

tcc ttc acc gat gtc atc ggc cac tac atc agc ggt gag cgg ccc aaa      642

```

Ser	Phe	Thr	Asp	Val	Ile	Gly	His	Tyr	Ile	Ser	Gly	Glu	Arg	Pro	Lys				
165					170					175					180				
ggc atc caa gag acc gag gag atg ctg aag gtg ggg gcc acc ctc aca	690																		
Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly Ala Thr Leu Thr				185					190						195				
ggg gtt ggc gaa ctg gtc ctg gac aac aac tct gtc cgc ctg cag ccg	738																		
Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val Arg Leu Gln Pro				200				205					210						
ccc aaa caa ggc atg cag tac tat cta agc agc cag gac ttc gac agc	786																		
Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln Asp Phe Asp Ser				215			220					225							
ctg ctg cag agg cag gag tcg agc gtc agg ctc tgg aag gtg ctg gcg	834																		
Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp Lys Val Leu Ala						235				240									
ctg gtt ttt ggc ttt gcc aca tgt gcc acc ctc ttc ttc att ctc cgg	882																		
Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe Phe Ile Leu Arg				250					255										
245																			
aag cag tat ctg cag cgg cag gag cgc ctg cgc ctc aag cag atg cag	930																		
Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu Lys Gln Met Gln				265				270						275					
gag gag ttc cag gag cat gag gcc cag ctg ctg agc cga gcc aag cct	978																		
Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser Arg Ala Lys Pro				280			285						290						
gag gac agg gag agt ctg aag agc gcc tgt gta gtg tgt ctg agc agc	1026																		
Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val Cys Leu Ser Ser				295			300				305								
ttc aag tcc tgc gtc ttt ctg gag tgt ggg cac gtt tgt tcc tgc acc	1074																		
Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val Cys Ser Cys Thr						315				320									
310																			
gag tgc tac cgc gcc ttg cca gag ccc aag aag tgc cct atc tgc aga	1122																		
Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys Pro Ile Cys Arg					330				335										
325																			
cag gcg atc acc cgg gtg ata ccc ctg tac aac agc taatagtttg	1168																		
Gln Ala Ile Thr Arg Val Ile Pro Leu Tyr Asn Ser				345			350												
gaagccgcac agcttgacct ggaagcaccc ctgccccctt ttcagggatt tttatctcga	1228																		
ggcctttgga ggagcagtgg tgggggtagc tgtcacctcc aggtatgatt gagggaggaa	1288																		
tcgggtagaa actctccaga cccatgcctc caatggcagg atgctgcctt tcccacctga	1348																		
gaggggaccc tgtccatgtg cagcctcatc agagcctcac cctgggagga tgccgtggcg	1408																		
tctcctccca ggagccagat cagtgcgagt gtgactgaaa atgcctcatc acttaagcac	1468																		

caaagccagt gatcagcage tcttetgttc ctgtgtcttc tgtttttttc tgggtgaatcg 1528
 ttgcttgctg tggacttggt ggaggactca gaggggagga aaggctgggc cccgagtaca 1588
 acggatgcct tgggtgctgc ctccgaagag actctgccgc agctttttctt ctttttcctc 1648
 atgccccggg aaacagtctt tcttcagaat tgtcaggctg ggcaggtcaa cttgtgttcc 1708
 tttccctca cctgcttgcc tccttaacgc ctgcacgtgt gtgtagagga caaaagaaag 1768
 tgaagtcagc acatccgctt ctgcccagat ggtcggggcc ccgggcaaca gattgaagag 1828
 agatcatgtg aagggcagtt ggtcaggcag gcctcctggt ttcgccactg gccctgattt 1888
 gaactcctgc cacttgggag agctcgggggt ggtccctggt tttccctcct ggagaatgag 1948
 gcgcagaggc ctgcctcct gaaggacgca gtgtggatgc cactggccta gtgtcctggc 2008
 ctcacagctt ccttgcaagg ctgtcacaag gaaaagcagc cggctggcac cctgagcata 2068
 tgccctcttg gggctccctc atccagcccg tcgcagcttt gacatcttggt tgtactcatg 2128
 tcgcttctcc ttgtgttacc cctcccaggt attaccattt gcccctcacc tgcccttggt 2188
 gagcctttta gtgcaagaca gatggggctg ttttccccca cctctgagta gttggaggtc 2248
 acatacacag ctcttttttt attgcccttt tctgcctctg aatgttcatc tctcgtcctc 2308
 ctttgtgcag gcgaggaagg ggtgccctca ggggccgaca ctagtgtgat gcagtgtcca 2368
 gtgtgaacag cagaaattaa acatgttgca acc 2401

<210> 77
 <211> 697
 <212> PRT
 <213> Homo sapiens

<400> 77
 Met Cys Lys Ser Leu Arg Tyr Cys Phe Ser His Cys Leu Tyr Leu Ala
 1 5 10 15
 Met Thr Arg Leu Glu Glu Val Asn Arg Glu Val Asn Met His Ser Ser
 20 25 30
 Val Arg Tyr Leu Gly Tyr Leu Ala Arg Ile Asn Leu Leu Val Ala Ile
 35 40 45
 Cys Leu Gly Leu Tyr Val Arg Trp Glu Lys Thr Ala Asn Ser Leu Ile
 50 55 60
 Leu Val Ile Phe Ile Leu Gly Leu Phe Val Leu Gly Ile Ala Ser Ile
 65 70 75 80
 Leu Tyr Tyr Tyr Phe Ser Met Glu Ala Ala Ser Leu Ser Leu Ser Asn
 85 90 95

Leu Trp Phe-Gly Phe-Leu Leu Gly-Leu Leu Cys Phe-Leu Asp Asn Ser
 100 105 110
 Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr Leu Leu Leu
 115 120 125
 Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu Arg Ile Ser
 130 135 140
 Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val Glu Phe Leu
 145 150 155 160
 Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu Val Glu Lys
 165 170 175
 Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met Leu Ile Ile
 180 185 190
 Asp Leu Arg Met Lys Ser Phe Leu Ala Ile Pro Asn Leu Val Ile Phe
 195 200 205
 Ala Val Leu Leu Phe Phe Ser Ser Leu Glu Thr Pro Lys Asn Pro Ile
 210 215 220
 Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro Phe Leu Asp
 225 230 235 240
 Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys Pro Phe Leu
 245 250 255
 Tyr Arg Gly Arg Ile Cys Arg Arg Leu Ser Val Val Phe Ala Gly Met
 260 265 270
 Ile Glu Leu Thr Phe Phe Ile Leu Ser Ala Phe Lys Leu Arg Asp Thr
 275 280 285
 His Leu Trp Tyr Phe Val Ile Pro Gly Phe Ser Ile Phe Gly Ile Phe
 290 295 300
 Trp Met Ile Cys His Ile Ile Phe Leu Leu Thr Leu Trp Gly Phe His
 305 310 315 320
 Thr Lys Leu Asn Asp Cys His Lys Val Tyr Phe Thr His Arg Thr Asp
 325 330 335
 Tyr Asn Ser Leu Asp Arg Ile Met Ala Ser Lys Gly Met Arg His Phe
 340 345 350
 Cys Leu Ile Ser Glu Gln Leu Val Phe Phe Ser Leu Leu Ala Thr Ala
 355 360 365
 Ile Leu Gly Ala Val Ser Trp Gln Pro Thr Asn Gly Ile Phe Leu Ser
 370 375 380
 Met Phe Leu Ile Val Leu Pro Leu Glu Ser Met Ala His Gly Leu Phe
 385 390 395 400

His Glu Leu Gly Asn Cys Leu Gly Gly Thr Ser Val Gly Tyr Ala Ile
 405 410 415
 Val Ile Pro Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro Thr Leu Leu
 420 425 430
 Pro Pro Glu His Val Gln Glu Leu Asn Leu Arg Ser Thr Gly Met Leu
 435 440 445
 Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu Thr Tyr Gly
 450 455 460
 Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu His Ser Lys
 465 470 475 480
 Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro Arg His Asp
 485 490 495
 Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr Gly Glu Trp
 500 505 510
 Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu Ile Glu Trp
 515 520 525
 Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile Ile Val Leu
 530 535 540
 Asp Ser Glu Asn Ser Thr Pro Trp Val Lys Glu Val Arg Lys Ile Asn
 545 550 555 560
 Asp Gln Tyr Ile Ala Val Gln Gly Ala Glu Leu Ile Lys Thr Val Asp
 565 570 575
 Ile Glu Glu Ala Asp Pro Pro Gln Leu Gly Asp Phe Thr Lys Asp Trp
 580 585 590
 Val Glu Tyr Asn Cys Asn Ser Ser Asn Asn Ile Cys Trp Thr Glu Lys
 595 600 605
 Gly Arg Thr Val Lys Ala Val Tyr Gly Val Ser Lys Arg Trp Ser Asp
 610 615 620
 Tyr Thr Leu His Leu Pro Thr Gly Ser Asp Val Ala Lys His Trp Met
 625 630 635 640
 Leu His Phe Pro Arg Ile Thr Tyr Pro Leu Val His Leu Ala Asn Trp
 645 650 655
 Leu Cys Gly Leu Asn Leu Phe Trp Ile Cys Lys Thr Cys Phe Arg Cys
 660 665 670
 Leu Lys Arg Leu Lys Met Ser Trp Phe Leu Pro Thr Val Leu Asp Thr
 675 680 685
 Gly Gln Gly Phe Lys Leu Val Lys Ser
 690 695

<210> 78
 <211> 3008
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (372)..(2462)

<400> 78
 cgtaccgtcg cggatttcgg cggcggaaac atggcggtcg cggccgggcc ggtaacggag 60
 aaagtttacg ccgacactgg cctgtattag cgcgtatggc ctcgggccct cgttccccc 120
 ggcggtgcgc ctccctgttc tcagtcgcag gctgaagcct tgtctgctct cctccttttt 180
 ggtttggttt tggaactgac tccgagggtt gggagagcgc gttggtggcg acggccgagt 240
 cagatcacta taaacaaaat ttccacaaga gaaaatgttg aaataggagt tgcggataca 300
 ttggatatac tggatgaaat acaagcgggtt aatttttgta acgtgaggga aaagcccaca 360
 ttgctgggta c atg tgt aaa tca ctg cgt tat tgc ttt agt cat tgt ctc 410
 Met Cys Lys Ser Leu Arg Tyr Cys Phe Ser His Cys Leu
 1 5 10
 tat tta gca atg aca aga ctg gaa gaa gta aat aga gaa gtg aac atg 458
 Tyr Leu Ala Met Thr Arg Leu Glu Glu Val Asn Arg Glu Val Asn Met
 15 20 25
 cat tct tca gtg cgg tat ctt ggc tat tta gcc aga atc aat tta ttg 506
 His Ser Ser Val Arg Tyr Leu Gly Tyr Leu Ala Arg Ile Asn Leu Leu
 30 35 40 45
 gtt gct ata tgc tta ggt cta tac gta aga tgg gaa aaa aca gca aat 554
 Val Ala Ile Cys Leu Gly Leu Tyr Val Arg Trp Glu Lys Thr Ala Asn
 50 55 60
 tcc tta att ttg gta att ttt att ctt ggt ctt ttt gtt ctt gga atc 602
 Ser Leu Ile Leu Val Ile Phe Ile Leu Gly Leu Phe Val Leu Gly Ile
 65 70 75
 gcc agc ata ctc tat tac tat ttt tca atg gaa gca gca agt tta agt 650
 Ala Ser Ile Leu Tyr Tyr Tyr Phe Ser Met Glu Ala Ala Ser Leu Ser
 80 85 90
 ctc tcc aat ctt tgg ttt gga ttc ttg ctt ggc ctc cta tgt ttt ctt 698
 Leu Ser Asn Leu Trp Phe Gly Phe Leu Leu Gly Leu Leu Cys Phe Leu
 95 100 105
 gat aat tca tcc ttt aaa aat gat gta aaa gaa gaa tca acc aaa tat 746
 Asp Asn Ser Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr
 110 115 120 125
 ttg ctt cta aca tcc ata gtg tta agg ata ttg tgc tct ctg gtg gag 794
 Leu Leu Leu Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu

	130	135	140	
aga att tct ggt tat gtc cgt cat cgg ccc act tta cta acc aca gtt				842
Arg Ile Ser Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val				
	145	150	155	
gaa ttt ctg gag ctt gtt gga ttt gcc att gcc agc aca act atg ttg				890
Glu Phe Leu Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu				
	160	165	170	
gtg gag aag tct ctg agt gtc att ttg ctt gtt gta gct ctg gct atg				938
Val Glu Lys Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met				
	175	180	185	
ctg att att gat ctg aga atg aaa tct ttc tta gct att cca aac tta				986
Leu Ile Ile Asp Leu Arg Met Lys Ser Phe Leu Ala Ile Pro Asn Leu				
	190	195	200	205
gtt att ttt gca gtt ttg tta ttt ttt tcc tca ttg gaa act ccc aaa				1034
Val Ile Phe Ala Val Leu Leu Phe Phe Ser Ser Leu Glu Thr Pro Lys				
	210	215	220	
aat ccg att gct ttt gcg tgt ttt ttt att tgc ctg ata act gat cct				1082
Asn Pro Ile Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro				
	225	230	235	
ttc ctt gac att tat ttt agt gga ctt tca gta act gaa aga tgg aaa				1130
Phe Leu Asp Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys				
	240	245	250	
ccc ttt ttg tac cgt gga aga att tgc aga aga ctt tca gtc gtt ttt				1178
Pro Phe Leu Tyr Arg Gly Arg Ile Cys Arg Arg Leu Ser Val Val Phe				
	255	260	265	
gct gga atg att gag ctt aca ttt ttt att ctt tcc gca ttc aaa ctt				1226
Ala Gly Met Ile Glu Leu Thr Phe Phe Ile Leu Ser Ala Phe Lys Leu				
	270	275	280	285
aga gac act cac ctc tgg tat ttt gta ata cct ggc ttt tcc att ttt				1274
Arg Asp Thr His Leu Trp Tyr Phe Val Ile Pro Gly Phe Ser Ile Phe				
	290	295	300	
gga att ttc tgg atg att tgt cat att att ttt ctt tta act ctt tgg				1322
Gly Ile Phe Trp Met Ile Cys His Ile Ile Phe Leu Leu Thr Leu Trp				
	305	310	315	
gga ttc cat acc aaa tta aat gac tgc cat aaa gta tat ttt act cac				1370
Gly Phe His Thr Lys Leu Asn Asp Cys His Lys Val Tyr Phe Thr His				
	320	325	330	
agg aca gat tac aat agc ctt gat aga atc atg gca tcc aaa ggg atg				1418
Arg Thr Asp Tyr Asn Ser Leu Asp Arg Ile Met Ala Ser Lys Gly Met				
	335	340	345	
cgc cat ttt tgc ttg att tca gag cag ttg gtg ttc ttt agt ctt ctt				1466
Arg His Phe Cys Leu Ile Ser Glu Gln Leu Val Phe Phe Ser Leu Leu				
	350	355	360	365

gca aca gcg att ttg gga gca gtt tcc tgg cag cca aca aat gga att	1514
Ala Thr Ala Ile Leu Gly Ala Val Ser Trp Gln Pro Thr Asn Gly Ile	
370 375 380	
ttc ttg agc atg ttt cta atc gtt ttg cca ttg gaa tcc atg gct cat	1562
Phe Leu Ser Met Phe Leu Ile Val Leu Pro Leu Glu Ser Met Ala His	
385 390 395	
ggg ctc ttc cat gaa ttg ggt aac tgt tta gga gga aca tct gtt gga	1610
Gly Leu Phe His Glu Leu Gly Asn Cys Leu Gly Gly Thr Ser Val Gly	
400 405 410	
tat gct att gtg att ccc acc aac ttc tgc agt cct gat ggt cag cca	1658
Tyr Ala Ile Val Ile Pro Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro	
415 420 425	
aca ctg ctt ccc cca gaa cat gta cag gag tta aat ttg agg tct act	1706
Thr Leu Leu Pro Pro Glu His Val Gln Glu Leu Asn Leu Arg Ser Thr	
430 435 440 445	
ggc atg ctc aat gct atc caa aga ttt ttt gca tat cat atg att gag	1754
Gly Met Leu Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu	
450 455 460	
acc tat gga tgt gac tat tcc aca agt gga ctg tca ttt gat act ctg	1802
Thr Tyr Gly Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu	
465 470 475	
cat tcc aaa cta aaa gct ttc ctc gaa ctt cgg aca gtg gat gga ccc	1850
His Ser Lys Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro	
480 485 490	
aga cat gat acg tat att ttg tat tac agt ggg cac acc cat ggt aca	1898
Arg His Asp Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr	
495 500 505	
gga gag tgg gct cta gca ggt gga gat aca cta cgc ctt gac aca ctt	1946
Gly Glu Trp Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu	
510 515 520 525	
ata gaa tgg tgg aga gaa aag aat ggt tcc ttt tgt tcc cgg ctt att	1994
Ile Glu Trp Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile	
530 535 540	
atc gta tta gac agc gaa aat tca acc cct tgg gtg aaa gaa gtg agg	2042
Ile Val Leu Asp Ser Glu Asn Ser Thr Pro Trp Val Lys Glu Val Arg	
545 550 555	
aaa att aat gac cag tat att gca gtg caa gga gca gag ttg ata aaa	2090
Lys Ile Asn Asp Gln Tyr Ile Ala Val Gln Gly Ala Glu Leu Ile Lys	
560 565 570	
aca gta gat att gaa gaa gct gac ccg cca cag cta ggt gac ttt aca	2138
Thr Val Asp Ile Glu Glu Ala Asp Pro Pro Gln Leu Gly Asp Phe Thr	
575 580 585	

```

aaa gac tgg gta gaa tat aac tgc aac tcc agt aat aac atc tgc tgg 2186
Lys Asp Trp Val Glu Tyr Asn Cys Asn Ser Ser Asn Asn Ile Cys Trp
590 595 600 605

act gaa aag gga cgc aca gtg aaa gca gta tat ggt gtg tca aaa cgg 2234
Thr Glu Lys Gly Arg Thr Val Lys Ala Val Tyr Gly Val Ser Lys Arg
610 615 620

tgg agt gac tac act ctg cat ttg cca acg gga agc gat gtg gcc aag 2282
Trp Ser Asp Tyr Thr Leu His Leu Pro Thr Gly Ser Asp Val Ala Lys
625 630 635

cac tgg atg tta cac ttt cct cgt att aca tat ccc cta gtg cat ttg 2330
His Trp Met Leu His Phe Pro Arg Ile Thr Tyr Pro Leu Val His Leu
640 645 650

gca aat tgg tta tgc ggt ctg aac ctt ttt tgg atc tgc aaa act tgt 2378
Ala Asn Trp Leu Cys Gly Leu Asn Leu Phe Trp Ile Cys Lys Thr Cys
655 660 665

ttt agg tgc ttg aaa aga tta aaa atg agt tgg ttt ctt cct act gtg 2426
Phe Arg Cys Leu Lys Arg Leu Lys Met Ser Trp Phe Leu Pro Thr Val
670 675 680 685

ctg gac aca gga caa ggc ttc aaa ctt gtc aaa tct taatttgac 2472
Leu Asp Thr Gly Gln Gly Phe Lys Leu Val Lys Ser
690 695

cccaaagcgg gatattaata agcactcata ctaccaatta tcactaactt gccatttttt 2532
gtatgctgta tttttatttg tggaaaatac cttgctactt ctgtagctgc tctcactttg 2592
tctttttctta agtaattatg gtatatataa ggcgttgggg aaaaacattt tataatgaaa 2652
gtatgtaggg agtcaaagtc ttactgtaaa tgcataagag acgttaaaaa taacactgca 2712
ctttcaggaa tgtttgctta tggctctgat tagaaagaaa cagttgtcta tgctctgcaa 2772
tggccaatga tgaattacta atgccttatt ttctaggoat ataataatag tttagagaat 2832
gtagaccaga taaatttggt tactgtttta agaaaactac cagtttactt acagaagatt 2892
cttttttcca aacagtaggt ttcattccaag accatttgaa gaactgcaaa ctctttctct 2952
tagaaaagaa agagggcagc ctaaaataaa cgcaaaattt gcttatactc catcac 3008

```

<210> 79

<211> 611

<212> PRT

<213> Homo sapiens

<400> 79

```

Met Glu Ala Ala Ser Leu Ser Leu Ser Asn Leu Trp Phe Gly Phe Leu
1 5 10 15

```

```

Leu Gly Leu Leu Cys Phe Leu Asp Asn Ser Ser Phe Lys Asn Asp Val

```

20 25 30
 Lys Glu Glu Ser Thr Lys Tyr Leu Leu Thr Ser Ile Val Leu Arg
 35 40 45
 Ile Leu Cys Ser Leu Val Glu Arg Ile Ser Gly Tyr Val Arg His Arg
 50 55 60
 Pro Thr Leu Leu Thr Thr Val Glu Phe Leu Glu Leu Val Gly Phe Ala
 65 70 75 80
 Ile Ala Ser Thr Thr Met Leu Val Glu Lys Ser Leu Ser Val Ile Leu
 85 90 95
 Leu Val Val Ala Leu Ala Met Leu Ile Ile Asp Leu Arg Met Lys Ser
 100 105 110
 Phe Leu Ala Ile Pro Asn Leu Val Ile Phe Ala Val Leu Leu Phe Phe
 115 120 125
 Ser Ser Leu Glu Thr Pro Lys Asn Pro Ile Ala Phe Ala Cys Phe Phe
 130 135 140
 Ile Cys Leu Ile Thr Asp Pro Phe Leu Asp Ile Tyr Phe Ser Gly Leu
 145 150 155 160
 Ser Val Thr Glu Arg Trp Lys Pro Phe Leu Tyr Arg Gly Arg Ile Cys
 165 170 175
 Arg Arg Leu Ser Val Val Phe Ala Gly Met Ile Glu Leu Thr Phe Phe
 180 185 190
 Ile Leu Ser Ala Phe Lys Leu Arg Asp Thr His Leu Trp Tyr Phe Val
 195 200 205
 Ile Pro Gly Phe Ser Ile Phe Gly Ile Phe Trp Met Ile Cys His Ile
 210 215 220
 Ile Phe Leu Leu Thr Leu Trp Gly Phe His Thr Lys Leu Asn Asp Cys
 225 230 235 240
 His Lys Val Tyr Phe Thr His Arg Thr Asp Tyr Asn Ser Leu Asp Arg
 245 250 255
 Ile Met Ala Ser Lys Gly Met Arg His Phe Cys Leu Ile Ser Glu Gln
 260 265 270
 Leu Val Phe Phe Ser Leu Leu Ala Thr Ala Ile Leu Gly Ala Val Ser
 275 280 285
 Trp Gln Pro Thr Asn Gly Ile Phe Leu Ser Met Phe Leu Ile Val Leu
 290 295 300
 Pro Leu Glu Ser Met Ala His Gly Leu Phe His Glu Leu Gly Asn Cys
 305 310 315 320
 Leu Gly Gly Thr Ser Val Gly Tyr Ala Ile Val Ile Pro Thr Asn Phe


```

<210> 80
<211> 3007
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (629)..(2461)

<400> 80
cgtaccgtcg cggatttcgg cggcggaaac atggcggtcg cggccgggcc ggtaacggag 60
aaagtttacg cggacactgg cctgtattag cgcgtatggc ctcgggccct cgttcccca 120
ggcgtgccgc ctccctgttc tcagtcgcag gctgaagcct tgtctgctct cctccttttt 180
ggtttggttt tggaactgac tccgaggggtt gggagagcgc gttggtggcg acggccgagt 240
cagatcacta taaacaaaat ttccacaaga gaaaatgttg aaataggagt tgcggataca 300
ttggatatac tggatgaaat acaagcgggtt aatttttgta acgtgagggg aaagcccaca 360
ttgctggtta catgtgtaaa tcaactgcgtt attgcttttag tcattgtctc tatttagcaa 420
tgacaagact ggaagaagta aatagagaag tgaacatgca ttcttcagtg cggatatcttg 480
ctattttagcc agaatcaatt tattggttgc tatatgctta ggtctatacg taagatggga 540
aaaaacagca aattccttaa ttttggtaat ttttattctt ggtctttttg ttcttggaat 600
cgccagcata ctctattact atttttca atg gaa gca gca agt tta agt ctc 652
                        Met Glu Ala Ala Ser Leu Ser Leu
                        1                      5

tcc aat ctt tgg ttt gga ttc ttg ctt ggc ctc cta tgt ttt ctt gat 700
Ser Asn Leu Trp Phe Gly Phe Leu Leu Gly Leu Leu Cys Phe Leu Asp
      10                      15                      20

aat tca tcc ttt aaa aat gat gta aaa gaa gaa tca acc aaa tat ttg 748
Asn Ser Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr Leu
      25                      30                      35                      40

ctt cta aca tcc ata gtg tta agg ata ttg tgc tct ctg gtg gag aga 796
Leu Leu Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu Arg
                        45                      50                      55

att tct ggt tat gtc cgt cat cgg ccc act tta cta acc aca gtt gaa 844
Ile Ser Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val Glu
                        60                      65                      70

ttt ctg gag ctt gtt gga ttt gcc att gcc agc aca act atg ttg gtg 892
Phe Leu Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu Val
                        75                      80                      85

gag aag tct ctg agt gtc att ttg ctt gtt gta gct ctg gct atg ctg 940
Glu Lys Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met Leu
      90                      95                      100

```

att att gat ctg aga atg aaa tct ttc tta gct att cca aac tta gtt	988
Ile Ile Asp Leu Arg Met Lys Ser Phe Leu Ala Ile Pro Asn Leu Val	
105 110 115 120	
att ttt gca gtt ttg tta ttt ttt tcc tca ttg gaa act ccc aaa aat	1036
Ile Phe Ala Val Leu Leu Phe Phe Ser Ser Leu Glu Thr Pro Lys Asn	
125 130 135	
cog att gct ttt gcg tgt ttt ttt att tgc ctg ata act gat cct ttc	1084
Pro Ile Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro Phe	
140 145 150	
ctt gac att tat ttt agt gga ctt tca gta act gaa aga tgg aaa ccc	1132
Leu Asp Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys Pro	
155 160 165	
ttt ttg tac cgt gga aga att tgc aga aga ctt tca gtc gtt ttt gct	1180
Phe Leu Tyr Arg Gly Arg Ile Cys Arg Arg Leu Ser Val Val Phe Ala	
170 175 180	
gga atg att gag ctt aca ttt ttt att ctt tcc gca ttc aaa ctt aga	1228
Gly Met Ile Glu Leu Thr Phe Phe Ile Leu Ser Ala Phe Lys Leu Arg	
185 190 195 200	
gac act cac ctc tgg tat ttt gta ata cct ggc ttt tcc att ttt gga	1276
Asp Thr His Leu Trp Tyr Phe Val Ile Pro Gly Phe Ser Ile Phe Gly	
205 210 215	
att ttc tgg atg att tgt cat att att ttt ctt tta act ctt tgg gga	1324
Ile Phe Trp Met Ile Cys His Ile Ile Phe Leu Leu Thr Leu Trp Gly	
220 225 230	
ttc cat acc aaa tta aat gac tgc cat aaa gta tat ttt act cac agg	1372
Phe His Thr Lys Leu Asn Asp Cys His Lys Val Tyr Phe Thr His Arg	
235 240 245	
aca gat tac aat agc ctt gat aga atc atg gca tcc aaa ggg atg cgc	1420
Thr Asp Tyr Asn Ser Leu Asp Arg Ile Met Ala Ser Lys Gly Met Arg	
250 255 260	
cat ttt tgc ttg att tca gag cag ttg gtg ttc ttt agt ctt ctt gca	1468
His Phe Cys Leu Ile Ser Glu Gln Leu Val Phe Phe Ser Leu Leu Ala	
265 270 275 280	
aca gcg att ttg gga gca gtt tcc tgg cag cca aca aat gga att ttc	1516
Thr Ala Ile Leu Gly Ala Val Ser Trp Gln Pro Thr Asn Gly Ile Phe	
285 290 295	
ttg agc atg ttt cta atc gtt ttg cca ttg gaa tcc atg gct cat ggg	1564
Leu Ser Met Phe Leu Ile Val Leu Pro Leu Glu Ser Met Ala His Gly	
300 305 310	
ctc ttc cat gaa ttg ggt aac tgt tta gga gga aca tct gtt gga tat	1612
Leu Phe His Glu Leu Gly Asn Cys Leu Gly Gly Thr Ser Val Gly Tyr	
315 320 325	

gct att gtg att ccc acc aac ttc tgc agt cct gat ggt cag cca aca	1660
Ala Ile Val Ile Pro Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro Thr	
330 335 340	
ctg ctt ccc cca gaa cat gta cag gag tta aat ttg agg tct act ggc	1708
Leu Leu Pro Pro Glu His Val Gln Glu Leu Asn Leu Arg Ser Thr Gly	
345 350 355 360	
atg ctc aat gct atc caa aga ttt ttt gca tat cat atg att gag acc	1756
Met Leu Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu Thr	
365 370 375	
tat gga tgt gac tat tcc aca agt gga ctg tca ttt gat act ctg cat	1804
Tyr Gly Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu His	
380 385 390	
tcc aaa cta aaa gct ttc ctc gaa ctt cgg aca gtg gat gga ccc aga	1852
Ser Lys Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro Arg	
395 400 405	
cat gat acg tat att ttg tat tac agt ggg cac acc cat ggt aca gga	1900
His Asp Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr Gly	
410 415 420	
gag tgg gct cta gca ggt gga gat aca cta cgc ctt gac aca ctt ata	1948
Glu Trp Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu Ile	
425 430 435 440	
gaa tgg tgg aga gaa aag aat ggt tcc ttt tgt tcc cgg ctt att atc	1996
Glu Trp Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile Ile	
445 450 455	
gta tta gac agc gaa aat tca acc cct tgg gtg aaa gaa gtg agg aaa	2044
Val Leu Asp Ser Glu Asn Ser Thr Pro Trp Val Lys Glu Val Arg Lys	
460 465 470	
att aat gac cag tat att gca gtg caa gga gca gag ttg ata aaa aca	2092
Ile Asn Asp Gln Tyr Ile Ala Val Gln Gly Ala Glu Leu Ile Lys Thr	
475 480 485	
gta gat att gaa gaa gct gac ccg cca cag cta ggt gac ttt aca aaa	2140
Val Asp Ile Glu Glu Ala Asp Pro Pro Gln Leu Gly Asp Phe Thr Lys	
490 495 500	
gac tgg gta gaa tat aac tgc aac tcc agt aat aac atc tgc tgg act	2188
Asp Trp Val Glu Tyr Asn Cys Asn Ser Ser Asn Asn Ile Cys Trp Thr	
505 510 515 520	
gaa aag gga cgc aca gtg aaa gca gta tat ggt gtg tca aaa cgg tgg	2236
Glu Lys Gly Arg Thr Val Lys Ala Val Tyr Gly Val Ser Lys Arg Trp	
525 530 535	
agt gac tac act ctg cat ttg cca acg gga agc gat gtg gcc aag cac	2284
Ser Asp Tyr Thr Leu His Leu Pro Thr Gly Ser Asp Val Ala Lys His	
540 545 550	
tgg atg tta cac ttt cct cgt att aca tat ccc cta gtg cat ttg gca	2332

```

-- Trp Met-Leu His Phe-Pro Arg Ile Thr Tyr-Pro Leu Val His Leu Ala
      555                      560                      565

aat tgg tta tgc ggt ctg aac ctt ttt tgg atc tgc aaa act tgt ttt 2380
Asn Trp Leu Cys Gly Leu Asn Leu Phe Trp Ile Cys Lys Thr Cys Phe
      570                      575                      580

agg tgc ttg aaa aga tta aaa atg agt tgg ttt ctt cct act gtg ctg 2428
Arg Cys Leu Lys Arg Leu Lys Met Ser Trp Phe Leu Pro Thr Val Leu
      585                      590                      595                      600

gac aca gga caa ggc ttc aaa ctt gtc aaa tct taatttggac cccaaagcgg 2481
Asp Thr Gly Gln Gly Phe Lys Leu Val Lys Ser
      605                      610

gatattaata agcactcata ctaccaatta tcaactaactt gccattttttt gtatgctgta 2541
tttttatttg tggaaaatac cttgctactt ctgtagctgc tctcactttg tcttttctta 2601
agtaattatg gtatatataa ggcgttggga aaaaacattt tataatgaaa gtatgtaggg 2661
agtcaaatgc ttactgtaaa tgcataagag acgttaaaaa taacactgca ctttcaggaa 2721
tgtttgctta tggctctgat tagaaagaaa cagttgtcta tgctctgcaa tgggtcaatga 2781
tgaattacta atgccttatt ttctaggcat ataataatag tttagagaat gtagaccaga 2841
taaatttggt tactgtttta agaaaactac cagtttactt acagaagatt cttttttcca 2901
aacagtaggt ttcattccaag accatttgaa gaactgcaaa ctctttctct tagaaaagaa 2961
agagggcagc ctaaaataaa cgcaaaattt gcttatactc catcac 3007

```

<210> 81
 <211> 184
 <212> PRT
 <213> Homo sapiens

```

<400> 81
Met Thr Ser Phe Glu Asp Ala Asp Thr Glu Glu Thr Val Thr Cys Leu
  1                      5                      10                      15

Gln Met Thr Val Tyr His Pro Gly Gln Leu Gln Cys Gly Ile Phe Gln
      20                      25                      30

Ser Ile Ser Phe Asn Arg Glu Lys Leu Pro Ser Ser Glu Val Val Lys
      35                      40                      45

Phe Gly Arg Asn Ser Asn Ile Cys His Tyr Thr Phe Gln Asp Lys Gln
      50                      55                      60

Val Ser Arg Val Gln Phe Ser Leu Gln Leu Phe Lys Lys Phe Asn Ser
      65                      70                      75                      80

Ser Val Leu Ser Phe Glu Ile Lys Asn Met Ser Lys Lys Thr Asn Leu
      85                      90                      95

```

Ile Val Asp Ser Arg Glu Leu Gly Tyr Leu Asn Lys Met Asp Leu Pro
 100 105 110
 Tyr Arg Cys Met Val Arg Phe Gly Glu Tyr Gln Phe Leu Met Glu Lys
 115 120 125
 Glu Asp Gly Glu Ser Leu Glu Phe Phe Glu Thr Gln Phe Ile Leu Ser
 130 135 140
 Pro Arg Ser Leu Leu Gln Glu Asn Asn Trp Pro Pro His Arg Pro Ile
 145 150 155 160
 Pro Glu Tyr Gly Thr Tyr Ser Leu Cys Ser Ser Gln Ser Ser Ser Pro
 165 170 175
 Thr Glu Met Asp Glu Asn Glu Ser
 180

<210> 82
 <211> 1617
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (285)..(836)

<400> 82
 tttttacaaa ggccccgggc gcgagaggac gtgctctgcc agccagtggg aaggcaggcc 60
 ggcgcgcgcg gagcgcggga ggatcggcgg ctgcggtca ctggtccctg gctcggttcc 120
 ccgcaccccg gggctcacac ttaccgcgcg ggaggagcag cggccgggtg tccacccccca 180
 tctgcgccc agtctcctcg attccctcg ctctgagccg ggagagccga acagctgaag 240
 agagttcact gactccccag cccaggtgg gccttgatgca catc atg acc agt ttt 296
 Met Thr Ser Phe
 1

gaa gat gct gac aca gaa gag aca gta act tgt ctc cag atg acg gtt 344
 Glu Asp Ala Asp Thr Glu Glu Thr Val Thr Cys Leu Gln Met Thr Val
 5 10 15 20

tac cat cct ggc cag ttg cag tgt gga ata ttt cag tca ata agt ttt 392
 Tyr His Pro Gly Gln Leu Gln Cys Gly Ile Phe Gln Ser Ile Ser Phe
 25 30 35

aac aga gag aaa ctc cct tcc agc gaa gtg gtg aaa ttt ggc cga aat 440
 Asn Arg Glu Lys Leu Pro Ser Ser Glu Val Val Lys Phe Gly Arg Asn
 40 45 50

tcc aac atc tgt cat tat act ttt cag gac aaa cag gtt tcc cga gtt 488
 Ser Asn Ile Cys His Tyr Thr Phe Gln Asp Lys Gln Val Ser Arg Val
 55 60 65

cag ttt tct ctg cag ctg ttt aaa aaa ttc aac agc tca gtt ctc tcc	536
Gln Phe Ser Leu Gln Leu Phe Lys Lys Phe Asn Ser Ser Val Leu Ser	
70 75 80	
ttt gaa ata aaa aat atg agt aaa aag acc aat ctg atc gtg gac agc	584
Phe Glu Ile Lys Asn Met Ser Lys Lys Thr Asn Leu Ile Val Asp Ser	
85 90 95 100	
aga gag ctg ggc tac cta aat aaa atg gac ctg cca tac agg tgc atg	632
Arg Glu Leu Gly Tyr Leu Asn Lys Met Asp Leu Pro Tyr Arg Cys Met	
105 110 115	
gtc aga ttc gga gag tat cag ttt ctg atg gag aag gaa gat ggc gag	680
Val Arg Phe Gly Glu Tyr Gln Phe Leu Met Glu Lys Glu Asp Gly Glu	
120 125 130	
tca ttg gaa ttt ttt gag act caa ttt att tta tct cca aga tca ctc	728
Ser Leu Glu Phe Phe Glu Thr Gln Phe Ile Leu Ser Pro Arg Ser Leu	
135 140 145	
ttg caa gaa aac aac tgg cca cca cac agg ccc ata ccg gag tat ggc	776
Leu Gln Glu Asn Asn Trp Pro Pro His Arg Pro Ile Pro Glu Tyr Gly	
150 155 160	
act tat tcg ctc tgc tcc tcc caa agc agt tct ccg aca gaa atg gat	824
Thr Tyr Ser Leu Cys Ser Ser Gln Ser Ser Ser Pro Thr Glu Met Asp	
165 170 175 180	
gaa aat gag tca tgaacacaga aagtctaaga ggagaaatat gatggatgaa 876	
Glu Asn Glu Ser	
gagctctgta gatgctgtat agacactaaa taagagttga ttagggtagt atattatagt 936	
catctgttat gctgtgaaat ttggaattca gtattatcat tttgaagtct gtaaattgtg 996	
ttagtcatta acttagtcac ctgttgattt ctggatctac acaaaattat ttttaactgct 1056	
cttattaatc tgtgaggatt aatatacaaaa aagtatcctt tgagatgaag tcgtgttctc 1116	
aaaataagggt tatattatatt tctttttctg cttgattttc atcttgtggt ttgctttggt 1176	
tttgtaagga accatctctt ggtttggtca catcagttca caacagccat ttgttttcaa 1236	
ggtcaagggt ccaggcaggt tgttactggt gtttgcagcc tgtcagtact tgcagtactg 1296	
gaatagggtc taggctagtg tctgcgcgtc actgtggttt tagcatggga ggacttatatt 1356	
gagaaatact accttacttt tctatgattt ctttttacag agttatagtg tgtttactcc 1416	
taagatgaca gttctctttg tctatattca gcatctaaga caaatattta aacattttta 1476	
agaaccactg tgttaagttt aggattatatt acttaccaaaa ttagaagttt gacttttatg 1536	
tgttatacac aatcttaaaaa ttacacgaat tcaccttttt aatagtatcc atgtacataa 1596	
taaaatcaaa gtttaattag c 1617	

<210> 83
 <211> 392
 <212> PRT
 <213> Homo sapiens

 <400> 83
 Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser
 1 5 10 15
 Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr
 20 25 30
 Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser
 35 40 45
 Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn
 50 55 60
 Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
 65 70 75 80
 Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro
 85 90 95
 Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu
 100 105 110
 Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val
 115 120 125
 Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser
 130 135 140
 Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
 145 150 155 160
 Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln
 165 170 175
 Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
 180 185 190
 Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
 195 200 205
 Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
 210 215 220
 Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
 225 230 235 240
 Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser
 245 250 255
 Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu

260 265 270
 Phe Thr Val Gly Ser Leu Leu Glu Gln Gly Ala Leu Leu Glu Gly Thr
 275 280 285
 Arg Phe Met Gly Arg His Ser Glu Phe Ala Ala His Ala Leu Leu Leu
 290 295 300
 Ser Ile Cys Ser Ala Cys Gly Gln Leu Phe Ile Phe Tyr Thr Ile Gly
 305 310 315 320
 Gln Phe Gly Ala Ala Val Phe Thr Ile Ile Met Thr Leu Arg Gln Ala
 325 330 335
 Phe Ala Ile Leu Leu Ser Cys Leu Leu Tyr Gly His Thr Val Thr Val
 340 345 350
 Val Gly Gly Leu Gly Val Ala Val Val Phe Ala Ala Leu Leu Leu Arg
 355 360 365
 Val Tyr Ala Arg Gly Arg Leu Lys Gln Arg Gly Lys Lys Ala Val Pro
 370 375 380
 Val Glu Ser Pro Val Gln Lys Val
 385 390

<210> 84
 <211> 1898
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (119)..(1294)

<400> 84
 atttccgctg gccgctggct cgctggccgc tcttgaggc ggcggcggga gcgcaggggg 60
 cgcgcgggccc ggggactcgc attccccggt tccccctcca cccacgcgg cctggacc 118
 atg gac gcc aga tgg tgg gca gtg gtg gtg ctg gct gcg ttc ccc tcc 166
 Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser
 1 5 10 15
 cta ggg gca ggt ggg gag act ccc gaa gcc cct ccg gag tca tgg acc 214
 Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr
 20 25 30
 cag cta tgg ttc ttc cga ttt gtg gtg aat gct gct ggc tat gcc agc 262
 Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser
 35 40 45
 ttt atg gta cct ggc tac ctc ctg gtg cag tac ttc agg cgg aag aac 310
 Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn
 50 55 60

tac	ctg	gag	acc	ggg	agg	ggc	ctc	tgc	ttt	ccc	ctg	gtg	aaa	gct	tgt	358
Tyr	Leu	Glu	Thr	Gly	Arg	Gly	Leu	Cys	Phe	Pro	Leu	Val	Lys	Ala	Cys	
65					70					75					80	
gtg	ttt	ggc	aat	gag	ccc	aag	gcc	tct	gat	gag	ggt	ccc	ctg	gcg	ccc	406
Val	Phe	Gly	Asn	Glu	Pro	Lys	Ala	Ser	Asp	Glu	Val	Pro	Leu	Ala	Pro	
				85					90						95	
cga	aca	gag	gcg	gca	gag	acc	acc	ccg	atg	tgg	cag	gcc	ctg	aag	ctg	454
Arg	Thr	Glu	Ala	Ala	Glu	Thr	Thr	Pro	Met	Trp	Gln	Ala	Leu	Lys	Leu	
			100					105					110			
ctc	ttc	tgt	gcc	aca	ggg	ctc	cag	gtg	tct	tat	ctg	act	tgg	ggg	gtg	502
Leu	Phe	Cys	Ala	Thr	Gly	Leu	Gln	Val	Ser	Tyr	Leu	Thr	Trp	Gly	Val	
		115					120					125				
ctg	cag	gaa	aga	gtg	atg	acc	cgc	agc	tat	ggg	gcc	aca	gcc	aca	tca	550
Leu	Gln	Glu	Arg	Val	Met	Thr	Arg	Ser	Tyr	Gly	Ala	Thr	Ala	Thr	Ser	
	130					135					140					
ccg	ggg	gag	cgc	ttt	acg	gac	tgc	cag	ttc	ctg	gtg	cta	atg	aac	cga	598
Pro	Gly	Glu	Arg	Phe	Thr	Asp	Ser	Gln	Phe	Leu	Val	Leu	Met	Asn	Arg	
145					150					155					160	
gtg	ctg	gca	ctg	att	gtg	gct	ggc	ctc	tcc	tgt	ggt	ctc	tgc	aag	cag	646
Val	Leu	Ala	Leu	Ile	Val	Ala	Gly	Leu	Ser	Cys	Val	Leu	Cys	Lys	Gln	
				165					170					175		
ccc	cgg	cat	ggg	gca	ccc	atg	tac	cgg	tac	tcc	ttt	gcc	agc	ctg	tcc	694
Pro	Arg	His	Gly	Ala	Pro	Met	Tyr	Arg	Tyr	Ser	Phe	Ala	Ser	Leu	Ser	
			180					185					190			
aat	gtg	ctt	agc	agc	tgg	tgc	caa	tac	gaa	gct	ctt	aag	ttc	gtc	agc	742
Asn	Val	Leu	Ser	Ser	Trp	Cys	Gln	Tyr	Glu	Ala	Leu	Lys	Phe	Val	Ser	
		195					200					205				
ttc	ccc	acc	cag	gtg	ctg	gcc	aag	gcc	tct	aag	gtg	atc	cct	gtc	atg	790
Phe	Pro	Thr	Gln	Val	Leu	Ala	Lys	Ala	Ser	Lys	Val	Ile	Pro	Val	Met	
	210					215					220					
ctg	atg	gga	aag	ctt	gtg	tct	cgg	cgc	agc	tac	gaa	cac	tgg	gag	tac	838
Leu	Met	Gly	Lys	Leu	Val	Ser	Arg	Arg	Ser	Tyr	Glu	His	Trp	Glu	Tyr	
225					230					235				240		
ctg	aca	gcc	acc	ctc	atc	tcc	att	ggg	gtc	agc	atg	ttt	ctg	cta	tcc	886
Leu	Thr	Ala	Thr	Leu	Ile	Ser	Ile	Gly	Val	Ser	Met	Phe	Leu	Leu	Ser	
				245					250					255		
agc	gga	cca	gag	ccc	cgc	agc	tcc	cca	gcc	acc	aca	ctc	tca	ggc	ctc	934
Ser	Gly	Pro	Glu	Pro	Arg	Ser	Ser	Pro	Ala	Thr	Thr	Leu	Ser	Gly	Leu	
			260					265					270			
ttc	aca	gtg	ggc	tca	ctg	cta	gaa	cag	ggg	gcc	cta	ctg	gag	gga	acc	982
Phe	Thr	Val	Gly	Ser	Leu	Leu	Glu	Gln	Gly	Ala	Leu	Leu	Glu	Gly	Thr	
		275					280					285				
cgc	ttc	atg	ggg	cga	cac	agt	gag	ttt	gct	gcc	cat	gcc	ctg	cta	ctc	1030

Arg	Phe	Met	Gly	Arg	His	Ser	Glu	Phe	Ala	Ala	His	Ala	Leu	Leu	Leu	
290						295					300					
tcc	atc	tgc	tcc	gca	tgt	ggc	cag	ctc	ttc	atc	ttt	tac	acc	att	ggg	1078
Ser	Ile	Cys	Ser	Ala	Cys	Gly	Gln	Leu	Phe	Ile	Phe	Tyr	Thr	Ile	Gly	
305					310					315					320	
cag	ttt	ggg	gct	gcc	gtc	ttc	acc	atc	atc	atg	acc	ctc	cgc	cag	gcc	1126
Gln	Phe	Gly	Ala	Ala	Val	Phe	Thr	Ile	Ile	Met	Thr	Leu	Arg	Gln	Ala	
				325						330					335	
ttt	gcc	atc	ctt	ctt	tcc	tgc	ctt	ctc	tat	ggc	cac	act	gtc	act	gtg	1174
Phe	Ala	Ile	Leu	Leu	Ser	Cys	Leu	Leu	Tyr	Gly	His	Thr	Val	Thr	Val	
			340							345					350	
gtg	gga	ggg	ctg	ggg	gtg	gct	gtg	gtc	ttt	gct	gcc	ctc	ctg	ctc	aga	1222
Val	Gly	Gly	Leu	Gly	Val	Ala	Val	Val	Phe	Ala	Ala	Leu	Leu	Leu	Arg	
		355						360							365	
gtc	tac	gcg	cgg	ggc	cgt	cta	aag	caa	cgg	gga	aag	aag	gct	gtg	cct	1270
Val	Tyr	Ala	Arg	Gly	Arg	Leu	Lys	Gln	Arg	Gly	Lys	Lys	Ala	Val	Pro	
	370						375								380	
gtt	gag	tct	cct	gtg	cag	aag	gtt	tgagggtgga	aagggcctga	ggggtgaagt						1324
Val	Glu	Ser	Pro	Val	Gln	Lys	Val									
385						390										
gaaataggac cctccaccca tccccttctg ctgtaacctc tgaggagct ggctgaaagg 1384																
gcaaaatgca ggtgttttct cagtatcaca gaccagctct gcagcagggg attggggagc 1444																
ccaggaggca gccttccctt ttgccttaag tcacccatct tccagtaagc agttttattct 1504																
gagccccggg ggtagacagt cctcagtgag gggttttggg gagtttgggg tcaagagagc 1564																
ataggtaggt tccacagtta ctcttccac aagttccctt aagtcttgcc ctagctgtgc 1624																
tctgccacct tccagactca ctcccctctg caaataacctg catttcttac cctggtgaga 1684																
aaagcacaag cgggtgtaggc tccaatgctg ctttcccagg aggggtgaaga tgggtgctgtg 1744																
ctgaggaaag gggatgcaga gccctgcccc gcaccaccac ctctatgct cctggatccc 1804																
taggctctgt tccatgagcc tgttgcaggt tttggtactt tagaaatgta actttttgct 1864																
cttataattt tattttatta aattaaatta ctgc 1898																
<210> 85																
<211> 432																
<212> PRT																
<213> Homo sapiens																
<400> 85																
Met	Asp	Ala	Arg	Trp	Trp	Ala	Val	Val	Val	Leu	Ala	Ala	Phe	Pro	Ser	
1				5					10					15		

Gln	Gly	Ala	Leu	Leu	Glu	Gly	Thr	Arg	Phe	Met	Gly	Arg	His	Ser	Glu
			325						330					335	
Phe	Ala	Ala	His	Ala	Leu	Leu	Leu	Ser	Ile	Cys	Ser	Ala	Cys	Gly	Gln
			340					345					350		
Leu	Phe	Ile	Phe	Tyr	Thr	Ile	Gly	Gln	Phe	Gly	Ala	Ala	Val	Phe	Thr
		355					360					365			
Ile	Ile	Met	Thr	Leu	Arg	Gln	Ala	Phe	Ala	Ile	Leu	Leu	Ser	Cys	Leu
	370					375					380				
Leu	Tyr	Gly	His	Thr	Val	Thr	Val	Val	Gly	Gly	Leu	Gly	Val	Ala	Val
385					390					395					400
Val	Phe	Ala	Ala	Leu	Leu	Leu	Arg	Val	Tyr	Ala	Arg	Gly	Arg	Leu	Lys
			405						410					415	
Gln	Arg	Gly	Lys	Lys	Ala	Val	Pro	Val	Glu	Ser	Pro	Val	Gln	Lys	Val
			420					425					430		

<210> 86
 <211> 2018
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (119)..(1414)

<400> 86
 acttccgctg gccgctggct cgctggccgc tcctggaggc ggcggcggga gcgcaggggg 60
 cgcgcgggccc ggggaactgc attccccggt tccccctcca cccacgcgg cctggacc 118
 atg gac gcc aga tgg tgg gca gtg gtg gtg ctg gct gcg ttc ccc tcc 166
 Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser
 1 5 10 15
 cta ggg gca ggt ggg gag act ccc gaa gcc cct ccg gag tca tgg acc 214
 Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr
 20 25 30
 cag cta tgg ttc ttc cga ttt gtg gtg aat gct gct ggc tat gcc agc 262
 Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser
 35 40 45
 ttt atg gta cct ggc tac ctc ctg gtg cag tac ttc agg cgg aag aac 310
 Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn
 50 55 60
 tac ctg gag acc ggt agg ggc ctc tgc ttt ccc ctg gtg aaa gct tgt 358
 Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
 65 70 75 80
 gtg ttt ggc aat gag ccc aag gcc tct gat gag gtt ccc ctg gcg ccc 406

Val	Phe	Gly	Asn	Glu	Pro	Lys	Ala	Ser	Asp	Glu	Val	Pro	Leu	Ala	Pro	-		
85																90	95	
cga	aca	gag	gcg	gca	gag	acc	acc	ccg	atg	tgg	cag	gcc	ctg	aag	ctg	454		
Arg	Thr	Glu	Ala	Ala	Glu	Thr	Thr	Pro	Met	Trp	Gln	Ala	Leu	Lys	Leu			
100																105	110	
ctc	ttc	tgt	gcc	aca	ggg	ctc	cag	gtg	tct	tat	ctg	act	tgg	ggg	gtg	502		
Leu	Phe	Cys	Ala	Thr	Gly	Leu	Gln	Val	Ser	Tyr	Leu	Thr	Trp	Gly	Val			
115																120	125	
ctg	cag	gaa	aga	gtg	atg	acc	cgc	agc	tat	ggg	gcc	aca	gcc	aca	tca	550		
Leu	Gln	Glu	Arg	Val	Met	Thr	Arg	Ser	Tyr	Gly	Ala	Thr	Ala	Thr	Ser			
130																135	140	
ccg	ggg	gag	cgc	ttt	acg	gac	tcg	cag	ttc	ctg	gtg	cta	atg	aac	cga	598		
Pro	Gly	Glu	Arg	Phe	Thr	Asp	Ser	Gln	Phe	Leu	Val	Leu	Met	Asn	Arg			
145																150	155	160
gtg	ctg	gca	ctg	att	gtg	gct	ggc	ctc	tcc	tgt	gtt	ctc	tgc	aag	cag	646		
Val	Leu	Ala	Leu	Ile	Val	Ala	Gly	Leu	Ser	Cys	Val	Leu	Cys	Lys	Gln			
165																170	175	
ccc	cgg	cat	ggg	gca	ccc	atg	tac	cgg	tac	tcc	ttt	gcc	agc	ctg	tcc	694		
Pro	Arg	His	Gly	Ala	Pro	Met	Tyr	Arg	Tyr	Ser	Phe	Ala	Ser	Leu	Ser			
180																185	190	
aat	gtg	ctt	agc	agc	tgg	tgc	caa	tac	gaa	gct	ctt	aag	ttc	gtc	agc	742		
Asn	Val	Leu	Ser	Ser	Trp	Cys	Gln	Tyr	Glu	Ala	Leu	Lys	Phe	Val	Ser			
195																200	205	
ttc	ccc	acc	cag	gtg	ctg	gcc	aag	gcc	tct	aag	gtg	atc	cct	gtc	atg	790		
Phe	Pro	Thr	Gln	Val	Leu	Ala	Lys	Ala	Ser	Lys	Val	Ile	Pro	Val	Met			
210																215	220	
ctg	atg	gga	aag	ctt	gtg	tct	cgg	cgc	agc	tac	gaa	cac	tgg	gag	tac	838		
Leu	Met	Gly	Lys	Leu	Val	Ser	Arg	Arg	Ser	Tyr	Glu	His	Trp	Glu	Tyr			
225																230	235	240
ctg	aca	gcc	acc	ctc	atc	tcc	att	ggg	gtc	agc	atg	ttt	ctg	cta	tcc	886		
Leu	Thr	Ala	Thr	Leu	Ile	Ser	Ile	Gly	Val	Ser	Met	Phe	Leu	Leu	Ser			
245																250	255	
agc	gga	cca	gag	ccc	cgc	agc	tcc	cca	gcc	acc	aca	ctc	tca	ggc	ctc	934		
Ser	Gly	Pro	Glu	Pro	Arg	Ser	Ser	Pro	Ala	Thr	Thr	Leu	Ser	Gly	Leu			
260																265	270	
atc	tta	ctg	gca	ggg	tat	att	gct	ttt	gac	agc	ttc	acc	tca	aac	tgg	982		
Ile	Leu	Leu	Ala	Gly	Tyr	Ile	Ala	Phe	Asp	Ser	Phe	Thr	Ser	Asn	Trp			
275																280	285	
cag	gat	gcc	ctg	ttt	gcc	tat	aag	atg	tca	tcg	gtg	cag	atg	atg	ttt	1030		
Gln	Asp	Ala	Leu	Phe	Ala	Tyr	Lys	Met	Ser	Ser	Val	Gln	Met	Met	Phe			
290																295	300	
ggg	gtc	aat	ttc	ttc	tcc	tgc	ctc	ttc	aca	gtg	ggc	tca	ctg	cta	gaa	1078		
Gly	Val	Asn	Phe	Phe	Ser	Cys	Leu	Phe	Thr	Val	Gly	Ser	Leu	Leu	Glu			

305	310	315	320	
cag ggg gcc cta ctg gag gga acc cgc ttc atg ggg cga cac agt gag				1126
Gln Gly Ala Leu Leu Glu Gly Thr Arg Phe Met Gly Arg His Ser Glu				
325		330	335	
ttt gct gcc cat gcc ctg cta ctc tcc atc tgc tcc gca tgt ggc cag				1174
Phe Ala Ala His Ala Leu Leu Leu Ser Ile Cys Ser Ala Cys Gly Gln				
340		345	350	
ctc ttc atc ttt tac acc att ggg cag ttt ggg gct gcc gtc ttc acc				1222
Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala Ala Val Phe Thr				
355		360	365	
atc atc atg acc ctc cgc cag gcc ttt gcc atc ctt ctt tcc tgc ctt				1270
Ile Ile Met Thr Leu Arg Gln Ala Phe Ala Ile Leu Leu Ser Cys Leu				
370		375	380	
ctc tat ggc cac act gtc act gtg gtg gga ggg ctg ggg gtg gct gtg				1318
Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val				
385		390	400	
gtc ttt gct gcc ctc ctg ctc aga gtc tac gcg cgg ggc cgt cta aag				1366
Val Phe Ala Ala Leu Leu Leu Arg Val Tyr Ala Arg Gly Arg Leu Lys				
405		410	415	
caa cgg gga aag aag gct gtg cct gtt gag tct cct gtg cag aag gtt				1414
Gln Arg Gly Lys Lys Ala Val Pro Val Glu Ser Pro Val Gln Lys Val				
420		425	430	
tgagggtgga aagggcctga ggggtgaagt gaaataggac cctcccacca tccccttctg				1474
ctgtaacctc tgaggagct ggctgaaagg gcaaaatgca ggtgttttct cagtatcaca				1534
gaccagctct gcagcagggg attggggagc ccaggaggca gccttccctt ttgccttaag				1594
tcacccatct tccagtaagc agttttattct gagccccggg ggtagacagt cctcagtgag				1654
gggttttgagg gagtttgagg tcaagagagc ataggtaggt tccacagtta ctcttcccac				1714
aagttccctt aagtcttgcc ctagctgtgc tctgccacct tccagactca ctcccctctg				1774
caaatacctg catttcttac cctggtgaga aaagcacaag cgggtgtaggc tccaatgctg				1834
ctttcccagg aggggtgaaga tgggtgctgtg ctgaggaaag gggatgcaga gccctgccc				1894
gcaccaccac ctctatgct cctggatccc taggctctgt tccatgagcc tgttgacaggt				1954
tttggtactt tagaaatgta actttttgct cttataattt tattttatta aattaaatta				2014
ctgc				2018

<210> 87
 <211> 235
 <212> PRT
 <213> Homo sapiens

<400> 87

Met Gly Ile Gly Lys Ser Lys Ile Asn Ser Cys Pro Leu Ser Leu Ser
1 5 10 15

Trp Gly Lys Arg His Ser Val Asp Thr Ser Pro Gly Tyr His Glu Ser
20 25 30

Asp Ser Lys Lys Ser Glu Asp Leu Ser Leu Cys Asn Val Ala Glu His
35 40 45

Ser Asn Thr Thr Glu Gly Pro Thr Gly Lys Gln Glu Gly Ala Gln Ser
50 55 60

Val Glu Glu Met Phe Glu Glu Glu Ala Glu Glu Glu Val Phe Leu Lys
65 70 75 80

Phe Val Ile Leu His Ala Glu Asp Asp Thr Asp Glu Ala Leu Arg Val
85 90 95

Gln Asn Leu Leu Gln Asp Asp Phe Gly Ile Lys Pro Gly Ile Ile Phe
100 105 110

Ala Glu Met Pro Cys Gly Arg Gln His Leu Gln Asn Leu Asp Asp Ala
115 120 125

Val Asn Gly Ser Ala Trp Thr Ile Leu Leu Leu Thr Glu Asn Phe Leu
130 135 140

Arg Asp Thr Trp Cys Asn Phe Gln Phe Tyr Thr Ser Leu Met Asn Ser
145 150 155 160

Val Asn Arg Gln His Lys Tyr Asn Ser Val Ile Pro Met Arg Pro Leu
165 170 175

Asn Asn Pro Leu Pro Arg Glu Arg Thr Pro Phe Ala Leu Gln Thr Ile
180 185 190

Asn Ala Leu Glu Glu Glu Ser Arg Gly Phe Pro Thr Gln Val Glu Arg
195 200 205

Ile Phe Gln Glu Ser Val Tyr Lys Thr Gln Gln Thr Ile Trp Lys Glu
210 215 220

Thr Arg Asn Met Val Gln Arg Gln Phe Ile Ala
225 230 235

<210> 88

<211> 2717

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (111)..(815)

<400> 88

```

aaaaggaaga cagaaaagcc gcgggctgac tgtggtggcg ctgcctgca gattgaaaag 60

aaatgctgag aaatacataa agttttcctc ttctgccttg gatatttata atg ggt      116
                                   Met Gly
                                   1

atc ggg aag tct aaa ata aat tcc tgc cct ctt tct ctc tct tgg ggt      164
Ile Gly Lys Ser Lys Ile Asn Ser Cys Pro Leu Ser Leu Ser Trp Gly
      5                                10                                15

aaa agg cac agt gtg gat aca agt cca gga tat cat gag tca gat tcc      212
Lys Arg His Ser Val Asp Thr Ser Pro Gly Tyr His Glu Ser Asp Ser
      20                                25                                30

aag aag tct gaa gat cta tcc ttg tgt aat gtt gct gag cac agc aat      260
Lys Lys Ser Glu Asp Leu Ser Leu Cys Asn Val Ala Glu His Ser Asn
      35                                40                                45                                50

aca aca gag ggg cca aca gga aag cag gag gga gct cag agc gtg gaa      308
Thr Thr Glu Gly Pro Thr Gly Lys Gln Glu Gly Ala Gln Ser Val Glu
      55                                60                                65

gag atg ttt gaa gaa gaa gct gaa gaa gag gtg ttc ctc aaa ttt gtg      356
Glu Met Phe Glu Glu Glu Ala Glu Glu Glu Val Phe Leu Lys Phe Val
      70                                75                                80

ata ttg cat gca gaa gat gac aca gat gaa gcc ctc aga gtc cag aat      404
Ile Leu His Ala Glu Asp Asp Thr Asp Glu Ala Leu Arg Val Gln Asn
      85                                90                                95

ctg cta caa gat gac ttt ggt atc aaa ccc gga ata atc ttt gct gag      452
Leu Leu Gln Asp Asp Phe Gly Ile Lys Pro Gly Ile Ile Phe Ala Glu
      100                                105                                110

atg cca tgt ggc aga cag cat tta cag aat tta gat gat gct gta aat      500
Met Pro Cys Gly Arg Gln His Leu Gln Asn Leu Asp Asp Ala Val Asn
      115                                120                                125                                130

ggg tct gca tgg aca atc tta tta ctg act gaa aac ttt tta aga gat      548
Gly Ser Ala Trp Thr Ile Leu Leu Leu Thr Glu Asn Phe Leu Arg Asp
      135                                140                                145

act tgg tgt aat ttc cag ttc tat acg tcc cta atg aac tcc gtt aac      596
Thr Trp Cys Asn Phe Gln Phe Tyr Thr Ser Leu Met Asn Ser Val Asn
      150                                155                                160

agg cag cat aaa tac aac tct gtt ata ccc atg cgg ccc ctg aac aat      644
Arg Gln His Lys Tyr Asn Ser Val Ile Pro Met Arg Pro Leu Asn Asn
      165                                170                                175

ccc ctt ccc cga gaa agg act ccc ttt gcc ctc caa acc atc aat gcc      692
Pro Leu Pro Arg Glu Arg Thr Pro Phe Ala Leu Gln Thr Ile Asn Ala
      180                                185                                190

tta gag gaa gaa agt cgt gga ttt cct aca caa gta gaa aga att ttt      740
Leu Glu Glu Glu Ser Arg Gly Phe Pro Thr Gln Val Glu Arg Ile Phe

```


195	200	205	210	
cag gag tct gtg tat aag aca caa caa act ata tgg aaa gag aca aga				788
Gln Glu Ser Val Tyr Lys Thr Gln Gln Thr Ile Trp Lys Glu Thr Arg				
	215	220	225	
aat atg gta caa aga caa ttt att gcc tgagatgaaa catataacat				835
Asn Met Val Gln Arg Gln Phe Ile Ala				
	230	235		
gtggctggct cttgttttgt aaaccaaattg attaatcttc acttgagaaa gcagtttcta				895
ggaaatgttt aaataaaaga gagtcttcac cttaaagaaa cctatggagc acaagaaaga				955
taaatttctg caggacagcc tataaaattg tggtaactttt tgatgtttca gtaaacttga				1015
cattgtcaga gtttcaagga cttttctttc acaattttcc tagttcatgg atatgaaaaa				1075
ggaattctca atccatattc cttgtattga accttgaaca aaaacttgta tgacagacat				1135
ttttaaaaaat gtgacaacac ttttattctc tgaattttga tctcaaagga cacagaaaaa				1195
aaatggcccc aggagatctg atcacacttc ctctgaggc acctctcatg gatgttgcaa				1255
taagcattcg ggtactatca cccagaaata tgaattgcca gaatagaaca tttagcatgt				1315
taagcgttga tgcatataaa atcagaaata gatgtgagaa tgggtggaact ttttaaaaga				1375
accagtcaa atgtattttc tgctgaaatc tgcatatttg gaggcatttc ccaccaccga				1435
ttcacagccc atttgatagt gtggtagtta gggacttcgt ggagtgggtg tcagacgtcc				1495
cctggggctt aaatctcttc atattagtca tcatttgtaa ctatggcttt atttgcagag				1555
cttctaaaag gcgtataact gtgtgagtgg ccagatattc actttttaga tcaaaaacct				1615
ctcttatgga agctttaaaa gtttccgtca cacacaattc tcttctcagg aagtatttct				1675
catttaggtc ttcaaagtag cctgactgtg tgcatgtgtg tgtgtgatag gttatttata				1735
aagactttgg atagaaggag atgtatttta ttacctcta ttctagagcc ccatgctcct				1795
aacaagccag agaggcccca aacaggattg tttctttcct ccacagccct tctgcccac				1855
tgagattgag ggagcatcgt ccacttgaga tcagggatgg ggtggagaat gggatcatgtc				1915
atgtaatgag aaaagccctc ttcgggatca tgagacttgg ttctagtcca atttctgcc				1975
ctgaggatga atgtaactgt gggcaaaacta tttaccctcc tttatctgtg aaatgaaagg				2035
gttgaattga tggatctcta aaggcttttg tcctctatga ggatgtgaaa aactagggac				2095
cacaaaaggg aacaagcaaa aaagtttgga ttcgataaag tgatatgtaa tagttgcaga				2155
aggctttata tatgcttata atgaaaagat attttttgta tattgacagc ataatttatt				2215
tttaatgctg tcattacact taaagtcaca ggaaaaaat atacatgctt actcaggctt				2275

tcttaaaaat aaatttttat agagatcctt gagtaaagac attttgctta atttcttttt 2335
 tcttattccc cacttgtata tcccctacca gtaccgggat ctgcacacat ctttttgag 2395
 ttacctcttc atagccatga accaaaacgt tctatgagga gcatgcaagt aagtcaagcc 2455
 tcctattctg ttagtactta ttagaggagg agatgggttt cattgcatag tgacattttc 2515
 ttagccttaa cgttctgata gtagcttact actcacttct ctttttcagt tttcataata 2575
 agtattcatt tttttgccat aatgcttcct gtaaagccaa ttttatatac taataaaaca 2635
 tgaactgccc actcttcatg cctgccaaac ttggggcaat tgatgctaaa tgggtattttt 2695
 aaaataaatg tttttattct tt 2717

<210> 89
 <211> 245
 <212> PRT
 <213> Homo sapiens

<400> 89
 Met Ala Ser Pro Ser Arg Arg Leu Gln Thr Lys Pro Val Ile Thr Cys
 1 5 10 15
 Phe Lys Ser Val Leu Leu Ile Tyr Thr Phe Ile Phe Trp Ile Thr Gly
 20 25 30
 Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser Leu Glu Asn
 35 40 45
 Tyr Phe Ser Leu Leu Asn Glu Lys Ala Thr Asn Val Pro Phe Val Leu
 50 55 60
 Ile Ala Thr Gly Thr Val Ile Ile Leu Leu Gly Thr Phe Gly Cys Phe
 65 70 75 80
 Ala Thr Cys Arg Ala Ser Ala Trp Met Leu Lys Leu Tyr Ala Met Phe
 85 90 95
 Leu Thr Leu Val Phe Leu Val Glu Leu Val Ala Ala Ile Val Gly Phe
 100 105 110
 Val Phe Arg His Glu Ile Lys Asn Ser Phe Lys Asn Asn Tyr Glu Lys
 115 120 125
 Ala Leu Lys Gln Tyr Asn Ser Thr Gly Asp Tyr Arg Ser His Ala Val
 130 135 140
 Asp Lys Ile Gln Asn Thr Leu His Cys Cys Gly Val Thr Asp Tyr Arg
 145 150 155 160
 Asp Trp Thr Asp Thr Asn Tyr Tyr Ser Glu Lys Gly Phe Pro Lys Ser
 165 170 175

Cys	Cys	Lys	Leu	Glu	Asp	Cys	Thr	Pro	Gln	Arg	Asp	Ala	Asp	Lys	Val
			180					185					190		
Asn	Asn	Glu	Gly	Cys	Phe	Ile	Lys	Val	Met	Thr	Ile	Ile	Glu	Ser	Glu
		195					200					205			
Met	Gly	Val	Val	Ala	Gly	Ile	Ser	Phe	Gly	Val	Ala	Cys	Phe	Gln	Leu
	210					215					220				
Ile	Gly	Ile	Phe	Leu	Ala	Tyr	Cys	Leu	Ser	Arg	Ala	Ile	Thr	Asn	Asn
225					230					235					240
Gln	Tyr	Glu	Ile	Val											
				245											

<210> 90
 <211> 1793
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (60)..(794)

<400> 90
 gcgtctcgct ctctgtgttc caatcgcccg gtgcggtggt gcagggtctc gggctagtc 59
 atg gcg tcc ccg tct cgg aga ctg cag act aaa cca gtc att act tgt 107
 Met Ala Ser Pro Ser Arg Arg Leu Gln Thr Lys Pro Val Ile Thr Cys
 1 5 10 15
 ttc aag agc gtt ctg cta atc tac act ttt att ttc tgg atc act ggc 155
 Phe Lys Ser Val Leu Leu Ile Tyr Thr Phe Ile Phe Trp Ile Thr Gly
 20 25 30
 gtt atc ctt ctt gca gtt ggc att tgg ggc aag gtg agc ctg gag aat 203
 Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser Leu Glu Asn
 35 40 45
 tac ttt tct ctt tta aat gag aag gcc acc aat gtc ccc ttc gtg ctc 251
 Tyr Phe Ser Leu Leu Asn Glu Lys Ala Thr Asn Val Pro Phe Val Leu
 50 55 60
 att gct act ggt acc gtc att att ctt ttg ggc acc ttt ggt tgt ttt 299
 Ile Ala Thr Gly Thr Val Ile Ile Leu Leu Gly Thr Phe Gly Cys Phe
 65 70 75 80
 gct acc tgc cga gct tct gca tgg atg cta aaa ctg tat gca atg ttt 347
 Ala Thr Cys Arg Ala Ser Ala Trp Met Leu Lys Leu Tyr Ala Met Phe
 85 90 95
 ctg act ctc gtt ttt ttg gtc gaa ctg gtc gct gcc atc gta gga ttt 395
 Leu Thr Leu Val Phe Leu Val Glu Leu Val Ala Ala Ile Val Gly Phe
 100 105 110
 gtt ttc aga cat gag att aag aac agc ttt aag aat aat tat gag aag 443

_actactgatg-ttctgtgata catcagggttt cagcacacaa cttacatttc tttagcctcca 1554
 aattgaggca tttattatga tgttcatact ttccctcttg ttgaaagtt tctaattatt 1614
 aaatggtgtc ggaattgttg tattttcctt aggaattcag tggaacttat cttcattaaa 1674
 tttagctggt accaggttga tatgacttgt caatattatg gtcaacttta agtcttagtt 1734
 ttcgtttgtg cctttgatta ataagtataa ctcttataca ataaatactg ctttcctct 1793

<210> 91
 <211> 180
 <212> PRT
 <213> Homo sapiens

<400> 91
 Met Ala Ser Thr Ser Tyr Asp Tyr Cys Arg Val Pro Met Glu Asp Gly
 1 5 10 15
 Asp Lys Arg Cys Lys Leu Leu Leu Gly Ile Gly Ile Leu Val Leu Leu
 20 25 30
 Ile Ile Val Ile Leu Gly Val Pro Leu Ile Ile Phe Thr Ile Lys Ala
 35 40 45
 Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg
 50 55 60
 Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly
 65 70 75 80
 Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met
 85 90 95
 Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys
 100 105 110
 Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln
 115 120 125
 Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu
 130 135 140
 Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser
 145 150 155 160
 Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser
 165 170 175
 Ala Leu Leu Gln
 180

<210> 92
 <211> 970
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (26)..(565)

<400> 92

```
tttttcagct aaaggggaga tctgg atg gca tct act tcg tat gac tat tgc 52
                        Met Ala Ser Thr Ser Tyr Asp Tyr Cys
                          1                      5

aga gtg ccc atg gaa gac ggg gat aag cgc tgt aag ctt ctg ctg ggg 100
Arg Val Pro Met Glu Asp Gly Asp Lys Arg Cys Lys Leu Leu Leu Gly
 10                      15                      20                      25

ata gga att ctg gtg ctc ctg atc atc gtg att ctg ggg gtg ccc ttg 148
Ile Gly Ile Leu Val Leu Leu Ile Ile Val Ile Leu Gly Val Pro Leu
                      30                      35                      40

att atc ttc acc atc aag gcc aac agc gag gcc tgc cgg gac ggc ctt 196
Ile Ile Phe Thr Ile Lys Ala Asn Ser Glu Ala Cys Arg Asp Gly Leu
                      45                      50                      55

cgg gca gtg atg gag tgt cgc aat gtc acc cat ctc ctg caa caa gag 244
Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu Leu Gln Gln Glu
                      60                      65                      70

ctg acc gag gcc cag aag ggc ttt cag gat gtg gag gcc cag gct gcc 292
Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu Ala Gln Ala Ala
                      75                      80                      85

acc tgc aac cac act gtg atg gcc cta atg gct tcc ctg gat gca gag 340
Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser Leu Asp Ala Glu
                      90                      95                      100                      105

aag gcc caa gga caa aag aaa gtg gag gag ctt gag gga gag atc act 388
Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu Gly Glu Ile Thr
                      110                      115                      120

aca tta aac cat aag ctt cag gac gcg tct gca gag gtg gag cga ctg 436
Thr Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu Val Glu Arg Leu
                      125                      130                      135

aga aga gaa aac cag gtc tta agc gtg aga atc gcg gac aag aag tac 484
Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala Asp Lys Lys Tyr
                      140                      145                      150

tac ccc agc tcc cag gac tcc agc tcc gct gcg gcg ccc cag ctg ctg 532
Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala Ala Ala Pro Gln Leu Leu
                      155                      160                      165

att gtg ctg ctg ggc ctc agc gct ctg ctg cag tgagatccca ggaagctggc 585
Ile Val Leu Leu Gly Leu Ser Ala Leu Leu Gln
170                      175                      180

acatcttgga aggtccgtcc tgctcggctt ttcgcttgaa cattcccttg atctcatcag 645
```

ttctgagcgg gtcattggggc aacacgggta gcggggagag caeggggtag ccggagaagg 705
 gcctctggag caggtctgga ggggccatgg ggcagtcctg ggtgtgggga cacagtcggg 765
 ttgaccaggg gctgtctccc tccagagcct ccctccggac aatgagtcct ccctcttctc 825
 tcccaccctg agattgggca tgggggtgcgg tgtggggggc atgtgctgcc tgttggttatg 885
 ggtttttttt gcgggggggg ttgctttttt ctgggggtctt tgagctccaa aaaataaaca 945
 ctctctttga gggagagcac acctt 970

<210> 93
 <211> 331
 <212> PRT
 <213> Homo sapiens

<400> 93
 Met Asp Ser Glu Lys Lys Arg Phe Thr Glu Glu Ala Thr Lys Tyr Phe
 1 5 10 15
 Arg Glu Arg Val Ser Pro Val His Leu Gln Ile Leu Leu Thr Asn Asn
 20 25 30
 Glu Ala Trp Lys Arg Phe Val Thr Ala Ala Glu Leu Pro Arg Asp Glu
 35 40 45
 Ala Asp Ala Leu Tyr Glu Ala Leu Lys Lys Leu Arg Thr Tyr Ala Ala
 50 55 60
 Ile Glu Asp Glu Tyr Val Gln Gln Lys Asp Glu Gln Phe Arg Glu Trp
 65 70 75 80
 Phe Leu Lys Glu Phe Pro Gln Val Lys Arg Lys Ile Gln Glu Ser Ile
 85 90 95
 Glu Lys Leu Arg Ala Leu Ala Asn Gly Ile Glu Glu Val His Arg Gly
 100 105 110
 Cys Thr Ile Ser Asn Val Val Ser Ser Ser Thr Gly Ala Ala Ser Gly
 115 120 125
 Ile Met Ser Leu Ala Gly Leu Val Leu Ala Pro Phe Thr Ala Gly Thr
 130 135 140
 Ser Leu Ala Leu Thr Ala Ala Gly Val Gly Leu Gly Ala Ala Ser Ala
 145 150 155 160
 Val Thr Gly Ile Thr Thr Ser Ile Val Glu His Ser Tyr Thr Ser Ser
 165 170 175
 Ala Glu Ala Glu Ala Ser Arg Leu Thr Ala Thr Ser Ile Asp Arg Leu
 180 185 190
 Lys Val Phe Lys Glu Val Met Arg Asp Ile Thr Pro Asn Leu Leu Ser
 195 200 205

Leu Leu Asn Asn Tyr Tyr Glu Ala Thr Gln Thr Ile Gly Ser Glu Ile
 210 215 220
 Arg Ala Ile Arg Gln Ala Arg Ala Arg Ala Arg Leu Pro Val Thr Thr
 225 230 235 240
 Trp Arg Ile Ser Ala Gly Ser Gly Gly Gln Ala Glu Arg Thr Ile Ala
 245 250 255
 Gly Thr Thr Arg Ala Val Ser Arg Gly Ala Arg Ile Leu Ser Ala Thr
 260 265 270
 Thr Ser Gly Ile Phe Leu Ala Leu Asp Val Val Asn Leu Val Tyr Glu
 275 280 285
 Ser Lys His Leu His Glu Gly Ala Lys Ser Ala Ser Ala Glu Glu Leu
 290 295 300
 Arg Arg Gln Ala Gln Glu Leu Glu Glu Asn Leu Met Glu Leu Thr Gln
 305 310 315 320
 Ile Tyr Gln Arg Leu Asn Pro Cys His Thr His
 325 330

<210> 94
 <211> 2039
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (175)..(1167)

<400> 94
 attatgcaga tgcacggctg gaggtgggat ccacacagct cagaacagct ggatcttgct 60
 cacactcttt caagagaagc ttccttgggt taagaaaaaa aacgaaccct tccagtcagg 120
 tcagtgactg gagagctcca aggaaagtct ctcagtgacc tggctgctgg cacc atg 177
 Met
 1
 gac tca gaa aag aaa cgc ttt act gaa gag gcc acc aaa tac ttc cgg 225
 Asp Ser Glu Lys Lys Arg Phe Thr Glu Glu Ala Thr Lys Tyr Phe Arg
 5 10 15
 gag aga gtc agc cca gtg cat ctg caa atc ctg ctg act aac aat gaa 273
 Glu Arg Val Ser Pro Val His Leu Gln Ile Leu Leu Thr Asn Asn Glu
 20 25 30
 gcc tgg aag aga ttc gtg act gcg gct gaa ttg ccc agg gat gag gca 321
 Ala Trp Lys Arg Phe Val Thr Ala Ala Glu Leu Pro Arg Asp Glu Ala
 35 40 45
 gat gct ctc tac gaa gct ctg aag aag ctt aga aca tat gca gct att 369

Asp	Ala	Leu	Tyr	Glu	Ala	Leu	Lys	Lys	Leu	Arg	Thr	Tyr	Ala	Ala	Ile	—
50					55					60					65	
gag	gac	gaa	tat	gtg	cag	cag	aaa	gat	gag	cag	ttt	agg	gaa	tgg	ttt	417
Glu	Asp	Glu	Tyr	Val	Gln	Gln	Lys	Asp	Glu	Gln	Phe	Arg	Glu	Trp	Phe	
				70					75					80		
ttg	aaa	gag	ttt	ccc	caa	gtc	aag	agg	aag	atc	cag	gag	tcc	ata	gaa	465
Leu	Lys	Glu	Phe	Pro	Gln	Val	Lys	Arg	Lys	Ile	Gln	Glu	Ser	Ile	Glu	
			85					90					95			
aag	ctt	cgt	gcc	ctt	gca	aat	ggt	att	gaa	gag	gtc	cac	aga	ggc	tgc	513
Lys	Leu	Arg	Ala	Leu	Ala	Asn	Gly	Ile	Glu	Glu	Val	His	Arg	Gly	Cys	
		100					105					110				
acc	atc	tcc	aac	gtg	gtg	tcc	agc	tcc	act	ggc	gct	gcc	tct	ggc	atc	561
Thr	Ile	Ser	Asn	Val	Val	Ser	Ser	Ser	Thr	Gly	Ala	Ala	Ser	Gly	Ile	
	115					120					125					
atg	tcc	ctt	gct	ggt	ctt	gtt	ttg	gca	cca	ttt	aca	gca	ggg	acg	agt	609
Met	Ser	Leu	Ala	Gly	Leu	Val	Leu	Ala	Pro	Phe	Thr	Ala	Gly	Thr	Ser	
130					135					140					145	
ctg	gcc	ctt	act	gca	gct	ggg	gta	ggg	ctg	gga	gca	gcg	tct	gct	gtg	657
Leu	Ala	Leu	Thr	Ala	Ala	Gly	Val	Gly	Leu	Gly	Ala	Ala	Ser	Ala	Val	
				150					155					160		
act	ggg	atc	acc	acc	agc	atc	gtg	gag	cac	tca	tac	aca	tca	tca	gca	705
Thr	Gly	Ile	Thr	Thr	Ser	Ile	Val	Glu	His	Ser	Tyr	Thr	Ser	Ser	Ala	
			165					170					175			
gaa	gct	gaa	gcc	agc	agg	ctg	act	gca	acc	agc	att	gac	cga	ttg	aag	753
Glu	Ala	Glu	Ala	Ser	Arg	Leu	Thr	Ala	Thr	Ser	Ile	Asp	Arg	Leu	Lys	
		180				185						190				
gta	ttt	aag	gaa	gtt	atg	cgt	gac	atc	aca	ccc	aac	tta	ctt	tcc	ctt	801
Val	Phe	Lys	Glu	Val	Met	Arg	Asp	Ile	Thr	Pro	Asn	Leu	Leu	Ser	Leu	
	195					200					205					
ctt	aat	aat	tat	tac	gaa	gcc	aca	caa	acc	att	ggg	agt	gaa	atc	cgt	849
Leu	Asn	Asn	Tyr	Tyr	Glu	Ala	Thr	Gln	Thr	Ile	Gly	Ser	Glu	Ile	Arg	
210					215					220					225	
gcc	atc	agg	caa	gcc	aga	gcc	agg	gcc	cga	ctc	cct	gtg	acc	acc	tgg	897
Ala	Ile	Arg	Gln	Ala	Arg	Ala	Arg	Ala	Arg	Leu	Pro	Val	Thr	Thr	Trp	
				230				235						240		
cga	atc	tca	gct	gga	agt	ggt	ggt	caa	gca	gag	aga	acg	att	gca	ggc	945
Arg	Ile	Ser	Ala	Gly	Ser	Gly	Gly	Gln	Ala	Glu	Arg	Thr	Ile	Ala	Gly	
			245					250					255			
acc	acc	cgg	gca	gtg	agc	aga	gga	gcc	cgg	atc	ctg	agt	gcg	acc	act	993
Thr	Thr	Arg	Ala	Val	Ser	Arg	Gly	Ala	Arg	Ile	Leu					

```

- - - - - 275 - - - - - 280 - - - - - 285 - - - - -
aag cac ttg cat gag ggg gca aag tct gca tct gct gag gag ctg agg 1089
Lys His Leu His Glu Gly Ala Lys Ser Ala Ser Ala Glu Glu Leu Arg
290                295                300                305

cgg cag gct cag gag ctg gag gag aat cta atg gag ctc act cag atc 1137
Arg Gln Ala Gln Glu Leu Glu Glu Asn Leu Met Glu Leu Thr Gln Ile
                310                315                320

tat cag cgt ctg aat cca tgc cat acc cac tgaccccaga ccagtgcagc 1187
Tyr Gln Arg Leu Asn Pro Cys His Thr His
                325                330

cagcagggga ggtgagccat acacaggcca cgacaaaatg caggcatttt attaggggga 1247

taaagagggc aaggtaaagt ttatggagct gagtgttagt gactttggca tttctgtagc 1307

tgagcacagc aggggagggg ttaatgcaga tggcaagtgc accaaggaga aggcaggaat 1367

gctggagcct ggaataaggg aggagagggg actggagagt gtggggaata ggaagaagaa 1427

atttccttta gactaacgaa tatattgggg ggaggaatag aggggaggtg tgcaggaacc 1487

agcaatgaga aggccaggaa aagaaagagc tgaaaatgca gaaagccgaa gagttagaac 1547

ttttggatac agcagaagaa acagcggctc cactaccgac ctgcccccg ttcgatgtcc 1607

ttccaagaat gaagtctttc cctggtgatg gtccccctgcc ctgtctttcc agcatccact 1667

ctgtcttgtc ctctggaag tgtatctcag tcagccagtg gcttcttgat gatggcggtg 1727

gaggtggtgg ttgtagtgtg atggatcccc tttaggttat ttaggggtat atgtccccctg 1787

cttgaaccct gaaggccagg taatgagcca tggccattgt cccagctga ggaccaggtg 1847

tctctaaaaa cccaacatc ctggagagta tgcgagaacc taccaagaaa aacagtctca 1907

ttactcatat acagcaggca aagagacaga aaattaactg aaaagcagtt tagagactgg 1967

gggaggccgg atctctagag ccattctgct gagtgccttg tgtgtaagtc ctaataaact 2027

cacctactca cc 2039

```

```

<210> 95
<211> 407
<212> PRT
<213> Homo sapiens

```

```

<400> 95
Met Glu Leu Leu Glu Glu Asp Leu Thr Cys Pro Ile Cys Cys Ser Leu
  1                5                10                15

Phe Asp Asp Pro Arg Val Leu Pro Cys Ser His Asn Phe Cys Lys Lys
 20                25                30

```

Cys	Leu	Glu	Gly	Ile	Leu	Glu	Gly	Ser	Val	Arg	Asn	Ser	Leu	Trp	Arg
		35					40					45			
Pro	Ala	Pro	Phe	Lys	Cys	Pro	Thr	Cys	Arg	Lys	Glu	Thr	Ser	Ala	Thr
	50					55					60				
Gly	Ile	Asn	Ser	Leu	Gln	Val	Asn	Tyr	Ser	Leu	Lys	Gly	Ile	Val	Glu
	65				70					75					80
Lys	Tyr	Asn	Lys	Ile	Lys	Ile	Ser	Pro	Lys	Met	Pro	Val	Cys	Lys	Gly
				85					90					95	
His	Leu	Gly	Gln	Pro	Leu	Asn	Ile	Phe	Cys	Leu	Thr	Asp	Met	Gln	Leu
			100					105					110		
Ile	Cys	Gly	Ile	Cys	Ala	Thr	Arg	Gly	Glu	His	Thr	Lys	His	Val	Phe
		115					120					125			
Cys	Ser	Ile	Glu	Asp	Ala	Tyr	Ala	Gln	Glu	Arg	Asp	Ala	Phe	Glu	Ser
	130					135					140				
Leu	Phe	Gln	Ser	Phe	Glu	Thr	Trp	Arg	Arg	Gly	Asp	Ala	Leu	Ser	Arg
	145				150					155					160
Leu	Asp	Thr	Leu	Glu	Thr	Ser	Lys	Arg	Lys	Ser	Leu	Gln	Leu	Leu	Thr
				165					170					175	
Lys	Asp	Ser	Asp	Lys	Val	Lys	Glu	Phe	Phe	Glu	Lys	Leu	Gln	His	Thr
			180					185					190		
Leu	Asp	Gln	Lys	Lys	Asn	Glu	Ile	Leu	Ser	Asp	Phe	Glu	Thr	Met	Lys
		195					200					205			
Leu	Ala	Val	Met	Gln	Ala	Tyr	Asp	Pro	Glu	Ile	Asn	Lys	Leu	Asn	Thr
	210					215					220				
Ile	Leu	Gln	Glu	Gln	Arg	Met	Ala	Phe	Asn	Ile	Ala	Glu	Ala	Phe	Lys
	225				230					235					240
Asp	Val	Ser	Glu	Pro	Ile	Val	Phe	Leu	Gln	Gln	Met	Gln	Glu	Phe	Arg
				245					250					255	
Glu	Lys	Ile	Lys	Val	Ile	Lys	Glu	Thr	Pro	Leu	Pro	Pro	Ser	Asn	Leu
			260					265					270		
Pro	Ala	Ser	Pro	Leu	Met	Lys	Asn	Phe	Asp	Thr	Ser	Gln	Trp	Glu	Asp
		275					280					285			
Ile	Lys	Leu	Val	Asp	Val	Asp	Lys	Leu	Ser	Leu	Pro	Gln	Asp	Thr	Gly
	290					295					300				
Thr	Phe	Ile	Ser	Lys	Ile	Pro	Trp	Ser	Phe	Tyr	Lys	Leu	Phe	Leu	Leu
	305				310					315					320
Ile	Leu	Leu	Leu	Gly	Leu	Val	Ile	Val	Phe	Gly	Pro	Thr	Met	Phe	Leu
				325					330					335	

_ Glu _ Trp Ser Leu Phe Asp Asp Leu Ala Thr Trp Lys Gly Cys Leu Ser --
 340 345 350

 Asn Phe Ser Ser Tyr Leu Thr Lys Thr Ala Asp Phe Ile Glu Gln Ser
 355 360 365

 Val Phe Tyr Trp Glu Gln Val Thr Asp Gly Phe Phe Ile Phe Asn Glu
 370 375 380

 Arg Phe Lys Asn Phe Thr Leu Val Val Leu Asn Asn Val Ala Glu Phe
 385 390 395 400

 Val Cys Lys Tyr Lys Leu Leu
 405

<210> 96
 <211> 1409
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (181)..(1401)

<400> 96
 gctgtgcttg gcgcgtagcg tgcgggtccct gtagttggag gacgggacggt cgcgcggcct 60

 ttcccactag ccggagtagc ctctagttcg ttagtcaaaa cgtgaaaaaa aaagacctgc 120

 ttggccctgg gaaatagtaa ccctgccaaa tacatcagct tgtaggagac agaggatgtg 180

 atg gag ctg ctt gaa gaa gat ctc aca tgc cct att tgt tgt agt ctg 228
 Met Glu Leu Leu Glu Glu Asp Leu Thr Cys Pro Ile Cys Cys Ser Leu
 1 5 10 15

 ttt gat gat cca cgg gtt ttg cct tgc tcc cac aac ttc tgc aaa aaa 276
 Phe Asp Asp Pro Arg Val Leu Pro Cys Ser His Asn Phe Cys Lys Lys
 20 25 30

 tgc tta gaa ggt atc tta gaa ggg agt gtg cgg aat tcc ttg tgg aga 324
 Cys Leu Glu Gly Ile Leu Glu Gly Ser Val Arg Asn Ser Leu Trp Arg
 35 40 45

 cca gct cca ttc aag tgt cct aca tgc cgt aag gaa act tca gct act 372
 Pro Ala Pro Phe Lys Cys Pro Thr Cys Arg Lys Glu Thr Ser Ala Thr
 50 55 60

 gga att aat agc ctg cag gtt aat tac tcc ctg aag ggt att gtg gaa 420
 Gly Ile Asn Ser Leu Gln Val Asn Tyr Ser Leu Lys Gly Ile Val Glu
 65 70 75 80

 aag tat aac aag atc aag atc tct ccc aaa atg cca gta tgc aaa gga 468
 Lys Tyr Asn Lys Ile Lys Ile Ser Pro Lys Met Pro Val Cys Lys Gly
 85 90 95

 cac ttg ggg cag cct ctc aac att ttc tgc ctg act gat atg cag ctg 516

His 101	Leu 102	Gly 103	Gln 100	Pro 104	Leu 105	Asn 106	Ile 107	Phe 105	Cys 108	Leu 109	Thr 110	Asp 111	Met 110	Gln 112	Leu 113	- 114	- 115
att Ile	tgt Cys	ggg Gly 115	atc Ile	tgt Cys	gct Ala	act Thr	cgt Arg 120	ggg Gly	gag Glu	cac His	acc Thr	aaa Lys 125	cat His	gtc Val	ttc Phe		564
tgt Cys	tct Ser 130	att Ile	gaa Glu	gat Asp	gcc Ala	tat Tyr 135	gct Ala	cag Gln	gaa Glu	agg Arg	gat Asp 140	gcc Ala	ttt Phe	gag Glu	tcc Ser		612
ctc Leu 145	ttc Phe	cag Gln	agc Ser	ttt Phe	gag Glu 150	acc Thr	tgg Trp	cgt Arg	cgg Arg	gga Gly 155	gat Asp	gct Ala	ctt Leu	tct Ser	cgc Arg 160		660
ttg Leu	gat Asp	acc Thr	ttg Leu	gaa Glu 165	act Thr	agt Ser	aag Lys	agg Arg	aaa Lys 170	tcc Ser	cta Leu	cag Gln	tta Leu	ctg Leu 175	act Thr		708
aaa Lys	gat Asp	tca Ser 180	gat Asp	aaa Lys	gtg Val	aag Lys	gaa Glu	ttt Phe 185	ttt Phe	gag Glu	aag Lys	tta Leu 190	caa Gln	cac His	aca Thr		756
ctg Leu	gat Asp	caa Gln 195	aag Lys	aag Lys	aat Asn	gaa Glu	att Ile 200	ctg Leu	tct Ser	gac Asp	ttt Phe 205	gag Glu 205	acc Thr	atg Met	aaa Lys		804
ctt Leu 210	gct Ala	gtt Val	atg Met	caa Gln	gca Ala	tat Tyr 215	gac Asp	cca Pro	gag Glu	atc Ile	aac Asn 220	aaa Lys	ctc Leu	aac Asn	acc Thr		852
atc Ile 225	ttg Leu	cag Gln	gag Glu	caa Gln	cgg Arg 230	atg Met	gcc Ala	ttt Phe	aac Asn	att Ile	gct Ala 235	gag Glu	gct Ala	ttc Phe	aaa Lys 240		900
gat Asp	gtg Val	tca Ser	gaa Glu	ccc Pro 245	att Ile	gta Val	ttt Phe	ctg Leu	caa Gln 250	cag Gln	atg Met	cag Gln	gag Glu 255	ttt Phe	aga Arg		948
gag Glu	aaa Lys	atc Ile 260	aaa Lys	gta Val	atc Ile	aag Lys	gaa Glu	act Thr 265	cct Pro	tta Leu	cct Pro	ccc Pro 270	tct Ser	aat Asn	ttg Leu		996
cct Pro	gca Ala 275	agc Ser	cct Pro	tta Leu	atg Met	aag Lys	aac Asn 280	ttt Phe	gat Asp	acc Thr	agt Ser	cag Gln 285	tgg Trp	gaa Glu	gac Asp		1044
ata Ile 290	aaa Lys	cta Leu	gtc Val	gat Asp	gtg Val	gat Asp 295	aaa Lys	ctt Leu	tct Ser	ttg Leu 300	cct Pro	caa Gln	gac Asp	act Thr	ggc Gly		1092
aca Thr 305	ttc Phe	att Ile	agc Ser	aag Lys	att Ile 310	ccc Pro	tgg Trp	agc Ser	ttt Phe 315	tat Tyr	aag Lys	tta Leu	ttt Phe	ttg Leu 320	cta Leu		1140
atc Ile	ctt Leu	ctg Leu	ctt Leu	ggc Gly	ctt Leu	gtc Val	att Ile	gtc Val	ttt Phe	ggg Gly	cct Pro	acc Thr	atg Met	ttc Phe	cta Leu		1188

```

      325      330      335
gaa tgg tca tta ttt gat gac ctg gca act tgg aaa ggc tgt ctt tca 1236
Glu Trp Ser Leu Phe Asp Asp Leu Ala Thr Trp Lys Gly Cys Leu Ser
      340      345      350

aac ttc agt tcc tat ctg act aaa aca gcc gat ttc ata gaa caa tca 1284
Asn Phe Ser Ser Tyr Leu Thr Lys Thr Ala Asp Phe Ile Glu Gln Ser
      355      360      365

gtt ttt tac tgg gaa cag gtg aca gat ggg ttt ttc att ttc aat gaa 1332
Val Phe Tyr Trp Glu Gln Val Thr Asp Gly Phe Phe Ile Phe Asn Glu
      370      375      380

aga ttc aag aat ttt act ttg gtg gta ctg aac aat gtg gca gaa ttt 1380
Arg Phe Lys Asn Phe Thr Leu Val Val Leu Asn Asn Val Ala Glu Phe
      385      390      395      400

gtg tgc aaa tat aaa cta tta taaaatcg 1409
Val Cys Lys Tyr Lys Leu Leu
      405

```

<210> 97
 <211> 465
 <212> PRT
 <213> Homo sapiens

```

<400> 97
Met Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys
  1          5          10          15

Ser Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly
  20          25          30

His Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser
  35          40          45

Gln Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala
  50          55          60

Pro Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu
  65          70          75          80

Ile Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His
  85          90          95

Gly Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys
 100          105          110

Trp Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu
 115          120          125

Val Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Glu Ala Val
 130          135          140

Thr Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser

```

145	150	155	160
Thr Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg	165	170	175
Gln Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu	180	185	190
Glu Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr	195	200	205
Leu Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn	210	215	220
Glu Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser	225	230	235
Ala Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp	245	250	255
Ala Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr	260	265	270
Met Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg	275	280	285
Ser His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu	290	295	300
Leu Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln	305	310	315
Glu Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val	325	330	335
Leu Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp	340	345	350
Val Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val	355	360	365
Gln Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr	370	375	380
Leu Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro	385	390	395
Thr Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu	405	410	415
Asp Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys	420	425	430
His Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro	435	440	445
Tyr Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly			

```

450      455      460
Asp
465

<210> 98
<211> 1940
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (477)..(1871)

<400> 98
gttaacttcc tgaccagga agtggcagca acagagggga ctagcagcga atatacttta 60
caccaaattc cagaagattc agaacttaga tgagtggggc ccaggacagg aaccctggag 120
ccttggaagg aggggagccc catctcccca gaagagcagt gaccccagca gagagggggc 180
tggtgtatca ctggaggaaa tagcctgcc aaggaatacac gtcttcagaa gaagttctgt 240
gtggcttcaa gagactgata aaattgtgag aggaaaacag cctacccggt cctcttttct 300
tcaatacaaa atgagataat aggggttgga aggaaaacct tcaagaccta tggaagtcag 360
ttgcagccag ctcatcacat agaggtgcag gtgaggtgta ttttcatcac ggtggaaaat 420
tctggctgct tcattccat ctctagagcc aatattggag cttttcaata aaagct atg 479
                                         Met
                                         1

gcc tca acc acc agc acc aag aag atg atg gag gaa gcc acc tgc tcc 527
Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys Ser
                    5                      10                      15

atc tgc ctg agc ctg atg acg aac cca gta agc atc aac tgt gga cac 575
Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly His
                    20                      25                      30

agc tac tgc cac ttg tgt ata aca gac ttc ttt aaa aac cca agc caa 623
Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser Gln
                    35                      40                      45

aag caa ctg agg cag gag aca ttc tgc tgt ccc cag tgt cgg gct cca 671
Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala Pro
                    50                      55                      60                      65

ttt cat atg gat agc ctc cga ccc aac aag cag ctg gga agc ctc att 719
Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu Ile
                    70                      75                      80

gaa gcc ctc aaa gag acg gat caa gaa atg tca tgt gag gaa cac gga 767
Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His Gly
                    85                      90                      95

```


gag cag ttc cac ctg ttc tgc gaa gac gag ggg cag ctc atc tgc tgg	815
Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys Trp	
100 105 110	
cgc tgt gag cgg gca cca cag cac aaa ggg cac acc aca gct ctt gtt	863
Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu Val	
115 120 125	
gaa gac gta tgc cag ggc tac aag gaa aag ctc cag gaa gct gtg aca	911
Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Glu Ala Val Thr	
130 135 140 145	
aaa ctg aag caa ctt gaa gac aga tgt acg gag cag aag ctg tcc aca	959
Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser Thr	
150 155 160	
gca atg cga ata act aaa tgg aaa gag aag gta cag att cag aga caa	1007
Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg Gln	
165 170 175	
aaa atc cgg tct gac ttt aag aat ctc cag tgt ttc cta cat gag gaa	1055
Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu Glu	
180 185 190	
gag aag tct tat ctc tgg agg ctg gag aaa gaa gaa caa cag act ctg	1103
Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr Leu	
195 200 205	
agt aga ctg agg gac tat gag gct ggt ctg ggg ctg aag agc aat gaa	1151
Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn Glu	
210 215 220 225	
ctc aag agc cac atc ctg gaa ctg gag gaa aaa tgt cag ggc tca gcc	1199
Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser Ala	
230 235 240	
cag aaa ttg ctg cag aat gtg aat gac act ttg agc agg agt tgg gct	1247
Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp Ala	
245 250 255	
gtg aag ctg gaa aca tca gag gct gtc tcc ttg gaa ctt cat act atg	1295
Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr Met	
260 265 270	
tgc aat gtt tcc aag ctt tac ttc gat gtg aag aaa atg tta agg agt	1343
Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg Ser	
275 280 285	
cat caa gtt agt gtg act ctg gat cca gat aca gct cat cac gaa cta	1391
His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu Leu	
290 295 300 305	
att ctc tct gag gat cgg aga caa gtg act cgt gga tac acc cag gag	1439
Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln Glu	
310 315 320	

aat cag gac aca tct tcc agg aga ttt act gcc ttc ccc tgt gtc ttg	1487-
Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val Leu	
325 330 335	
ggt tgt gaa ggc ttc acc tca gga aga cgt tac ttt gaa gtg gat gtt	1535
Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp Val	
340 345 350	
ggc gaa gga acc gga tgg gat tta gga gtt tgt atg gaa aat gtg cag	1583
Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val Gln	
355 360 365	
agg ggc act ggc atg aag caa gag cct cag tct gga ttc tgg acc ctc	1631
Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr Leu	
370 375 380 385	
agg ctg tgc aaa aag aaa ggc tat gta gca ctt act tct ccc cca act	1679
Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro Thr	
390 395 400	
tcc ctt cat ctg cat gag cag ccc ctg ctt gtg gga att ttt ctg gac	1727
Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu Asp	
405 410 415	
tat gag gcc gga gtt gta tcc ttt tat aac ggg aat act ggc tgc cac	1775
Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys His	
420 425 430	
atc ttt act ttc ccg aag gct tcc ttc tct gat act ctc cgg ccc tat	1823
Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro Tyr	
435 440 445	
ttc cag gtt tat caa tat tct cct ttg ttt ctg cct ccc cca ggt gac	1871
Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly Asp	
450 455 460 465	
taaggaaaag agcagaagct ccttggttta accagcacag agaaaataat ataaatccca	1931
taagggcag	1940
<210> 99	
<211> 465	
<212> PRT	
<213> Homo sapiens	
<400> 99	
Met Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys	
1 5 10 15	
Ser Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly	
20 25 30	
His Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser	
35 40 45	
Gln Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala	

50	55	60																	
Pro	Phe	His	Met	Asp	Ser	Leu	Arg	Pro	Asn	Lys	Gln	Leu	Gly	Ser	Leu				
65					70					75					80				
Ile	Glu	Ala	Leu	Lys	Glu	Thr	Asp	Gln	Glu	Met	Ser	Cys	Glu	Glu	His				
				85					90					95					
Gly	Glu	Gln	Phe	His	Leu	Phe	Cys	Glu	Asp	Glu	Gly	Gln	Leu	Ile	Cys				
			100					105					110						
Trp	Arg	Cys	Glu	Arg	Ala	Pro	Gln	His	Lys	Gly	His	Thr	Thr	Ala	Leu				
		115					120					125							
Val	Glu	Asp	Val	Cys	Gln	Gly	Tyr	Lys	Glu	Lys	Leu	Gln	Lys	Ala	Val				
	130					135					140								
Thr	Lys	Leu	Lys	Gln	Leu	Glu	Asp	Arg	Cys	Thr	Glu	Gln	Lys	Leu	Ser				
145					150					155					160				
Thr	Ala	Met	Arg	Ile	Thr	Lys	Trp	Lys	Glu	Lys	Val	Gln	Ile	Gln	Arg				
				165					170					175					
Gln	Lys	Ile	Arg	Ser	Asp	Phe	Lys	Asn	Leu	Gln	Cys	Phe	Leu	His	Glu				
			180					185					190						
Glu	Glu	Lys	Ser	Tyr	Leu	Trp	Arg	Leu	Glu	Lys	Glu	Glu	Gln	Gln	Thr				
		195					200					205							
Leu	Ser	Arg	Leu	Arg	Asp	Tyr	Glu	Ala	Gly	Leu	Gly	Leu	Lys	Ser	Asn				
	210					215					220								
Glu	Leu	Lys	Ser	His	Ile	Leu	Glu	Leu	Glu	Glu	Lys	Cys	Gln	Gly	Ser				
225					230				235						240				
Ala	Gln	Lys	Leu	Leu	Gln	Asn	Val	Asn	Asp	Thr	Leu	Ser	Arg	Ser	Trp				
			245						250					255					
Ala	Val	Lys	Leu	Glu	Thr	Ser	Glu	Ala	Val	Ser	Leu	Glu	Leu	His	Thr				
			260					265					270						
Met	Cys	Asn	Val	Ser	Lys	Leu	Tyr	Phe	Asp	Val	Lys	Lys	Met	Leu	Arg				
		275					280					285							
Ser	His	Gln	Val	Ser	Val	Thr	Leu	Asp	Pro	Asp	Thr	Ala	His	His	Glu				
	290					295					300								
Leu	Ile	Leu	Ser	Glu	Asp	Arg	Arg	Gln	Val	Thr	Arg	Gly	Tyr	Thr	Gln				
305					310					315					320				
Glu	Asn	Gln	Asp	Thr	Ser	Ser	Arg	Arg	Phe	Thr	Ala	Phe	Pro	Cys	Val				
				325					330					335					
Leu	Gly	Cys	Glu	Gly	Phe	Thr	Ser	Gly	Arg	Arg	Tyr	Phe	Glu	Val	Asp				
			340					345					350						
Val	Gly	Glu	Gly	Thr	Gly	Trp	Asp	Leu	Gly	Val	Cys	Met	Glu	Asn	Val				

355 360 365
 Gln Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr
 370 375 380
 Leu Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro
 385 390 395 400
 Thr Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu
 405 410 415
 Asp Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys
 420 425 430
 His Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro
 435 440 445
 Tyr Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly
 450 455 460

Asp
 465

<210> 100
 <211> 1940
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (477)..(1871)

<400> 100
 gttaacttcc tgaccagga agtggcagca acagagggga ctagcagcga atatacttta 60
 caccaaattc cagaagattc agaacttaga tgagtggggc ccaggacagg aaccctggag 120
 ccttgaagg aggggagccc catctcccca gaagagcagt gacccagca gagagggggc 180
 tgggtgtatca ctggaggaaa tagcctgcc aggaatacac gtcttcagaa gaagttctgt 240
 gtggcttcaa gagactgac aaattgtgag aggaaaacag cctaccggg cctcttttct 300
 tcaatacaaa atgagataat aggggttgga aggaaaacct tcaagaccta tggaagtcag 360
 ttgcagccag ctcatcacat agaggtgcag gtgaggtgta ttttcatcac ggtggaaaat 420
 tctggctgct tcattccat ctctagagcc aatattggag cttttcaata aaagct atg 479
 Met
 1

gcc tca acc acc agc acc aag aag atg atg gag gaa gcc acc tgc tcc 527
 Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys Ser
 5 10 15

atc tgc ctg agc ctg atg acg aac cca gta agc atc aac tgt gga cac 575

Ile	Cys	Leu	Ser	Leu	Met	Thr	Asn	Pro	Val	Ser	Ile	Asn	Cys	Gly	His	
	20						25					30				
agc	tac	tgc	cac	ttg	tgt	ata	aca	gac	ttc	ttt	aaa	aac	cca	agc	caa	623
Ser	Tyr	Cys	His	Leu	Cys	Ile	Thr	Asp	Phe	Phe	Lys	Asn	Pro	Ser	Gln	
	35					40					45					
aag	caa	ctg	agg	cag	gag	aca	ttc	tgc	tgt	ccc	cag	tgt	cgg	gct	cca	671
Lys	Gln	Leu	Arg	Gln	Glu	Thr	Phe	Cys	Cys	Pro	Gln	Cys	Arg	Ala	Pro	
	50				55					60					65	
ttt	cat	atg	gat	agc	ctc	cga	ccc	aac	aag	cag	ctg	gga	agc	ctc	att	719
Phe	His	Met	Asp	Ser	Leu	Arg	Pro	Asn	Lys	Gln	Leu	Gly	Ser	Leu	Ile	
				70					75					80		
gaa	gcc	ctc	aaa	gag	acg	gat	caa	gaa	atg	tca	tgt	gag	gaa	cac	gga	767
Glu	Ala	Leu	Lys	Glu	Thr	Asp	Gln	Glu	Met	Ser	Cys	Glu	Glu	His	Gly	
			85					90						95		
gag	cag	ttc	cac	ctg	ttc	tgc	gaa	gac	gag	ggg	cag	ctc	atc	tgc	tgg	815
Glu	Gln	Phe	His	Leu	Phe	Cys	Glu	Asp	Glu	Gly	Gln	Leu	Ile	Cys	Trp	
		100					105					110				
cgc	tgt	gag	cgg	gca	cca	cag	cac	aaa	ggg	cac	acc	aca	gct	ctt	gtt	863
Arg	Cys	Glu	Arg	Ala	Pro	Gln	His	Lys	Gly	His	Thr	Thr	Ala	Leu	Val	
	115					120					125					
gaa	gac	gta	tgc	cag	ggc	tac	aag	gaa	aag	ctc	cag	aaa	gct	gtg	aca	911
Glu	Asp	Val	Cys	Gln	Gly	Tyr	Lys	Glu	Lys	Leu	Gln	Lys	Ala	Val	Thr	
	130				135					140					145	
aaa	ctg	aag	caa	ctt	gaa	gac	aga	tgt	acg	gag	cag	aag	ctg	tcc	aca	959
Lys	Leu	Lys	Gln	Leu	Glu	Asp	Arg	Cys	Thr	Glu	Gln	Lys	Leu	Ser	Thr	
			150						155					160		
gca	atg	cga	ata	act	aaa	tgg	aaa	gag	aag	gta	cag	att	cag	aga	caa	1007
Ala	Met	Arg	Ile	Thr	Lys	Trp	Lys	Glu	Lys	Val	Gln	Ile	Gln	Arg	Gln	
			165					170					175			
aaa	atc	cgg	tct	gac	ttt	aag	aat	ctc	cag	tgt	ttc	cta	cat	gag	gaa	1055
Lys	Ile	Arg	Ser	Asp	Phe	Lys	Asn	Leu	Gln	Cys	Phe	Leu	His	Glu	Glu	
		180					185					190				
gag	aag	tct	tat	ctc	tgg	agg	ctg	gag	aaa	gaa	gaa	caa	cag	act	ctg	1103
Glu	Lys	Ser	Tyr	Leu	Trp	Arg	Leu	Glu	Lys	Glu	Glu	Gln	Gln	Thr	Leu	
	195					200						205				
agt	aga	ctg	agg	gac	tat	gag	gct	ggc	ctg	ggg	ctg	aag	agc	aat	gaa	1151
Ser	Arg	Leu	Arg	Asp	Tyr	Glu	Ala	Gly	Leu	Gly	Leu	Lys	Ser	Asn	Glu	
	210				215					220					225	
ctc	aag	agc	cac	atc	ctg	gaa	ctg	gag	gaa	aaa	tgt	cag	ggc	tca	gcc	1199
Leu	Lys	Ser	His	Ile	Leu	Glu	Leu	Glu	Glu	Lys	Cys	Gln	Gly	Ser	Ala	
			230						235					240		
cag	aaa	ttg	ctg	cag	aat	gtg	aat	gac	act	ttg	agc	agg	agt	tgg	gct	1247
Gln	Lys	Leu	Leu	Gln	Asn	Val	Asn	Asp	Thr	Leu	Ser	Arg	Ser	Trp	Ala	

245										250										255										
gtg	aag	ctg	gaa	aca	tca	gag	gct	gtc	tcc	ttg	gaa	ctt	cat	act	atg	1295														
Val	Lys	Leu	Glu	Thr	Ser	Glu	Ala	Val	Ser	Leu	Glu	Leu	His	Thr	Met															
		260					265					270																		
tgc	aat	gtt	tcc	aag	ctt	tac	ttc	gat	gtg	aag	aaa	atg	tta	agg	agt	1343														
Cys	Asn	Val	Ser	Lys	Leu	Tyr	Phe	Asp	Val	Lys	Lys	Met	Leu	Arg	Ser															
	275					280					285																			
cat	caa	gtt	agt	gtg	act	ctg	gat	cca	gat	aca	gct	cat	cac	gaa	cta	1391														
His	Gln	Val	Ser	Val	Thr	Leu	Asp	Pro	Asp	Thr	Ala	His	His	Glu	Leu															
	290				295					300					305															
att	ctc	tct	gag	gat	cgg	aga	caa	gtg	act	cgt	gga	tac	acc	cag	gag	1439														
Ile	Leu	Ser	Glu	Asp	Arg	Arg	Gln	Val	Thr	Arg	Gly	Tyr	Thr	Gln	Glu															
			310						315					320																
aat	cag	gac	aca	tct	tcc	agg	aga	ttt	act	gcc	ttc	ccc	tgt	gtc	ttg	1487														
Asn	Gln	Asp	Thr	Ser	Ser	Arg	Arg	Phe	Thr	Ala	Phe	Pro	Cys	Val	Leu															
			325					330					335																	
ggt	tgt	gaa	ggc	ttc	acc	tca	gga	aga	cgt	tac	ttt	gaa	gtg	gat	gtt	1535														
Gly	Cys	Glu	Gly	Phe	Thr	Ser	Gly	Arg	Arg	Tyr	Phe	Glu	Val	Asp	Val															
		340					345					350																		
ggc	gaa	gga	acc	gga	tgg	gat	tta	gga	gtt	tgt	atg	gaa	aat	gtg	cag	1583														
Gly	Glu	Gly	Thr	Gly	Trp	Asp	Leu	Gly	Val	Cys	Met	Glu	Asn	Val	Gln															
	355					360					365																			
agg	ggc	act	ggc	atg	aag	caa	gag	cct	cag	tct	gga	ttc	tgg	acc	ctc	1631														
Arg	Gly	Thr	Gly	Met	Lys	Gln	Glu	Pro	Gln	Ser	Gly	Phe	Trp	Thr	Leu															
	370				375					380					385															
agg	ctg	tgc	aaa	aag	aaa	ggc	tat	gta	gca	ctt	act	tct	ccc	cca	act	1679														
Arg	Leu	Cys	Lys	Lys	Lys	Gly	Tyr	Val	Ala	Leu	Thr	Ser	Pro	Pro	Thr															
			390						395					400																
tcc	ctt	cat	ctg	cat	gag	cag	ccc	ctg	ctt	gtg	gga	att	ttt	ctg	gac	1727														
Ser	Leu	His	Leu	His	Glu	Gln	Pro	Leu	Leu	Val	Gly	Ile	Phe	Leu	Asp															
			405					410					415																	
tat	gag	gcc	gga	gtt	gta	tcc	ttt	tat	aac	ggg	aat	act	ggc	tgc	cac	1775														
Tyr	Glu	Ala	Gly	Val	Val	Ser	Phe	Tyr	Asn	Gly	Asn	Thr	Gly	Cys	His															
		420					425					430																		
atc	ttt	act	ttc	ccg	aag	gct	tcc	ttc	tct	gat	act	ctc	cgg	ccc	tat	1823														
Ile	Phe	Thr	Phe	Pro	Lys	Ala	Ser	Phe	Ser	Asp	Thr	Leu	Arg	Pro	Tyr															
	435					440				445																				
ttc	cag	gtt	tat	caa	tat	tct	cct	ttg	ttt	ctg	cct	ccc	cca	ggt	gac	1871														
Phe	Gln	Val	Tyr	Gln	Tyr	Ser	Pro	Leu	Phe	Leu	Pro	Pro	Pro	Gly	Asp															
	450				455					460					465															
taaggaaaag agcagaagct ccttggttta accagcacag agaaaataat ataaatccca																1931														
taagggcag																1940														

<210> 101
 <211> 685
 <212> PRT
 <213> Homo sapiens

<400> 101
 Met Glu Leu Leu Arg Thr Ile Thr Tyr Gln Pro Ala Ala Ser Thr Lys
 1 5 10 15
 Met Cys Glu Gln Ala Leu Gly Lys Gly Cys Gly Ala Asp Ser Lys Lys
 20 25 30
 Lys Arg Pro Pro Gln Pro Pro Glu Glu Ser Gln Pro Pro Gln Ser Gln
 35 40 45
 Ala Gln Val Pro Pro Ala Ala Pro His His His His His His Ser His
 50 55 60
 Ser Gly Pro Glu Ile Ser Arg Ile Ile Val Asp Pro Thr Thr Gly Lys
 65 70 75 80
 Arg Tyr Cys Arg Gly Lys Val Leu Gly Lys Gly Gly Phe Ala Lys Cys
 85 90 95
 Tyr Glu Met Thr Asp Leu Thr Asn Asn Lys Val Tyr Ala Ala Lys Ile
 100 105 110
 Ile Pro His Ser Arg Val Ala Lys Pro His Gln Arg Glu Lys Ile Asp
 115 120 125
 Lys Glu Ile Glu Leu His Arg Ile Leu His His Lys His Val Val Gln
 130 135 140
 Phe Tyr His Tyr Phe Glu Asp Lys Glu Asn Ile Tyr Ile Leu Leu Glu
 145 150 155 160
 Tyr Cys Ser Arg Arg Ser Met Ala His Ile Leu Lys Ala Arg Lys Val
 165 170 175
 Leu Thr Glu Pro Glu Val Arg Tyr Tyr Leu Arg Gln Ile Val Ser Gly
 180 185 190
 Leu Lys Tyr Leu His Glu Gln Glu Ile Leu His Arg Asp Leu Lys Leu
 195 200 205
 Gly Asn Phe Phe Ile Asn Glu Ala Met Glu Leu Lys Val Gly Asp Phe
 210 215 220
 Gly Leu Ala Ala Arg Leu Glu Pro Leu Glu His Arg Arg Arg Thr Ile
 225 230 235 240
 Cys Gly Thr Pro Asn Tyr Leu Ser Pro Glu Val Leu Asn Lys Gln Gly
 245 250 255
 His Gly Cys Glu Ser Asp Ile Trp Ala Leu Gly Cys Val Met Tyr Thr

565 570 575
 His Tyr Met Glu Glu Asn Leu Met Asp Gly Gly Asp Leu Pro Ser Val
 580 585 590
 Thr Asp Ile Arg Arg Pro Arg Leu Tyr Leu Leu Gln Trp Leu Lys Ser
 595 600 605
 Asp Lys Ala Leu Met Met Leu Phe Asn Asp Gly Thr Phe Gln Val Asn
 610 615 620
 Phe Tyr His Asp His Thr Lys Ile Ile Ile Cys Ser Gln Asn Glu Glu
 625 630 635 640
 Tyr Leu Leu Thr Tyr Ile Asn Glu Asp Arg Ile Ser Thr Thr Phe Arg
 645 650 655
 Leu Thr Thr Leu Leu Met Ser Gly Cys Ser Ser Glu Leu Lys Asn Arg
 660 665 670
 Met Glu Tyr Ala Leu Asn Met Leu Leu Gln Arg Cys Asn
 675 680 685

<210> 102
 <211> 2783
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (128)..(2182)

<400> 102
 gcacaagtgg accggggtgt tgggtgctag tcggcaccag aggcaagggt gcgaggacca 60
 cgggcggctc ggacgtgtga ccgcgcctag ggggtggcag cgggcagtgc ggggcggcaa 120
 ggcgacc atg gag ctt ttg cgg act atc acc tac cag cca gcc gcc agc 169
 Met Glu Leu Leu Arg Thr Ile Thr Tyr Gln Pro Ala Ala Ser
 1 5 10
 acc aaa atg tgc gag cag gcg ctg ggc aag ggt tgc gga gca gac tcg 217
 Thr Lys Met Cys Glu Gln Ala Leu Gly Lys Gly Cys Gly Ala Asp Ser
 15 20 25 30
 aag aag aag cgg ccg ccg cag ccc ccc gag gaa tcg cag cca cct cag 265
 Lys Lys Lys Arg Pro Pro Gln Pro Pro Glu Glu Ser Gln Pro Pro Gln
 35 40 45
 tcc cag gcg caa gtg ccc ccg gcg gcc cct cac cac cat cac cac cat 313
 Ser Gln Ala Gln Val Pro Pro Ala Ala Pro His His His His His His
 50 55 60
 tcg cac tcg ggg ccg gag atc tcg cgg att atc gtc gac ccc acg act 361
 Ser His Ser Gly Pro Glu Ile Ser Arg Ile Ile Val Asp Pro Thr Thr
 65 70 75

ggg aag cgc tac tgc cgg ggc aaa gtg ctg gga aag ggt ggc ttt gca	409
Gly Lys Arg Tyr Cys Arg Gly Lys Val Leu Gly Lys Gly Gly Phe Ala	
80 85 90	
aaa tgt tac gag atg aca gat ttg aca aat aac aaa gtc tac gcc gca	457
Lys Cys Tyr Glu Met Thr Asp Leu Thr Asn Asn Lys Val Tyr Ala Ala	
95 100 105 110	
aaa att att cct cac agc aga gta gct aaa cct cat caa agg gaa aag	505
Lys Ile Ile Pro His Ser Arg Val Ala Lys Pro His Gln Arg Glu Lys	
115 120 125	
att gac aaa gaa ata gag ctt cac aga att ctt cat cat aag cat gta	553
Ile Asp Lys Glu Ile Glu Leu His Arg Ile Leu His His Lys His Val	
130 135 140	
gtg cag ttt tac cac tac ttc gag gac aaa gaa aac att tac att ctc	601
Val Gln Phe Tyr His Tyr Phe Glu Asp Lys Glu Asn Ile Tyr Ile Leu	
145 150 155	
ttg gaa tac tgc agt aga agg tca atg gct cat att ttg aaa gca aga	649
Leu Glu Tyr Cys Ser Arg Arg Ser Met Ala His Ile Leu Lys Ala Arg	
160 165 170	
aag gtg ttg aca gag cca gaa gtt cga tac tac ctc agg cag att gtg	697
Lys Val Leu Thr Glu Pro Glu Val Arg Tyr Tyr Leu Arg Gln Ile Val	
175 180 185 190	
tct gga ctg aaa tac ctt cat gaa caa gaa atc ttg cac aga gat ctc	745
Ser Gly Leu Lys Tyr Leu His Glu Gln Glu Ile Leu His Arg Asp Leu	
195 200 205	
aaa cta ggg aac ttt ttt att aat gaa gcc atg gaa cta aaa gtt ggg	793
Lys Leu Gly Asn Phe Phe Ile Asn Glu Ala Met Glu Leu Lys Val Gly	
210 215 220	
gac ttc ggt ctg gca gcc agg cta gaa ccc ttg gaa cac aga agg aga	841
Asp Phe Gly Leu Ala Ala Arg Leu Glu Pro Leu Glu His Arg Arg Arg	
225 230 235	
acg ata tgt ggt acc cca aat tat ctc tct cct gaa gtc ctc aac aaa	889
Thr Ile Cys Gly Thr Pro Asn Tyr Leu Ser Pro Glu Val Leu Asn Lys	
240 245 250	
caa gga cat ggc tgt gaa tca gac att tgg gcc ctg ggc tgt gta atg	937
Gln Gly His Gly Cys Glu Ser Asp Ile Trp Ala Leu Gly Cys Val Met	
255 260 265 270	
tat aca atg tta cta ggg agg ccc cca ttt gaa act aca aat ctc aaa	985
Tyr Thr Met Leu Leu Gly Arg Pro Pro Phe Glu Thr Thr Asn Leu Lys	
275 280 285	
gaa act tat agg tgc ata agg gaa gca agg tat aca atg ccg tcc tca	1033
Glu Thr Tyr Arg Cys Ile Arg Glu Ala Arg Tyr Thr Met Pro Ser Ser	
290 295 300	

ttg ctg gct cct gcc aag cac tta att gct agt atg ttg tcc aaa aac	1081
Leu Leu Ala Pro Ala Lys His Leu Ile Ala Ser Met Leu Ser Lys Asn	
305 310 315	
cca gag gat cgt ccc agt ttg gat gac atc att cga cat gac ttt ttt	1129
Pro Glu Asp Arg Pro Ser Leu Asp Asp Ile Ile Arg His Asp Phe Phe	
320 325 330	
ttg cag ggc ttc act ccg gac aga ctg tct tct agc tgt tgt cat aca	1177
Leu Gln Gly Phe Thr Pro Asp Arg Leu Ser Ser Ser Cys Cys His Thr	
335 340 345 350	
gtt cca gat ttc cac tta tca agc cca gct aag aat ttc ttt aag aaa	1225
Val Pro Asp Phe His Leu Ser Ser Pro Ala Lys Asn Phe Phe Lys Lys	
355 360 365	
gca gct gct gct ctt ttt ggt ggc aaa aaa gac aaa gca aga tat att	1273
Ala Ala Ala Ala Leu Phe Gly Gly Lys Lys Asp Lys Ala Arg Tyr Ile	
370 375 380	
gac aca cat aat aga gtg tct aaa gaa gat gaa gac atc tac aag ctt	1321
Asp Thr His Asn Arg Val Ser Lys Glu Asp Glu Asp Ile Tyr Lys Leu	
385 390 395	
agg cat gat ttg aaa aag act tca ata act cag caa ccc agc aaa cac	1369
Arg His Asp Leu Lys Lys Thr Ser Ile Thr Gln Gln Pro Ser Lys His	
400 405 410	
agg aca gat gag gag ctc cag cca cct acc acc aca gtt gcc agg tct	1417
Arg Thr Asp Glu Glu Leu Gln Pro Pro Thr Thr Thr Val Ala Arg Ser	
415 420 425 430	
gga aca ccc gca gta gaa aac aag cag cag att ggg gat gct att cgg	1465
Gly Thr Pro Ala Val Glu Asn Lys Gln Gln Ile Gly Asp Ala Ile Arg	
435 440 445	
atg ata gtc aga ggg act ctt ggc agc tgt agc agc agc agt gaa tgc	1513
Met Ile Val Arg Gly Thr Leu Gly Ser Cys Ser Ser Ser Ser Glu Cys	
450 455 460	
ctt gaa gac agt acc atg gga agt gtt gca gac aca gtg gca agg gtt	1561
Leu Glu Asp Ser Thr Met Gly Ser Val Ala Asp Thr Val Ala Arg Val	
465 470 475	
ctt cgg gga tgt ctg gaa aac atg ccg gaa gct gat tgc att ccc aaa	1609
Leu Arg Gly Cys Leu Glu Asn Met Pro Glu Ala Asp Cys Ile Pro Lys	
480 485 490	
gag cag ctg agc aca tca ttt cag tgg gtc acc aaa tgg gtt gat tac	1657
Glu Gln Leu Ser Thr Ser Phe Gln Trp Val Thr Lys Trp Val Asp Tyr	
495 500 505 510	
tct aac aaa tat ggc ttt ggg tac cag ctc tca gac cac acc gtc ggt	1705
Ser Asn Lys Tyr Gly Phe Gly Tyr Gln Leu Ser Asp His Thr Val Gly	
515 520 525	
gtc ctt ttc aac aat ggt gct cac atg agc ctc ctt cca gac aaa aaa	1753

-	Val	Leu	Phe	Asn	Asn	Gly	Ala	His	Met	Ser	Leu	Leu	Pro	Asp	Lys	Lys	-
				530					535					540			
	aca	gtt	cac	tat	tac	gca	gag	ctt	ggc	caa	tgc	tca	gtt	ttc	cca	gca	1801
	Thr	Val	His	Tyr	Tyr	Ala	Glu	Leu	Gly	Gln	Cys	Ser	Val	Phe	Pro	Ala	
			545					550					555				
	aca	gat	gct	cct	gag	caa	ttt	att	agt	caa	gtg	acg	gtg	ctg	aaa	tac	1849
	Thr	Asp	Ala	Pro	Glu	Gln	Phe	Ile	Ser	Gln	Val	Thr	Val	Leu	Lys	Tyr	
		560					565					570					
	ttt	tct	cat	tac	atg	gag	gag	aac	ctc	atg	gat	ggg	gga	gat	ctg	cct	1897
	Phe	Ser	His	Tyr	Met	Glu	Glu	Asn	Leu	Met	Asp	Gly	Gly	Asp	Leu	Pro	
	575					580					585					590	
	agt	gtt	act	gat	att	cga	aga	cct	cgg	ctc	tac	ctc	ctt	cag	tgg	cta	1945
	Ser	Val	Thr	Asp	Ile	Arg	Arg	Pro	Arg	Leu	Tyr	Leu	Leu	Gln	Trp	Leu	
				595					600						605		
	aaa	tct	gat	aag	gcc	cta	atg	atg	ctc	ttt	aat	gat	ggc	acc	ttt	cag	1993
	Lys	Ser	Asp	Lys	Ala	Leu	Met	Met	Leu	Phe	Asn	Asp	Gly	Thr	Phe	Gln	
				610					615					620			
	gtg	aat	ttc	tac	cat	gat	cat	aca	aaa	atc	atc	atc	tgt	agc	caa	aat	2041
	Val	Asn	Phe	Tyr	His	Asp	His	Thr	Lys	Ile	Ile	Ile	Cys	Ser	Gln	Asn	
			625					630					635				
	gaa	gaa	tac	ctt	ctc	acc	tac	atc	aat	gag	gat	agg	ata	tct	aca	act	2089
	Glu	Glu	Tyr	Leu	Leu	Thr	Tyr	Ile	Asn	Glu	Asp	Arg	Ile	Ser	Thr	Thr	
		640					645					650					
	ttc	agg	ctg	aca	act	ctg	ctg	atg	tct	ggc	tgt	tca	tca	gaa	tta	aaa	2137
	Phe	Arg	Leu	Thr	Thr	Leu	Leu	Met	Ser	Gly	Cys	Ser	Ser	Glu	Leu	Lys	
	655					660					665					670	
	aat	cga	atg	gaa	tat	gcc	ctg	aac	atg	ctc	tta	caa	aga	tgt	aac		2182
	Asn	Arg	Met	Glu	Tyr	Ala	Leu	Asn	Met	Leu	Leu	Gln	Arg	Cys	Asn		
				675					680						685		
	tgaaagactt	ttcgaatgga	ccctatggga	ctcctctttt	ccactgtgag	atctacaggg	2242										
	aacccaaaag	aatgatctag	agtatggtga	agaagatgga	catgtggtgg	tacgaaaaaca	2302										
	attcccctgt	ggcctgctgg	actgggtgga	accagaacag	gctaaggcat	acagttcttg	2362										
	actttggaca	atccaagagt	gaaccagaat	gcagttttcc	ttgagatacc	tgttttaaaa	2422										
	ggtttttcag	acaattttgc	agaaaggtgc	attgattctt	aaattctctc	tgttgagagc	2482										
	atttcagcca	gaggactttg	gaactgtgaa	tatacttcct	gaagggggagg	gagaagggag	2542										
	gaagctccca	tgttgtttaa	aggctgtaat	tggagcagct	tttggtctgcg	taactgtgaa	2602										
	ctatggccat	atataatttt	ttttcattaa	tttttgaaga	tacttgtggc	tggaagggtg	2662										
	cattccttgt	taataaaactt	tttattttatt	acagcccaaa	gagcagttatt	tatttatcaaa	2722		</								

_atgtcttttt ttttatgttg accatttttaa accgttggca ataaagagta tgaaaacgca-2782-

g

2783

<210> 103
<211> 161
<212> PRT
<213> Homo sapiens

<400> 103
Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser Ser Ala
1 5 10 15
Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn Ser Tyr
20 25 30
Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly Leu Val
35 40 45
Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr Thr Gln
50 55 60
Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr Val Tyr
65 70 75 80
Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Ile Gln Met Cys Cys
85 90 95
Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn Ala Gly
100 105 110
Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly Cys Ile
115 120 125
Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln Asp Val
130 135 140
Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr Lys Arg
145 150 155 160

Leu

<210> 104
<211> 1589
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (70)..(552)

<400> 104
ccttttctcg gggcgcccga aggccagctc agacctcccg gctcgacagg cggcgcgggc 60

```

ggcggtaaa atg tgc gtt cca gga cct tac cag gcg gcc act ggg cct tcc 111
Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser
1 5 10

tca gca cca tcc gca cct cca tcc tat gaa gag aca gtg gct gtt aac 159
Ser Ala Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn
15 20 25 30

agt tat tac ccc aca cct cca gct ccc atg cct ggg cca act acg ggg 207
Ser Tyr Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly
35 40 45

ctt gtg acg ggg cct gat ggg aag ggc atg aat cct cct tgc tat tat 255
Leu Val Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr
50 55 60

acc cag cca gcg ccc atc ccc aat aac aat cca att acc gtg cag acg 303
Thr Gln Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr
65 70 75

gtc tac gtg cag cac ccc atc acc ttt ttg gac cgc cct atc caa atg 351
Val Tyr Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Ile Gln Met
80 85 90

tgt tgt cct tcc tgc aac aag atg atc gtg agt cag ctg tcc tat aac 399
Cys Cys Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn
95 100 105 110

gcc ggt gct ctg acc tgg ctg tcc tgc ggg agc ctg tgc ctg ctg ggg 447
Ala Gly Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly
115 120 125

tgc ata gcg ggc tgc tgc ttc atc ccc ttc tgc gtg gat gcc ctg cag 495
Cys Ile Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln
130 135 140

gac gtg gac cat tac tgt ccc aac tgc aga gct ctc ctg ggc acc tac 543
Asp Val Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr
145 150 155

aag cgt ttg taggactcag ccagacgtgg agggagccgg gtgccgcagg 592
Lys Arg Leu
160

aagtcctttc cacctctcat ccagcttcac gcctggtgga ggttctgccc tgggtggtctc 652
acctctccag ggggccacc ttcattgtctt cttttggggg gaatacgtcg caaaactaac 712
aaatctccaa accccagaaa ttgtgcttg gagtcgtgca taggacttgc aaagacattc 772
cccttgagtgc tcagttccac ggtttcctgc ctccctgaga cctgagttcc tgccattctaa 832
ctgtgatcat tgccctatcc gaatatcttc ctgtgatctg ccatcagttg ctcttttttc 892
ctgcttccat gggcctttct ggtggcagtc tcaaactgag aagccacagt tgccttattt 952
ttgaggctgt tctgccaga gctcggctga accagccttt agtgcctacc attatcttat 1012

```

ccgtctcttc ccgtccctga tgacaaagat cttgccttac agactttaca ggcttggctt 1072
 tgagattctg taactgcaga cttcattagc acacagattc actttaattt ctttaattttt 1132
 tttttaaata caaggagggg gctattaaca ccagtagacg acatatccac aaggtcgtaa 1192
 atgcatgcta gaaaaatagg gctggatctt atcactgccc tgtctcccct tgtttctctg 1252
 tgccagatct tcagtgcgcc tttccataca gggatttttt tctcatagag taattatatg 1312
 aacagttttt atgacctcct tttggtctga aatactttcg aacagaattt ctttttttta 1372
 aaaaaaaca gagatggggg cttactatgt tgcccaggct ggtgtcgaac tcctgggctc 1432
 aagcgatcct tctgccttgg cctcccgaag tgctgggatt gcaggcataa gctaccatgc 1492
 tgggcctgaa cataatttca agaggaggat ttataaaacc attttctgta atcaaatgat 1552
 tgggtgtcatt ttcccatttg ccaatgtagt ctcaatt 1589

<210> 105
 <211> 161
 <212> PRT
 <213> Homo sapiens

<400> 105
 Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser Ser Ala
 1 5 10 15
 Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn Ser Tyr
 20 25 30
 Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly Leu Val
 35 40 45
 Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr Thr Gln
 50 55 60
 Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr Val Tyr
 65 70 75 80
 Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Val Gln Met Cys Cys
 85 90 95
 Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn Ala Gly
 100 105 110
 Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly Cys Ile
 115 120 125
 Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln Asp Val
 130 135 140
 Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr Lys Arg
 145 150 155 160

Leu

<210> 106
<211> 1589
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (70)..(552)

<400> 106
ccttttctcg gggcgccccga aggccagctc agacctcccg gctcgacagg cggcgcgggc 60

ggcggtaaa atg tcg gtt cca gga cct tac cag gcg gcc act ggg cct tcc 111
Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser
1 5 10

tca gca cca tcc gca cct cca tcc tat gaa gag aca gtg gct gtt aac 159
Ser Ala Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn
15 20 25 30

agt tat tac ccc aca cct cca gct ccc atg cct ggg cca act acg ggg 207
Ser Tyr Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly
35 40 45

ctt gtg acg ggg cct gat ggg aag ggc atg aat cct cct tcg tat tat 255
Leu Val Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr
50 55 60

acc cag cca gcg ccc atc ccc aat aac aat cca att acc gtg cag acg 303
Thr Gln Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr
65 70 75

gtc tac gtg cag cac ccc atc acc ttt ttg gac cgc cct gtc caa atg 351
Val Tyr Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Val Gln Met
80 85 90

tgt tgt cct tcc tgc aac aag atg atc gtg agt cag ctg tcc tat aac 399
Cys Cys Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn
95 100 105 110

gcc ggt gct ctg acc tgg ctg tcc tgc ggg agc ctg tgc ctg ctg ggg 447
Ala Gly Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly
115 120 125

tgc ata gcg ggc tgc tgc ttc atc ccc ttc tgc gtg gat gcc ctg cag 495
Cys Ile Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln
130 135 140

gac gtg gac cat tac tgt ccc aac tgc aga gct ctc ctg ggc acc tac 543
Asp Val Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr
145 150 155

aag-cgt ttg taggactcag ccagacgtgg agggagccgg gtgccgcagg 592
 Lys Arg Leu
 160

aagtcctttc cacctctcat ccagcttcac gcttgggtga ggttctgccc tgggtgtctc 652
 acctctccag ggggcccacc ttcattgtctt cttttggggg gaatacgtcg caaaactaac 712
 aaatctccaa accccagaaa ttgctgcttg gagtcgtgca taggacttgc aaagacattc 772
 cccttgagtg tcagttccac ggtttctctg ctccttgaga ccctgagtc tgccatctaa 832
 ctgtgatcat tgccctatcc gaatatcttc ctgtgatctg ccatcagtggt ctcttttttc 892
 ctgcttccat gggcctttct ggtggcagtc tcaaactgag aagccacagt tgccattattt 952
 ttgaggctgt tctgcccaga gctcggctga accagccttt agtgccctacc attatcttat 1012
 ccgtctcttc ccgtccctga tgacaaagat cttgccttac agactttaca ggcttggctt 1072
 tgagattctg taactgcaga cttcattagc acacagattc actttaattt ctttaattttt 1132
 tttttaaata caaggagggg gctattaaca ccagtacag acatatccac aaggtcgtaa 1192
 atgcatgcta gaaaaatagg gctggatctt atcactgccc tgtctcccct tgtttctctg 1252
 tgccagatct tcagtgcacc tttccatata gggatttttt tctcatagag taattatatg 1312
 aacagttttt atgacctctt tttggtctga aatactttcg aacagaattt ctttttttta 1372
 aaaaaaaaca gagatggggg cttactatgt tgccaggct ggtgtcgaac tcctgggctc 1432
 aagcgatcct tctgccttgg cctcccgaag tgctgggatt gcaggcataa gctaccatgc 1492
 tgggcctgaa cataatttca agaggaggat ttataaaacc attttctgta atcaaatgat 1552
 tgggtgtcatt ttcccatttg ccaatgtagt ctcaactt 1589

<210> 107
 <211> 249
 <212> PRT
 <213> Homo sapiens

<400> 107
 Met Ala Ser Ala Ser Gly Ala Met Ala Lys His Glu Gln Ile Leu Val
 1 5 10 15
 Leu Asp Pro Pro Thr Asp Leu Lys Phe Lys Gly Pro Phe Thr Asp Val
 20 25 30
 Val Thr Thr Asn Leu Lys Leu Arg Asn Pro Ser Asp Arg Lys Val Cys
 35 40 45
 Phe Lys Val Lys Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn
 50 55 60

tcc gcc tca ggg gcc atg gcg aag cac gag cag atc ctg gtc ctc gat	285
Ser Ala Ser Gly Ala Met Ala Lys His Glu Gln Ile Leu Val Leu Asp	
5 10 15	
ccg ccc aca gac ctc aaa ttc aaa ggc ccc ttc aca gat gta gtc act	333
Pro Pro Thr Asp Leu Lys Phe Lys Gly Pro Phe Thr Asp Val Val Thr	
20 25 30	
aca aat ctt aaa ttg cga aat cca tcg gat aga aaa gtg tgt ttc aaa	381
Thr Asn Leu Lys Leu Arg Asn Pro Ser Asp Arg Lys Val Cys Phe Lys	
35 40 45 50	
gtg aag act aca gca cct cgc cgg tac tgt gtg agg ccc aac agt gga	429
Val Lys Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn Ser Gly	
55 60 65	
att att gac cca ggg tca act gtg act gtt tca gta atg cta cag ccc	477
Ile Ile Asp Pro Gly Ser Thr Val Thr Val Ser Val Met Leu Gln Pro	
70 75 80	
ttt gac tat gat ccg aat gaa aag agt aaa cac aag ttt atg gta cag	525
Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met Val Gln	
85 90 95	
aca att ttt gct cca cca aac act tca gat atg gaa gct gtg tgg aaa	573
Thr Ile Phe Ala Pro Pro Asn Thr Ser Asp Met Glu Ala Val Trp Lys	
100 105 110	
gag gca aaa cct gat gaa tta atg gat tcc aaa ttg aga tgc gta ttt	621
Glu Ala Lys Pro Asp Glu Leu Met Asp Ser Lys Leu Arg Cys Val Phe	
115 120 125 130	
gaa atg ccc aat gaa aat gat aaa ttg aat gat atg gaa cct agc aaa	669
Glu Met Pro Asn Glu Asn Asp Lys Leu Asn Asp Met Glu Pro Ser Lys	
135 140 145	
gct gtt cca ctg aat gca tct aag caa gat gga cct atg cca aaa cca	717
Ala Val Pro Leu Asn Ala Ser Lys Gln Asp Gly Pro Met Pro Lys Pro	
150 155 160	
cac agt gtt tca ctt aat gat acc gaa aca agg aaa cta atg gaa gag	765
His Ser Val Ser Leu Asn Asp Thr Glu Thr Arg Lys Leu Met Glu Glu	
165 170 175	
tgt aaa aga ctt cag gga gaa atg atg aag cta tca gaa gaa aat cgg	813
Cys Lys Arg Leu Gln Gly Glu Met Met Lys Leu Ser Glu Glu Asn Arg	
180 185 190	
cac ctg aga gat gaa ggt tta agg ctc aga aag gta gca cat tcg gat	861
His Leu Arg Asp Glu Gly Leu Arg Leu Arg Lys Val Ala His Ser Asp	
195 200 205 210	
aaa cct gga tca acc tca act gca tcc ttc aga gat aat gtc acc agt	909
Lys Pro Gly Ser Thr Ser Thr Ala Ser Phe Arg Asp Asn Val Thr Ser	
215 220 225	
cct ctt cct tca ctt ctt gtt gta att gca gcc att ttc att gga ttc	957

Pro Leu-Pro Ser Leu Leu Val Val Ile Ala Ala-Ile Phe Ile Gly Phe
 230 235 240

ttt cta ggg aaa ttc atc ttg tagagtgaag catgcagagt gctgtttcctt 1008
 Phe Leu Gly Lys Phe Ile Leu
 245

tttttttttt tctcttgacc agaaaaagat ttgtttacct accatttcac tggtagtatg 1068
 gccacgggtg accatttttt tgtgtgtaca ggcgcataata ggctttgcct ttaatgatct 1128
 cttacgggta gaaaacacaa taaaaacaaa ctgttcggct actggacagg ttgtatatta 1188
 ccagatcatc actagcagat gtcagttgca cattgagtc tttatgaaat tcataaataa 1248
 agaattgttc tttctttgtg gttttaataa gagttcaaga attgttcaga gtcttgtaaa 1308
 tgttattttta ataatccctt taaattttat ctgttgctgt tacctcttga aatatgattt 1368
 atttagattg ctaatcccac tcattcagga aatgccaaaga ggtattcctt ggggaaatgg 1428
 tgccctcttac agtgtaaatt tttcctcctt tacctttgct aatatcatgg cagaattttt 1488
 cttatccctt gtgaggcagt tgttgactga gtttttcac cttacaatcc tgtcccatgg 1548
 tatttaacat aaaaaaaaaat aaaactgtta acagattcctt gctcgat 1595

<210> 109
 <211> 540
 <212> PRT
 <213> Homo sapiens

<400> 109
 Met Gly Thr Thr Ala Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val
 1 5 10 15
 Ala Ser Ala Ala Ser Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln
 20 25 30
 Leu Arg Pro Glu His Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser
 35 40 45
 Pro Pro Leu Ser Arg Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln
 50 55 60
 His Gly Pro Pro Phe Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser
 65 70 75 80
 Gln Glu Ala Thr Pro Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu
 85 90 95
 Pro Ala Glu Lys Glu Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro
 100 105 110
 Leu Gln Lys Glu Leu Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu
 115 120 125

Gly	Thr	Pro	Ala	Pro	Phe	Gly	Asp	Gln	Ser	His	Pro	Glu	Pro	Glu	Ser	130	135	140
Trp	Asn	Ala	Ala	Gln	His	Cys	Gln	Gln	Asp	Arg	Ser	Gln	Gly	Gly	Trp	145	150	155
Gly	His	Arg	Leu	Asp	Gly	Phe	Pro	Pro	Gly	Arg	Pro	Ser	Pro	Asp	Asn	165	170	175
Leu	Asn	Gln	Ile	Cys	Leu	Pro	Asn	Arg	Gln	His	Val	Val	Tyr	Gly	Pro	180	185	190
Trp	Asn	Leu	Pro	Gln	Ser	Ser	Tyr	Ser	His	Leu	Thr	Arg	Gln	Gly	Glu	195	200	205
Thr	Leu	Asn	Phe	Leu	Glu	Ile	Gly	Tyr	Ser	Arg	Cys	Cys	His	Cys	Arg	210	215	220
Ser	His	Thr	Asn	Arg	Leu	Glu	Cys	Ala	Lys	Leu	Val	Trp	Glu	Glu	Ala	225	230	235
Met	Ser	Arg	Phe	Cys	Glu	Ala	Glu	Phe	Ser	Val	Lys	Thr	Arg	Pro	His	245	250	255
Trp	Cys	Cys	Thr	Arg	Gln	Gly	Glu	Ala	Arg	Phe	Ser	Cys	Phe	Gln	Glu	260	265	270
Glu	Ala	Pro	Gln	Pro	His	Tyr	Gln	Leu	Arg	Ala	Cys	Pro	Ser	His	Gln	275	280	285
Pro	Asp	Ile	Ser	Ser	Gly	Leu	Glu	Leu	Pro	Phe	Pro	Pro	Gly	Val	Pro	290	295	300
Thr	Leu	Asp	Asn	Ile	Lys	Asn	Ile	Cys	His	Leu	Arg	Arg	Phe	Arg	Ser	305	310	315
Val	Pro	Arg	Asn	Leu	Pro	Ala	Thr	Asp	Pro	Leu	Gln	Arg	Glu	Leu	Leu	325	330	335
Ala	Leu	Ile	Gln	Leu	Glu	Arg	Glu	Phe	Gln	Arg	Cys	Cys	Arg	Gln	Gly	340	345	350
Asn	Asn	His	Thr	Cys	Thr	Trp	Lys	Ala	Trp	Glu	Asp	Thr	Leu	Asp	Lys	355	360	365
Tyr	Cys	Asp	Arg	Glu	Tyr	Ala	Val	Lys	Thr	His	His	His	Leu	Cys	Cys	370	375	380
Arg	His	Pro	Pro	Ser	Pro	Thr	Arg	Asp	Glu	Cys	Phe	Ala	Arg	Arg	Ala	385	390	395
Pro	Tyr	Pro	Asn	Tyr	Asp	Arg	Asp	Ile	Leu	Thr	Ile	Asp	Ile	Gly	Arg	405	410	415
Val	Thr	Pro	Asn	Leu	Met	Gly	His	Leu	Cys	Gly	Asn	Gln	Arg	Val	Leu	420	425	430

Thr	Lys	His	Lys	His	Ile	Pro	Gly	Leu	Ile	His	Asn	Met	Thr	Ala	Arg	
		435					440					445				
Cys	Cys	Asp	Leu	Pro	Phe	Pro	Glu	Gln	Ala	Cys	Cys	Ala	Glu	Glu	Glu	
		450				455					460					
Lys	Leu	Thr	Phe	Ile	Asn	Asp	Leu	Cys	Gly	Pro	Arg	Arg	Asn	Ile	Trp	
465					470					475					480	
Arg	Asp	Pro	Ala	Leu	Cys	Cys	Tyr	Leu	Ser	Pro	Gly	Asp	Glu	Gln	Val	
				485					490						495	
Asn	Cys	Phe	Asn	Ile	Asn	Tyr	Leu	Arg	Asn	Val	Ala	Leu	Val	Ser	Gly	
			500					505						510		
Asp	Thr	Glu	Asn	Ala	Lys	Gly	Gln	Gly	Glu	Gln	Gly	Ser	Thr	Gly	Gly	
		515					520					525				
Thr	Asn	Ile	Ser	Ser	Thr	Ser	Glu	Pro	Lys	Glu	Glu					
	530					535					540					

<210> 110
 <211> 1810
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (102)..(1721)

<400> 110
 aaccgtaaca gccaccagac aagcttcagt ggccggccct tcacatccag acttgccctga 60
 gaggacccac ctctgagtgt ccagtgggtca gttgccccag g atg ggg acc aca gcc 116
 Met Gly Thr Thr Ala
 1 5
 aga gca gcc ttg gtc ttg acc tat ttg gct gtt gct tct gct gcc tct 164
 Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val Ala Ser Ala Ala Ser
 10 15 20
 gag gga ggc ttc acg gct aca gga cag agg cag ctg agg cca gag cac 212
 Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln Leu Arg Pro Glu His
 25 30 35
 ttt caa gaa gtt ggc tac gca gct ccc ccc tcc cca ccc cta tcc cga 260
 Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser Pro Pro Leu Ser Arg
 40 45 50
 agc ctc ccc atg gat cac cct gac tcc tct cag cat ggc cct ccc ttt 308
 Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln His Gly Pro Pro Phe
 55 60 65
 gag gga cag agt caa gtg cag ccc cct ccc tct cag gag gcc acc cct 356
 Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser Gln Glu Ala Thr Pro

70	75	80	85	
ctc caa cag gaa aag ctg cta cct gcc caa ctc cct gct gaa aag gaa	404			
Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu Pro Ala Glu Lys Glu				
90 95 100				
gtg ggt ccc cct ctc cct cag gaa gct gtc ccc ctc caa aaa gag ctg	452			
Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro Leu Gln Lys Glu Leu				
105 110 115				
ccc tct ctc cag cac ccc aat gaa cag aag gaa gga acg cca gct cca	500			
Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu Gly Thr Pro Ala Pro				
120 125 130				
ttt ggg gac cag agc cat cca gaa cct gag tcc tgg aat gca gcc cag	548			
Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser Trp Asn Ala Ala Gln				
135 140 145				
cac tgc caa cag gac cgg tcc caa ggg ggc tgg ggc cac cgg ctg gat	596			
His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp Gly His Arg Leu Asp				
150 155 160 165				
ggc ttc ccc cct ggg cgg cct tct cca gac aat ctg aac caa atc tgc	644			
Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn Leu Asn Gln Ile Cys				
170 175 180				
ctt cct aac cgt cag cat gtg gta tat ggt ccc tgg aac cta cca cag	692			
Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro Trp Asn Leu Pro Gln				
185 190 195				
tcc agc tac tcc cac ctc act cgc cag ggt gag acc ctc aat ttc ctg	740			
Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu Thr Leu Asn Phe Leu				
200 205 210				
gag att gga tat tcc cgc tgc tgc cac tgc cgc agc cac aca aac cgc	788			
Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg Ser His Thr Asn Arg				
215 220 225				
cta gag tgt gcc aaa ctt gtg tgg gag gaa gca atg agc cga ttc tgt	836			
Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala Met Ser Arg Phe Cys				
230 235 240 245				
gag gcc gag ttc tcg gtc aag acc cga ccc cac tgg tgc tgc acg cgg	884			
Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His Trp Cys Cys Thr Arg				
250 255 260				
cag ggg gag gct cgg ttc tcc tgc ttc cag gag gaa gct ccc cag cca	932			
Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu Glu Ala Pro Gln Pro				
265 270 275				
cac tac cag ctc cgg gcc tgc ccc agc cat cag cct gat att tcc tcg	980			
His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln Pro Asp Ile Ser Ser				
280 285 290				
ggc ctt gag ctg cct ttc cct cct ggg gtg ccc aca ttg gac aat atc	1028			
Gly Leu Glu Leu P				
ro Phe Pro Pro Gly Val Pro Thr Leu Asp Asn Ile				

295	300	305	
aag aac atc tgc cac ctg agg cgc ttc cgc tct gtg cca cgc aac ctg			1076
Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser Val Pro Arg Asn Leu			
310	315	320	325
cca gct act gac ccc cta caa agg gag ctg ctg gca ctg atc cag ctg			1124
Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Ala Leu Ile Gln Leu			
	330	335	340
gag agg gag ttc cag cgc tgc tgc cgc cag ggg aac aat cac acc tgt			1172
Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly Asn Asn His Thr Cys			
	345	350	355
aca tgg aag gcc tgg gag gat acc ctt gac aaa tac tgt gac cgg gag			1220
Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys Tyr Cys Asp Arg Glu			
	360	365	370
tat gct gtg aag acc cac cac cac ttg tgt tgc cgc cac cct ccc agc			1268
Tyr Ala Val Lys Thr His His His Leu Cys Cys Arg His Pro Pro Ser			
	375	380	385
cct act cgg gat gag tgc ttt gcc cgt cgg gct cct tac ccc aac tat			1316
Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala Pro Tyr Pro Asn Tyr			
	390	395	400
gac cgg gac atc ttg acc att gac atc ggt cga gtc acc ccc aac ctc			1364
Asp Arg Asp Ile Leu Thr Ile Asp Ile Gly Arg Val Thr Pro Asn Leu			
	410	415	420
atg ggc cac ctc tgt gga aac caa aga gtt ctc acc aag cat aaa cat			1412
Met Gly His Leu Cys Gly Asn Gln Arg Val Leu Thr Lys His Lys His			
	425	430	435
att cct ggg ctg atc cac aac atg act gcc cgc tgc tgt gac ctg cca			1460
Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg Cys Cys Asp Leu Pro			
	440	445	450
ttt cca gaa cag gcc tgc tgt gca gag gag gag aaa tta acc ttc atc			1508
Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu Lys Leu Thr Phe Ile			
	455	460	465
aat gat ctg tgt ggt ccc cga cgt aac atc tgg cga gac cct gcc ctc			1556
Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp Arg Asp Pro Ala Leu			
	470	475	480
tgc tgt tac ctg agt cct ggg gat gaa cag gtc aac tgc ttc aac atc			1604
Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val Asn Cys Phe Asn Ile			
	490	495	500
aat tat ctg agg aac gtg gct cta gtg tct gga gac act gag aac gcc			1652
Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly Asp Thr Glu Asn Ala			
	505	510	515
aag ggc cag ggg gag cag ggc tca act gga gga aca aat atc agc tcc			1700
Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly Thr Asn Ile Ser Ser			
	520	525	530

acc tct gag ccc aag gaa gaa tgagtcaccc cagagcccta gagggtcaga 1751
 Thr Ser Glu Pro Lys Glu Glu
 535 540

tggggggaac cccaccctgc cccacccatc tgaacactca ttacactaaa cacctcttg 1810

<210> 111
 <211> 540
 <212> PRT
 <213> Homo sapiens

<400> 111
 Met Gly Thr Thr Ala Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val
 1 5 10 15
 Ala Ser Ala Ala Ser Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln
 20 25 30
 Leu Arg Pro Glu His Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser
 35 40 45
 Pro Pro Leu Ser Arg Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln
 50 55 60
 His Gly Pro Pro Phe Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser
 65 70 75 80
 Gln Glu Ala Thr Pro Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu
 85 90 95
 Pro Ala Glu Lys Glu Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro
 100 105 110
 Leu Gln Lys Glu Leu Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu
 115 120 125
 Gly Thr Pro Ala Pro Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser
 130 135 140
 Trp Asn Ala Ala Gln His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp
 145 150 155 160
 Gly His Arg Leu Asp Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn
 165 170 175
 Leu Asn Gln Ile Cys Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro
 180 185 190
 Trp Asn Leu Pro Gln Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu
 195 200 205
 Thr Leu Asn Phe Leu Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg
 210 215 220
 Ser His Thr Asn Arg Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala

225					230					235					240
Met	Ser	Arg	Phe	Cys	Glu	Ala	Glu	Phe	Ser	Val	Lys	Thr	Arg	Pro	His
				245					250					255	
Trp	Cys	Cys	Thr	Arg	Gln	Gly	Glu	Ala	Arg	Phe	Ser	Cys	Phe	Gln	Glu
			260					265					270		
Glu	Ala	Pro	Gln	Pro	His	Tyr	Gln	Leu	Arg	Ala	Cys	Pro	Ser	His	Gln
		275					280					285			
Pro	Asp	Ile	Ser	Ser	Gly	Leu	Glu	Leu	Pro	Phe	Pro	Pro	Gly	Val	Pro
	290					295					300				
Thr	Leu	Asp	Asn	Ile	Lys	Asn	Ile	Cys	His	Leu	Arg	Arg	Phe	Arg	Ser
305					310					315					320
Val	Pro	Arg	Asn	Leu	Pro	Ala	Thr	Asp	Pro	Leu	Gln	Arg	Glu	Leu	Leu
			325						330					335	
Ala	Leu	Ile	Gln	Leu	Glu	Arg	Glu	Phe	Gln	Arg	Cys	Cys	Arg	Gln	Gly
			340					345					350		
Asn	Asn	His	Thr	Cys	Thr	Trp	Lys	Ala	Trp	Glu	Asp	Thr	Leu	Asp	Lys
		355					360					365			
Tyr	Cys	Asp	Arg	Glu	Tyr	Ala	Val	Lys	Thr	His	His	His	Leu	Cys	Cys
	370					375					380				
Arg	His	Pro	Pro	Ser	Pro	Thr	Arg	Asp	Glu	Cys	Phe	Ala	Arg	Arg	Ala
385					390					395					400
Pro	Tyr	Pro	Asn	Tyr	Asp	Arg	Asp	Ile	Leu	Thr	Ile	Asp	Ile	Ser	Arg
			405						410					415	
Val	Thr	Pro	Asn	Leu	Met	Gly	His	Leu	Cys	Gly	Asn	Gln	Arg	Val	Leu
			420					425					430		
Thr	Lys	His	Lys	His	Ile	Pro	Gly	Leu	Ile	His	Asn	Met	Thr	Ala	Arg
	435						440					445			
Cys	Cys	Asp	Leu	Pro	Phe	Pro	Glu	Gln	Ala	Cys	Cys	Ala	Glu	Glu	Glu
	450					455					460				
Lys	Leu	Thr	Phe	Ile	Asn	Asp	Leu	Cys	Gly	Pro	Arg	Arg	Asn	Ile	Trp
465					470					475					480
Arg	Asp	Pro	Ala	Leu	Cys	Cys	Tyr	Leu	Ser	Pro	Gly	Asp	Glu	Gln	Val
			485						490					495	
Asn	Cys	Phe	Asn	Ile	Asn	Tyr	Leu	Arg	Asn	Val	Ala	Leu	Val	Ser	Gly
			500					505					510		
Asp	Thr	Glu	Asn	Ala	Lys	Gly	Gln	Gly	Glu	Gln	Gly	Ser	Thr	Gly	Gly
	515						520					525			
Thr	Asn	Ile	Ser	Ser	Thr	Ser	Glu	Pro	Lys	Glu	Glu				

530

535

540

<210> 112
 <211> 1810
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (102)..(1721)

<400> 112
 aaccgtaaca gccaccagac aagcttcagt ggccggccct tcacatccag acttgccctga 60

gaggacccac ctctgagtgt ccagtgggtca gttgccccag g atg ggg acc aca gcc 116
 Met Gly Thr Thr Ala
 1 5

aga gca gcc ttg gtc ttg acc tat ttg gct gtt gct tct gct gcc tct 164
 Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val Ala Ser Ala Ala Ser
 10 15 20

gag gga ggc ttc acg gct aca gga cag agg cag ctg agg cca gag cac 212
 Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln Leu Arg Pro Glu His
 25 30 35

ttt caa gaa gtt ggc tac gca gct ccc ccc tcc cca ccc cta tcc cga 260
 Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser Pro Pro Leu Ser Arg
 40 45 50

agc ctc ccc atg gat cac cct gac tcc tct cag cat ggc cct ccc ttt 308
 Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln His Gly Pro Pro Phe
 55 60 65

gag gga cag agt caa gtg cag ccc cct ccc tct cag gag gcc acc cct 356
 Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser Gln Glu Ala Thr Pro
 70 75 80 85

ctc caa cag gaa aag ctg cta cct gcc caa ctc cct gct gaa aag gaa 404
 Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu Pro Ala Glu Lys Glu
 90 95 100

gtg ggt ccc cct ctc cct cag gaa gct gtc ccc ctc caa aaa gag ctg 452
 Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro Leu Gln Lys Glu Leu
 105 110 115

ccc tct ctc cag cac ccc aat gaa cag aag gaa gga acg cca gct cca 500
 Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu Gly Thr Pro Ala Pro
 120 125 130

ttt ggg gac cag agc cat cca gaa cct gag tcc tgg aat gca gcc cag 548
 Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser Trp Asn Ala Ala Gln
 135 140 145

cac tgc caa cag gac cgg tcc caa ggg ggc tgg ggc cac cgg ctg gat 596
 His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp Gly His Arg Leu Asp

150	155	160	165	
ggc ttc ccc cct ggg cgg cct tct cca gac aat ctg aac caa atc tgc				644
Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn Leu Asn Gln Ile Cys	170	175	180	
ctt cct aac cgt cag cat gtg gta tat ggt ccc tgg aac cta cca cag				692
Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro Trp Asn Leu Pro Gln	185	190	195	
tcc agc tac tcc cac ctc act cgc cag ggt gag acc ctc aat ttc ctg				740
Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu Thr Leu Asn Phe Leu	200	205	210	
gag att gga tat tcc cgc tgc tgc cac tgc cgc agc cac aca aac cgc				788
Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg Ser His Thr Asn Arg	215	220	225	
cta gag tgt gcc aaa ctt gtg tgg gag gaa gca atg agc cga ttc tgt				836
Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala Met Ser Arg Phe Cys	230	235	240	245
gag gcc gag ttc tcg gtc aag acc cga ccc cac tgg tgc tgc acg cgg				884
Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His Trp Cys Cys Thr Arg	250	255	260	
cag ggg gag gct cgg ttc tcc tgc ttc cag gag gaa gct ccc cag cca				932
Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu Glu Ala Pro Gln Pro	265	270	275	
cac tac cag ctc cgg gcc tgc ccc agc cat cag cct gat att tcc tcg				980
His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln Pro Asp Ile Ser Ser	280	285	290	
ggt ctt gag ctg cct ttc cct cct ggg gtg ccc aca ttg gac aat atc				1028
Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro Thr Leu Asp Asn Ile	295	300	305	
aag aac atc tgc cac ctg agg cgc ttc cgc tct gtg cca cgc aac ctg				1076
Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser Val Pro Arg Asn Leu	310	315	320	325
cca gct act gac ccc cta caa agg gag ctg ctg gca ctg atc cag ctg				1124
Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu Ala Leu Ile Gln Leu	330	335	340	
gag agg gag ttc cag cgc tgc tgc cgc cag ggg aac aat cac acc tgt				1172
Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly Asn Asn His Thr Cys	345	350	355	
aca tgg aag gcc tgg gag gat acc ctt gac aaa tac tgt gac cgg gag				1220
Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys Tyr Cys Asp Arg Glu	360	365	370	
tat gct gtg aag acc cac cac cac ttg tgt tgc cgc cac cct ccc agc				1268
Tyr Ala Val Lys Thr His His His Leu Cys Cys Arg His Pro Pro Ser	375	380	385	

cct act cgg gat gag tgc ttt gcc cgt cgg gct cct tac ccc aac tat	1316
Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala Pro Tyr Pro Asn Tyr	
390 395 400 405	
gac cgg gac atc ttg acc att gac atc agt cga gtc acc ccc aac ctc	1364
Asp Arg Asp Ile Leu Thr Ile Asp Ile Ser Arg Val Thr Pro Asn Leu	
410 415 420	
atg ggc cac ctc tgt gga aac caa aga gtt ctc acc aag cat aaa cat	1412
Met Gly His Leu Cys Gly Asn Gln Arg Val Leu Thr Lys His Lys His	
425 430 435	
att cct ggg ctg atc cac aac atg act gcc cgc tgc tgt gac ctg cca	1460
Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg Cys Cys Asp Leu Pro	
440 445 450	
ttt cca gaa cag gcc tgc tgt gca gag gag gag aaa tta acc ttc atc	1508
Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu Lys Leu Thr Phe Ile	
455 460 465	
aat gat ctg tgt ggt ccc cga cgt aac atc tgg cga gac cct gcc ctc	1556
Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp Arg Asp Pro Ala Leu	
470 475 480 485	
tgc tgt tac ctg agt cct ggg gat gaa cag gtc aac tgc ttc aac atc	1604
Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val Asn Cys Phe Asn Ile	
490 495 500	
aat tat ctg agg aac gtg gct cta gtg tct gga gac act gag aac gcc	1652
Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly Asp Thr Glu Asn Ala	
505 510 515	
aag ggc cag ggg gag cag ggc tca act gga gga aca aat atc agc tcc	1700
Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly Thr Asn Ile Ser Ser	
520 525 530	
acc tct gag ccc aag gaa gaa tgagtcaccc cagagcccta gagggtcaga	1751
Thr Ser Glu Pro Lys Glu Glu	
535 540	
tggggggaac cccaccctgc cccaccatc tgaacactca ttacactaaa cacctcttg	1810

<210> 113
 <211> 382
 <212> PRT
 <213> Homo sapiens

<400> 113
 Met Gly Asp Trp Ser Ala Leu Gly Lys Leu Leu Asp Lys Val Gln Ala
 1 5 10 15
 Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser Val Leu Phe Ile Phe
 20 25 30
 Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser Ala Trp Gly Asp Glu

35	40	45
Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro Gly Cys Glu Asn Val		
50	55	60
Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val Arg Phe Trp Val Leu		
65	70	75
Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu Tyr Leu Ala His Val		
85	90	95
Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn Lys Lys Glu Glu Glu		
100	105	110
Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val Asp Met His Leu Lys		
115	120	125
Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile Glu Glu His Gly Lys		
130	135	140
Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr Ile Ile Ser Ile Leu		
145	150	155
Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu Ile Gln Trp Tyr Ile		
165	170	175
Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys Lys Arg Asp Pro Cys		
180	185	190
Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro Thr Glu Lys Thr Ile		
195	200	205
Phe Ile Ile Phe Met Leu Val Val Ser Leu Val Ser Leu Ala Leu Asn		
210	215	220
Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly Val Lys Asp Arg Val		
225	230	235
Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser Gly Ala Leu Ser Pro		
245	250	255
Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr Phe Asn Gly Cys Ser		
260	265	270
Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro Pro Gly Tyr Lys Leu		
275	280	285
Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn Tyr Asn Lys Gln		
290	295	300
Ala Ser Glu Gln Thr Trp Ala Asn Tyr Ser Ala Glu Gln Asn Arg Met		
305	310	315
Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His Ala Gln Pro Phe Asp		
325	330	335
Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu Ala Ala Gly His Glu		

-----340-----345-----350-----
 Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro Ser Ser Arg Ala Ser
 355 360 365

Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp Leu Glu Ile
 370 375 380

<210> 114
 <211> 3074
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (201)..(1346)

<400> 114
 aacttttacg aggtatcagc actttttcttt cattagggggg aaggcgtgag gaaagtacca 60
 aacagcagcg gagtttttaa ctttaaatac acaggtctga gtgcctgaac ttgccttttc 120
 attttacttc atcctccaag gagttcaatc acttggcgtg acttcactac ttttaagcaa 180
 aagagtgggtg cccaggcaac atg ggt gac tgg agc gcc tta ggc aaa ctc ctt 233
 Met Gly Asp Trp Ser Ala Leu Gly Lys Leu Leu
 1 5 10
 gac aag gtt caa gcc tac tca act gct gga ggg aag gtg tgg ctg tca 281
 Asp Lys Val Gln Ala Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser
 15 20 25
 gta ctt ttc att ttc cga atc ctg ctg ctg ggg aca gcg gtt gag tca 329
 Val Leu Phe Ile Phe Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser
 30 35 40
 gcc tgg gga gat gag cag tct gcc ttt cgt tgt aac act cag caa cct 377
 Ala Trp Gly Asp Glu Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro
 45 50 55
 ggt tgt gaa aat gtc tgc tat gac aag tct ttc cca atc tct cat gtg 425
 Gly Cys Glu Asn Val Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val
 60 65 70 75
 cgc ttc tgg gtc ctg cag atc ata ttt gtg tct gta ccc aca ctc ttg 473
 Arg Phe Trp Val Leu Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu
 80 85 90
 tac ctg gct cat gtg ttc tat gtg atg cga aag gaa gag aaa ctg aac 521
 Tyr Leu Ala His Val Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn
 95 100 105
 aag aaa gag gaa gaa ctc aag gtt gcc caa act gat ggt gtc aat gtg 569
 Lys Lys Glu Glu Glu Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val
 110 115 120

gac_atg_cac_ttg_aag_cag_att_gag_ata_aag_aag_ttc_aag_tac_ggt_att-	617
Asp Met His Leu Lys Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile	
125 130 135	
gaa_gag_cat_ggt_aag_gtg_aaa_atg_cga_ggg_ggg_ttg_ctg_cga_acc_tac	665
Glu Glu His Gly Lys Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr	
140 145 150 155	
atc_atc_agt_atc_ctc_ttc_aag_tct_atc_ttt_gag_gtg_gcc_ttc_ttg_ctg	713
Ile Ile Ser Ile Leu Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu	
160 165 170	
atc_cag_tgg_tac_atc_tat_gga_ttc_agc_ttg_agt_gct_gtt_tac_act_tgc	761
Ile Gln Trp Tyr Ile Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys	
175 180 185	
aaa_aga_gat_ccc_tgc_cca_cat_cag_gtg_gac_tgt_ttc_ctc_tct_cgc_ccc	809
Lys Arg Asp Pro Cys Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro	
190 195 200	
acg_gag_aaa_acc_atc_ttc_atc_atc_ttc_atg_ctg_gtg_gtg_tcc_ttg_gtg	857
Thr Glu Lys Thr Ile Phe Ile Ile Phe Met Leu Val Val Ser Leu Val	
205 210 215	
tcc_ctg_gcc_ttg_aat_atc_att_gaa_ctc_ttc_tat_gtt_ttc_ttc_aag_ggc	905
Ser Leu Ala Leu Asn Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly	
220 225 230 235	
gtt_aag_gat_cgg_gtt_aag_gga_aag_agc_gac_cct_tac_cat_gcg_acc_agt	953
Val Lys Asp Arg Val Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser	
240 245 250	
ggt_gcg_ctg_agc_cct_gcc_aaa_gac_tgt_ggg_tct_caa_aaa_tat_gct_tat	1001
Gly Ala Leu Ser Pro Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr	
255 260 265	
ttc_aat_ggc_tgc_tcc_tca_cca_acc_gct_ccc_ctc_tcg_cct_atg_tct_cct	1049
Phe Asn Gly Cys Ser Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro	
270 275 280	
cct_ggg_tac_aag_ctg_gtt_act_ggc_gac_aga_aac_aat_tct_tct_tgc_cgc	1097
Pro Gly Tyr Lys Leu Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg	
285 290 295	
aat_tac_aac_aag_caa_gca_agt_gag_caa_acc_tgg_gct_aat_tac_agt_gca	1145
Asn Tyr Asn Lys Gln Ala Ser Glu Gln Thr Trp Ala Asn Tyr Ser Ala	
300 305 310 315	
gaa_caa_aat_cga_atg_ggg_cag_gcg_gga_agc_acc_atc_tct_aac_tcc_cat	1193
Glu Gln Asn Arg Met Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His	
320 325 330	
gca_cag_cct_ttt_gat_ttc_ccc_gat_gat_aac_cag_aat_tct_aaa_aaa_cta	1241
Ala Gln Pro Phe Asp Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu	
335 340 345	
gct_gct_gga_cat_gaa_tta_cag_cca_cta_gcc_att_gtg_gac_cag_cga_cct	1289

Ala	Ala	Gly	His	Glu	Leu	Gln	Pro	Leu	Ala	Ile	Val	Asp	Gln	Arg	Pro	—	—	—	—	—	—
		350					355					360									

tca agc aga gcc agc agt cgt gcc agc agc aga cct cgg cct gat gac 1337
Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp
365 370 375

ctg gag atc tagatacagg cttgaaagca tcaagattcc actcaattgt 1386
Leu Glu Ile
380

ggagaagaaa aaaggtgctg tagaaagtgc accaggtggt aattttgatc cgggtggaggt 1446
ggtactcaac agccttattc atgaggctta gaaaacacaa agacattaga atacctaggt 1506
tcaactggggg tgtatggggt agatgggtgg agagggaggg gataagagag gtgcatgttg 1566
gtatttaaag tagtggattc aaagaactta gattataaat aagagttcca ttaggtgata 1626
catagataag ggctttttct ccccgcaaac acccctaaga atggttctgt gtatgtgaat 1686
gagcgggtgg taattgtggc taaatatttt tgttttacca agaaactgaa ataattctgg 1746
ccaggaataa atacttcttg aacatcttag gtcttttcaa caagaaaaag acagaggatt 1806
gtccttaagt ccctgctaaa acattccatt gttaaaattt gcactttgaa ggtaagcttt 1866
ctaggcctga ccctccaggt gtcaatggac ttgtgctact atattttttt attcttggtg 1926
tcagttttaa attcagacaa ggcccacaga ataagatttt ccatgcattt gcaaatacgt 1986
atattctttt tccatccact tgcacaatat cattaccatc actttttcat cattcctcag 2046
ctactactca cattcattta atggtttctg taaacatttt taagacagtt gggatgtcac 2106
ttaacatttt ttttttgagc taaagtcagg gaatcaagcc atgcttaata tttacaatc 2166
acttatatgt gtgtcgaaga gtttgttttg tttgtcatgt attggtacaa gcagatacag 2226
tataaactca caaacacaga tttgaaaata atgcacatat ggtgttcaaa tttgaacctt 2286
tctcatggat ttttgtggtg tgggccaata tgggtgtttac attatataat tctgtctgtg 2346
gcaagtaaag cacacttttt ttttctccta aaatgttttt ccctgtgtat cctattatgg 2406
atactggttt tgttaattat gattctttat tttctctcct ttttttagga tatagcagta 2466
atgctattac tgaaatgaat ttcctttttc tgaaatgtaa tcattgatgc ttgaatgata 2526
gaattttagt actgtaaaca ggcttttagtc attaatgtga gagacttaga aaaaaatgct 2586
tagagtggac tattaaatgt gcctaaatga attttgcagt aactggtatt cttgggtttt 2646
cctacttaat acacagtaat tcagaacttg tattctatta tgagtttagc agtcttttgg 2706
agtgaccagc aactttgatg tttgcactaa gattttattt ggaatgcaag agaggttgaa 2766

agaggattca gtagtacaca tacaactaat ttatttgaac tatatgttga-agacatctac-2826-
 cagtttctcc aaatgccttt tttaaaactc atcacagaag attggtgaaa atgctgagta 2886
 tgacactttt cttcttgcac gcatgtcagc tacataaaca gttttgtaca atgaaaatta 2946
 ctaatttggt tgacattcca tgttaaacta cggatcatggt cagcttcatt gcatgtaatg 3006
 tagacctagt ccatcagatc atgtgttctg gagagtgttc ttatttcaat aaagttttta 3066
 tttagtat 3074

<210> 115
 <211> 382
 <212> PRT
 <213> Homo sapiens

<400> 115
 Met Gly Asp Trp Ser Ala Leu Gly Lys Leu Leu Asp Lys Val Gln Ala
 1 5 10 15
 Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser Val Leu Phe Ile Phe
 20 25 30
 Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser Ala Trp Gly Asp Glu
 35 40 45
 Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro Gly Cys Glu Asn Val
 50 55 60
 Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val Arg Phe Trp Val Leu
 65 70 75 80
 Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu Tyr Leu Ala His Val
 85 90 95
 Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn Lys Lys Glu Glu Glu
 100 105 110
 Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val Asp Met His Leu Lys
 115 120 125
 Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile Glu Glu His Gly Lys
 130 135 140
 Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr Ile Ile Ser Ile Leu
 145 150 155 160
 Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu Ile Gln Trp Tyr Ile
 165 170 175
 Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys Lys Arg Asp Pro Cys
 180 185 190
 Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro Thr Glu Lys Thr Ile
 195 200 205

	15	20	25	
gta ctt ttc att ttc cga atc ctg ctg ctg ggg aca gcg gtt gag tca	329			
Val Leu Phe Ile Phe Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser				
30 35 40				
gcc tgg gga gat gag cag tct gcc ttt cgt tgt aac act cag caa cct	377			
Ala Trp Gly Asp Glu Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro				
45 50 55				
ggt tgt gaa aat gtc tgc tat gac aag tct ttc cca atc tct cat gtg	425			
Gly Cys Glu Asn Val Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val				
60 65 70 75				
cgc ttc tgg gtc ctg cag atc ata ttt gtg tct gta ccc aca ctc ttg	473			
Arg Phe Trp Val Leu Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu				
80 85 90				
tac ctg gct cat gtg ttc tat gtg atg cga aag gaa gag aaa ctg aac	521			
Tyr Leu Ala His Val Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn				
95 100 105				
aag aaa gag gaa gaa ctc aag gtt gcc caa act gat ggt gtc aat gtg	569			
Lys Lys Glu Glu Glu Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val				
110 115 120				
gac atg cac ttg aag cag att gag ata aag aag ttc aag tac ggt att	617			
Asp Met His Leu Lys Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile				
125 130 135				
gaa gag cat ggt aag gtg aaa atg cga ggg ggg ttg ctg cga acc tac	665			
Glu Glu His Gly Lys Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr				
140 145 150 155				
atc atc agt atc ctc ttc aag tct atc ttt gag gtg gcc ttc ttg ctg	713			
Ile Ile Ser Ile Leu Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu				
160 165 170				
atc cag tgg tac atc tat gga ttc agc ttg agt gct gtt tac act tgc	761			
Ile Gln Trp Tyr Ile Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys				
175 180 185				
aaa aga gat ccc tgc cca cat cag gtg gac tgt ttc ctc tct cgc ccc	809			
Lys Arg Asp Pro Cys Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro				
190 195 200				
acg gag aaa acc atc ttc atc atc ttc atg ctg gtg gtg tcc ttg gtg	857			
Thr Glu Lys Thr Ile Phe Ile Ile Phe Met Leu Val Val Ser Leu Val				
205 210 215				
tcc ctg gcc ttg aat atc att gaa ctc ttc tat gtt ttc ttc aag ggc	905			
Ser Leu Ala Leu Asn Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly				
220 225 230 235				
gtt aag gat cgg gtt aag gga aag agc gac cct tac cat gcg acc agt	953			
Val Lys Asp Arg Val Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser				
240 245 250				

ggt gcg ctg agc cct gcc aaa gac tgt ggg tct caa aaa tat gct tat	1001
Gly Ala Leu Ser Pro Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr	
255 260 265	
ttc aat ggc tgc tcc tca cca acc gct ccc ctc tcg cct atg tct cct	1049
Phe Asn Gly Cys Ser Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro	
270 275 280	
cct ggg tac aag ctg gtt act ggc gac aga aac aat tct tct tgc cgc	1097
Pro Gly Tyr Lys Leu Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg	
285 290 295	
aat tac aac aag caa gca agt gag caa aac tgg gct aat tac agt gca	1145
Asn Tyr Asn Lys Gln Ala Ser Glu Gln Asn Trp Ala Asn Tyr Ser Ala	
300 305 310 315	
gaa caa aat cga atg ggg cag gcg gga agc acc atc tct aac tcc cat	1193
Glu Gln Asn Arg Met Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His	
320 325 330	
gca cag cct ttt gat ttc ccc gat gat aac cag aat tct aaa aaa cta	1241
Ala Gln Pro Phe Asp Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu	
335 340 345	
gct gct gga cat gaa tta cag cca cta gcc att gtg gac cag cga cct	1289
Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro	
350 355 360	
tca agc aga gcc agc agt cgt gcc agc agc aga cct cgg cct gat gac	1337
Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp	
365 370 375	
ctg gag atc tagatacagg cttgaaagca tcaagattcc actcaattgt	1386
Leu Glu Ile	
380	
ggagaagaaa aaaggtgctg tagaaagtgc accaggtggt aattttgatc cggtggaggt	1446
ggtactcaac agccttattc atgaggctta gaaaacacaa agacattaga atacctaggt	1506
tcaactggggg tgtatggggt agatgggtgg agagggaggg gataagagag gtgcatgttg	1566
gtattttaag tagtggattc aaagaactta gattataaat aagagttcca ttaggtgata	1626
catagataag ggctttttct ccccgcaaac acccctaaga atggttctgt gtatgtgaat	1686
gagcgggtgg taattgtggc taaatatttt tgttttacca agaaactgaa ataattctgg	1746
ccaggaataa atacttctg aacatcttag gtcttttcaa caagaaaaag acagaggatt	1806
gtccttaagt cctgctaaa acattccatt gttaaaattt gcactttgaa ggtaagcttt	1866
ctaggcctga cctccaggt gtcaatggac ttgtgctact atattttttt attcttggtg	1926
tcagttttaa attcagacaa ggcccacaga ataagatttt ccatgcattt gcaaatacgt	1986

~~atattctttt~~ ~~tccatccact~~ ~~tgacacaatat~~ ~~cattaccatc~~ ~~actttttcāt~~ ~~cāttcōctcāg~~ 2046
 ctactactca cattcattta atgggtttctg taaacatttt taagacagtt gggatgtcac 2106
 ttaacatttt ttttttgagc taaagtcagg gaatcaagcc atgcttaata tttacaatc 2166
 acttatatgt gtgtcgaaga gtttgttttg tttgtcatgt attggtacaa gcagatacag 2226
 tataaactca caaacacaga tttgaaaata atgcacatat ggtgttcaaa tttgaacctt 2286
 tctcatggat ttttgtggtg tgggccaaata tgggtgtttac attatataat tctgtgtgtg 2346
 gcaagtaaag cacacttttt ttttctccta aaatgttttt cctgtgtgtat cctattatgg 2406
 atactgggtt tgttaattat gattctttat tttctctcct ttttttagga tatagcagta 2466
 atgctattac tgaaatgaat ttcttttttc tgaaatgtaa tcattgatgc ttgaatgata 2526
 gaattttagt actgtaaaca ggcttttagtc attaatgtga gagacttaga aaaaaatgct 2586
 tagagtggac tattaaatgt gcctaaatga attttgcagt aactggtatt cttgggtttt 2646
 cctacttaat acacagtaat tcagaacttg tattctatta tgagtttagc agtcttttgg 2706
 agtgaccagc aactttgatg tttgcactaa gattttattt ggaatgcaag agaggttgaa 2766
 agaggattca gtagtacaca tacaactaat ttatttgaac tatatgttga agacatctac 2826
 cagtttctcc aaatgccttt tttaaaactc atcacagaag attggtgaaa atgctgagta 2886
 tgacactttt cttcttgcac gcatgtcagc tacataaaca gttttgtaca atgaaaatta 2946
 ctaatttggt tgacattcca tgttaaacta cgggtcatgtt cagcttcatt gcatgtaatg 3006
 tagacctagt ccatcagatc atgtgttctg gagagtgttc tttattcaat aaagttttta 3066
 tttagtat 3074

<210> 117
 <211> 398
 <212> PRT
 <213> Homo sapiens

<400> 117
 Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu Cys Ile Trp Met
 1 5 10 15
 Ser Ala Leu Phe Leu Gly Val Gly Val Arg Ala Glu Glu Ala Gly Ala
 20 25 30
 Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr Gly Asp Pro Gln
 35 40 45
 Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met Asp Pro Glu Ser
 50 55 60

-Ser	Ile	Phe	Ile	Glu	Asp	Ala	Ile	Lys	Tyr	Phe	Lys	Glu	Lys	Val	Ser	65	70	75	80
Thr	Gln	Asn	Leu	Leu	Leu	Leu	Leu	Thr	Asp	Asn	Glu	Ala	Trp	Asn	Gly	85	90	95	
Phe	Val	Ala	Ala	Ala	Glu	Leu	Pro	Arg	Asn	Glu	Ala	Asp	Glu	Leu	Arg	100	105	110	
Lys	Ala	Leu	Asp	Asn	Leu	Ala	Arg	Gln	Met	Ile	Met	Lys	Asp	Lys	Asn	115	120	125	
Trp	His	Asp	Lys	Gly	Gln	Gln	Tyr	Arg	Asn	Trp	Phe	Leu	Lys	Glu	Phe	130	135	140	
Pro	Arg	Leu	Lys	Ser	Lys	Leu	Glu	Asp	Asn	Ile	Arg	Arg	Leu	Arg	Ala	145	150	155	160
Leu	Ala	Asp	Gly	Val	Gln	Lys	Val	His	Lys	Gly	Thr	Thr	Ile	Ala	Asn	165	170	175	
Val	Val	Ser	Gly	Ser	Leu	Ser	Ile	Ser	Ser	Gly	Ile	Leu	Thr	Leu	Val	180	185	190	
Gly	Met	Gly	Leu	Ala	Pro	Phe	Thr	Glu	Gly	Gly	Ser	Leu	Val	Leu	Leu	195	200	205	
Glu	Pro	Gly	Met	Glu	Leu	Gly	Ile	Thr	Ala	Ala	Leu	Thr	Gly	Ile	Thr	210	215	220	
Ser	Ser	Thr	Ile	Asp	Tyr	Gly	Lys	Lys	Trp	Trp	Thr	Gln	Ala	Gln	Ala	225	230	235	240
His	Asp	Leu	Val	Ile	Lys	Ser	Leu	Asp	Lys	Leu	Lys	Glu	Val	Lys	Glu	245	250	255	
Phe	Leu	Gly	Glu	Asn	Ile	Ser	Asn	Phe	Leu	Ser	Leu	Ala	Gly	Asn	Thr	260	265	270	
Tyr	Gln	Leu	Thr	Arg	Gly	Ile	Gly	Lys	Asp	Ile	Arg	Ala	Leu	Arg	Arg	275	280	285	
Ala	Arg	Ala	Asn	Leu	Gln	Ser	Val	Pro	His	Ala	Ser	Ala	Ser	Arg	Pro	290	295	300	
Arg	Val	Thr	Glu	Pro	Ile	Ser	Ala	Glu	Ser	Gly	Glu	Gln	Val	Glu	Arg	305	310	315	320
Val	Asn	Glu	Pro	Ser	Ile	Leu	Glu	Met	Ser	Arg	Gly	Val	Lys	Leu	Thr	325	330	335	
Asp	Val	Ala	Pro	Val	Ser	Phe	Phe	Leu	Val	Leu	Asp	Val	Val	Tyr	Leu	340	345	350	
Val	Tyr	Glu	Ser	Lys	His	Leu	His	Glu	Gly	Ala	Lys	Ser	Glu	Thr	Ala	355	360	365	

Glu Glu Leu Lys Lys Val-Ala Gln-Glu-Leu-Glu-Glu Lys Leu Asn Ile
 370 375 380

Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln Glu Leu
 385 390 395

<210> 118
 <211> 2054
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (76)..(1269)

<400> 118
 cacacagctc agaacagctg gatcttgctc agtctctgcc aggggaagat tccttgagg 60

aggccctgca gcgac atg gag gga gct gct ttg ctg aga gtc tct gtc ctc 111
 Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu
 1 5 10

tgc atc tgg atg agt gca ctt ttc ctt ggt gtg gga gtg agg gca gag 159
 Cys Ile Trp Met Ser Ala Leu Phe Leu Gly Val Gly Val Arg Ala Glu
 15 20 25

gaa gct gga gcg agg gtg caa caa aac gtt cca agt ggg aca gat act 207
 Glu Ala Gly Ala Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr
 30 35 40

gga gat cct caa agt aag ccc ctc ggt gac tgg gct gct ggc acc atg 255
 Gly Asp Pro Gln Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met
 45 50 55 60

gac cca gag agc agt atc ttt att gag gat gcc att aag tat ttc aag 303
 Asp Pro Glu Ser Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys
 65 70 75

gaa aaa gtg agc aca cag aat ctg cta ctc ctg ctg act gat aat gag 351
 Glu Lys Val Ser Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu
 80 85 90

gcc tgg aac gga ttc gtg gct gct gct gaa ctg ccc agg aat gag gca 399
 Ala Trp Asn Gly Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala
 95 100 105

gat gag ctc cgt aaa gct ctg gac aac ctt gca aga caa atg atc atg 447
 Asp Glu Leu Arg Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met
 110 115 120

aaa gac aaa aac tgg cac gat aaa ggc cag cag tac aga aac tgg ttt 495
 Lys Asp Lys Asn Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe
 125 130 135 140

ctg aaa gag ttt cct cgg ttg aaa agt aag ctt gag gat aac ata aga 543
 Leu Lys Glu Phe Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg

	145		150		155	
agg ctc cgt gcc ctt gca gat ggg gtt cag aag gtc cac aaa ggc acc	591					
Arg Leu Arg Ala Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr						
160		165		170		
acc atc gcc aat gtg gtg tct ggc tct ctc agc att tcc tct ggc atc	639					
Thr Ile Ala Asn Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile						
175		180		185		
ctg acc ctc gtc ggc atg ggt ctg gca ccc ttc aca gag gga ggc agc	687					
Leu Thr Leu Val Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser						
190		195		200		
ctt gta ctc ttg gaa cct ggg atg gag ttg gga atc aca gca gct ttg	735					
Leu Val Leu Leu Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu						
205		210		215		220
acc ggg att acc agc agt acc ata gac tac gga aag aag tgg tgg aca	783					
Thr Gly Ile Thr Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr						
225		230		235		
caa gcc caa gcc cac gac ctg gtc atc aaa agc ctt gac aaa ttg aag	831					
Gln Ala Gln Ala His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys						
240		245		250		
gag gtg aag gag ttt ttg ggt gag aac ata tcc aac ttt ctt tcc tta	879					
Glu Val Lys Glu Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu						
255		260		265		
gct ggc aat act tac caa ctc aca cga ggc att ggg aag gac atc cgt	927					
Ala Gly Asn Thr Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg						
270		275		280		
gcc ctc aga cga gcc aga gcc aat ctt cag tca gta ccg cat gcc tca	975					
Ala Leu Arg Arg Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser						
285		290		295		300
gcc tca cgc ccc cgg gtc act gag cca atc tca gct gaa agc ggt gaa	1023					
Ala Ser Arg Pro Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu						
305		310		315		
cag gtg gag aga gtt aat gaa ccc agc atc ctg gaa atg agc aga gga	1071					
Gln Val Glu Arg Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly						
320		325		330		
gtc aag ctc acg gat gtg gcc cct gta agc ttc ttt ctt gtg ctg gat	1119					
Val Lys Leu Thr Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp						
335		340		345		
gta gtc tac ctc gtg tac gaa tca aag cac tta cat gag ggg gca aag	1167					
Val Val Tyr Leu Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys						
350		355		360		
tca gag aca gct gag gag ctg aag aag gtg gct cag gag ctg gag gag	1215					
Ser Glu Thr Ala Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu						
365		370		375		380

aag cta aac att ctc aac aat aat tat aag att ctg cag gcg gac caa 1263
 Lys Leu Asn Ile Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln
 385 390 395

gaa ctg tgaccacagg gcagggcagc caccaggaga gatatgcctg gcaggggcca 1319
 Glu Leu

ggacaaaatg caaacttttt ttttttctga gacagagtct tgctctgtcg ccaagttgca 1379

gtgagccgag atatcgccac tgcactccag cctgggtgac agagcgagac tccatctcaa 1439

aaaaaaaaa aaaaagaata tattgacgga agaatagaga ggaggcttga aggaaccagc 1499

aatgagaagg ccaggaaaag aaagagctga aaatggagaa agcccaagag ttagaacagt 1559

tggatacagg agaagaaaca gcggctccac tacagacca gccccagggt caatgtcctc 1619

cgaagaatga agtctttccc tggatgatgt cccctgccct gtctttccag catccactct 1679

cccttgtcct cctgggggca tatctcagtc aggcagcggc ttcttgatga tggtcgttgg 1739

ggtggttgtc atgtgatggg tccccctccag gttactaaag ggtgcatgtc cccctgcttga 1799

acactgaagg gcagggtggtg agccatggcc atgggtcccca gctgaggagc aggtgtccct 1859

gagaacccaa acttcccaga gagtatgtga gaaccaacca atgaaaacag tcccatcgct 1919

cttaccgggt aagtaaacag tcagaaaatt agcatgaaag cagtttagca ttggggaggaa 1979

gtcagatct ctagagctgt cttgtccccg ccaggattg acctgtgtaa gtcccaataa 2039

actcacctac tcac 2054

<210> 119
 <211> 398
 <212> PRT
 <213> Homo sapiens

<400> 119
 Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu Cys Ile Trp Met
 1 5 10 15
 Ser Ala Leu Phe Leu Gly Val Arg Val Arg Ala Glu Glu Ala Gly Ala
 20 25 30
 Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr Gly Asp Pro Gln
 35 40 45
 Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met Asp Pro Glu Ser
 50 55 60
 Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys Glu Lys Val Ser
 65 70 75 80
 Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu Ala Trp Asn Gly

385 390 395

<210> 120
 <211> 2054
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (76)..(1269)

<400> 120
 cacacagctc agaacagctg gatcttgctc agtctctgcc aggggaagat tccttgagg 60
 aggccctgca gcgac atg gag gga gct gct ttg ctg aga gtc tct gtc ctc 111
 Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu
 1 5 10
 tgc atc tgg atg agt gca ctt ttc ctt ggt gtg aga gtg agg gca gag 159
 Cys Ile Trp Met Ser Ala Leu Phe Leu Gly Val Arg Val Arg Ala Glu
 15 20 25
 gaa gct gga gcg agg gtg caa caa aac gtt cca agt ggg aca gat act 207
 Glu Ala Gly Ala Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr
 30 35 40
 gga gat cct caa agt aag ccc ctc ggt gac tgg gct gct ggc acc atg 255
 Gly Asp Pro Gln Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met
 45 50 55 60
 gac cca gag agc agt atc ttt att gag gat gcc att aag tat ttc aag 303
 Asp Pro Glu Ser Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys
 65 70 75
 gaa aaa gtg agc aca cag aat ctg cta ctc ctg ctg act gat aat gag 351
 Glu Lys Val Ser Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu
 80 85 90
 gcc tgg aac gga ttc gtg gct gct gct gaa ctg ccc agg aat gag gca 399
 Ala Trp Asn Gly Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala
 95 100 105
 gat gag ctc cgt aaa gct ctg gac aac ctt gca aga caa atg atc atg 447
 Asp Glu Leu Arg Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met
 110 115 120
 aaa gac aaa aac tgg cac gat aaa ggc cag cag tac aga aac tgg ttt 495
 Lys Asp Lys Asn Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe
 125 130 135 140
 ctg aaa gag ttt cct cgg ttg aaa agt aag ctt gag gat aac ata aga 543
 Leu Lys Glu Phe Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg
 145 150 155
 agg ctc cgt gcc ctt gca gat ggg gtt cag aag gtc cac aaa ggc acc 591
 Arg Leu Arg Ala Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr

gaa ctg tgaccacagg gcagggcagc caccaggaga gatatgcctg gcaggggccca 1319
 Glu Leu
 ggacaaaatg caaacttttt ttttttctga gacagagtct tgctctgtcg ccaagttgca 1379
 gtgagccgag atatcgccac tgcactccag cctgggtgac agagcgagac tccatctcaa 1439
 aaaaaaaaaa aaaaagaata tattgacgga agaatagaga ggaggcttga aggaaccagc 1499
 aatgagaagg ccaggaaaag aaagagctga aaatggagaa agcccaagag ttagaacagt 1559
 tggatacagg agaagaaaca gcggctccac tacagaccca gcccaggtt caatgtcctc 1619
 cgaagaatga agtctttccc tggatgatgt cccctgccct gtctttccag catccactct 1679
 ccttgtcct cctgggggca tatctcagtc aggcagcggc ttctgatga tggtcgttgg 1739
 ggtggttgtc atgtgatggg tcccctccag gttactaaag ggtgcatgtc ccctgcttga 1799
 aactgaagg gcagggtggtg agccatggcc atggtcccca gctgaggagc aggtgtccct 1859
 gagaacccaa acttcccaga gagtatgtga gaaccaacca atgaaaacag tcccatcgct 1919
 cttaccgggt aagtaaacag tcagaaaatt agcatgaaag cagtttagca ttgggaggaa 1979
 gctcagatct cttagagctgt cttgtccccg ccaggattg acctgtgtaa gtcccaataa 2039
 actcacctac tcatac 2054

<210> 121
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 121
 Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
 1 5 10 15
 Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
 20 25 30
 Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
 35 40 45
 Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
 50 55 60
 Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
 65 70 75 80
 Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
 85 90 95
 Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu
 100 105

<210> 122
 <211> 1546
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (89)..(412)

<400> 122
 actaggcaga gccgtggaac cgccgccagg tcgctgttgg tccacgccgc ccgtcgcgcc 60
 gcccgccgc tcagcgccg ccgccgcc atg gga gtg cag gtg gaa acc atc 112
 Met Gly Val Gln Val Glu Thr Ile
 1 5
 tcc cca gga gac ggg cgc acc ttc ccc aag cgc ggc cag acc tgc gtg 160
 Ser Pro Gly Asp Gly Arg Thr Phe Pro Lys Arg Gly Gln Thr Cys Val
 10 15 20
 gtg cac tac acc ggg atg ctt gaa gat gga aag aaa ttt gat tcc tcc 208
 Val His Tyr Thr Gly Met Leu Glu Asp Gly Lys Lys Phe Asp Ser Ser
 25 30 35 40
 cgg gac aga aac aag ccc ttt aag ttt atg cta ggc aag cag gag gtg 256
 Arg Asp Arg Asn Lys Pro Phe Lys Phe Met Leu Gly Lys Gln Glu Val
 45 50 55
 atc cga ggc tgg gaa gaa ggg gtt gcc cag atg agt gtg ggt cag aga 304
 Ile Arg Gly Trp Glu Glu Gly Val Ala Gln Met Ser Val Gly Gln Arg
 60 65 70
 gcc aaa ctg act ata tct cca gat tat gcc tat ggt gcc act ggg cac 352
 Ala Lys Leu Thr Ile Ser Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His
 75 80 85
 cca ggc atc atc cca cca cat gcc act ctc gtc ttc gat gtg gag ctt 400
 Pro Gly Ile Ile Pro Pro His Ala Thr Leu Val Phe Asp Val Glu Leu
 90 95 100
 cta aaa ctg gaa tgacaggaat ggccctctcc cttagctccc tgttcttggg 452
 Leu Lys Leu Glu
 105
 tctgccatgg agggatctgg tgccctcaga catgtgcaca tgaatccata tggagctttt 512
 cctgatgttc cactccactt tgtatagaca tctgccctga ctgaatgtgt tctgtcactc 572
 agctttgctt ccgacacctc tgtttctctt tcccctttct cctcgatatgt gtgtttacct 632
 aaactatatg ccataaacct caagttactc attttatttt gttttcattt tgggggtgaag 692
 attcagtttc agtcttttgg atataggttt ccaattaagt acatgggtcaa gtattaacag 752
 cacaagtggg aggttaacat tagaatagga attggtgttg gggggggggg ttgcaagaat 812

attttatttt aatttttttg atgaaatttt tatctattat atatttaaaca ttcttgctgc 872
 tgcgctgcaa agccatagca gatttgaggc gctgttgagg actgaattac tctccaagtt 932
 gagagatgtc tttgggttaa attaaaagcc ctacctaaaa ctgaggtggg gatggggaga 992
 gcctttgcct ccaccattcc caccaccct ccccttaaac cctctgcctt tgaaagtaga 1052
 tcatgttcac tgcaatgctg gacactacag gtatctgtcc ctgggccagc agggacctct 1112
 gaagccttct ttgtggcctt tttttttttt tcatcctgtg gtttttctaa tggactttca 1172
 ggaattttgt aatctcataa ctttccaagc tccaccactt cctaaatctt aagaacttta 1232
 attgacagtt tcaattgaag gtgctgtttg tagacttaac acccagtgaag agcccagcca 1292
 tcatgacaaa tccttgaatg ttctcttaag aaaatgatgc tggatcatgc agcttcagca 1352
 tctcctgttt ttgatgctt ggctccctct gctgatctca gtttctggc ttttctccc 1412
 tcagccctt ctcacccctt tgctgtcctg tgtagtgatt tggtgagaaa tcgttgctgc 1472
 acccttcccc cagcaccatt tatgagtctc aagttttatt attgcaataa aagtgcctta 1532
 tgccggcttt tctc 1546

<210> 123
 <211> 679
 <212> PRT
 <213> Homo sapiens

<400> 123
 Met Ala Thr Leu Ile Thr Ser Thr Thr Ala Ala Thr Ala Ala Ser Gly
 1 5 10 15
 Pro Leu Val Asp Tyr Leu Trp Met Leu Ile Leu Gly Phe Ile Ile Ala
 20 25 30
 Phe Val Leu Ala Phe Ser Val Gly Ala Asn Asp Val Ala Asn Ser Phe
 35 40 45
 Gly Thr Ala Val Gly Ser Gly Val Val Thr Leu Lys Gln Ala Cys Ile
 50 55 60
 Leu Ala Ser Ile Phe Glu Thr Val Gly Ser Val Leu Leu Gly Ala Lys
 65 70 75 80
 Val Ser Glu Thr Ile Arg Lys Gly Leu Ile Asp Val Glu Met Tyr Asn
 85 90 95
 Ser Thr Gln Gly Leu Leu Met Ala Gly Ser Val Ser Ala Met Phe Gly
 100 105 110
 Ser Ala Val Trp Gln Leu Val Ala Ser Phe Leu Lys Leu Pro Ile Ser
 115 120 125

Gly	Thr	His	Cys	Ile	Val	Gly	Ala	Thr	Ile	Gly	Phe	Ser	Leu	Val	Ala	
130						135					140					
Lys	Gly	Gln	Glu	Gly	Val	Lys	Trp	Ser	Glu	Leu	Ile	Lys	Ile	Val	Met	
145					150					155					160	
Ser	Trp	Phe	Val	Ser	Pro	Leu	Leu	Ser	Gly	Ile	Met	Ser	Gly	Ile	Leu	
				165					170					175		
Phe	Phe	Leu	Val	Arg	Ala	Phe	Ile	Leu	His	Lys	Ala	Asp	Pro	Val	Pro	
			180					185					190			
Asn	Gly	Leu	Arg	Ala	Leu	Pro	Val	Phe	Tyr	Ala	Cys	Thr	Val	Gly	Ile	
	195						200					205				
Asn	Leu	Phe	Ser	Ile	Met	Tyr	Thr	Gly	Ala	Pro	Leu	Leu	Gly	Phe	Asp	
	210					215					220					
Lys	Leu	Pro	Leu	Trp	Gly	Thr	Ile	Leu	Ile	Ser	Val	Gly	Cys	Ala	Val	
225					230					235					240	
Phe	Cys	Ala	Leu	Ile	Val	Trp	Phe	Phe	Val	Cys	Pro	Arg	Met	Lys	Arg	
			245						250					255		
Lys	Ile	Glu	Arg	Glu	Ile	Lys	Cys	Ser	Pro	Ser	Glu	Ser	Pro	Leu	Met	
			260					265					270			
Glu	Lys	Lys	Asn	Ser	Leu	Lys	Glu	Asp	His	Glu	Glu	Thr	Lys	Leu	Ser	
	275						280					285				
Val	Gly	Asp	Ile	Glu	Asn	Lys	His	Pro	Val	Ser	Glu	Val	Gly	Pro	Ala	
	290					295					300					
Thr	Val	Pro	Leu	Gln	Ala	Val	Val	Glu	Glu	Arg	Thr	Val	Ser	Phe	Lys	
305					310					315					320	
Leu	Gly	Asp	Leu	Glu	Glu	Ala	Pro	Glu	Arg	Glu	Arg	Leu	Pro	Ser	Val	
			325						330					335		
Asp	Leu	Lys	Glu	Glu	Thr	Ser	Ile	Asp	Ser	Thr	Val	Asn	Gly	Ala	Val	
			340					345					350			
Gln	Leu	Pro	Asn	Gly	Asn	Leu	Val	Gln	Phe	Ser	Gln	Ala	Val	Ser	Asn	
	355						360					365				
Gln	Ile	Asn	Ser	Ser	Gly	His	Tyr	Gln	Tyr	His	Thr	Val	His	Lys	Asp	
	370					375					380					
Ser	Gly	Leu	Tyr	Lys	Glu	Leu	Leu	His	Lys	Leu	His	Leu	Ala	Lys	Val	
385					390					395					400	
Gly	Asp	Cys	Met	Gly	Asp	Ser	Gly	Asp	Lys	Pro	Leu	Arg	Arg	Asn	Asn	
			405						410					415		
Ser	Tyr	Thr	Ser	Tyr	Thr	Met	Ala	Ile	Cys	Gly	Met	Pro	Leu	Asp	Ser	
			420					425					430			

Phe Arg Ala Lys Glu Gly Glu Gln Lys Gly Glu Glu Met Glu Lys Leu
435 440 445
Thr Trp Pro Asn Ala Asp Ser Lys Lys Arg Ile Arg Met Asp Ser Tyr
450 455 460
Thr Ser Tyr Cys Asn Ala Val Ser Asp Leu His Ser Ala Ser Glu Ile
465 470 475 480
Asp Met Ser Val Lys Ala Glu Met Gly Leu Gly Asp Arg Lys Gly Ser
485 490 495
Asn Gly Ser Leu Glu Glu Trp Tyr Asp Gln Asp Lys Pro Glu Val Ser
500 505 510
Leu Leu Phe Gln Phe Leu Gln Ile Leu Thr Ala Cys Phe Gly Ser Phe
515 520 525
Ala His Gly Gly Asn Asp Val Ser Asn Ala Ile Gly Pro Leu Val Ala
530 535 540
Leu Tyr Leu Val Tyr Asp Thr Gly Asp Val Ser Ser Lys Val Ala Thr
545 550 555 560
Pro Ile Trp Leu Leu Leu Tyr Gly Gly Val Gly Ile Cys Val Gly Leu
565 570 575
Trp Val Trp Gly Arg Arg Val Ile Gln Thr Met Gly Lys Asp Leu Thr
580 585 590
Pro Ile Thr Pro Ser Ser Gly Phe Ser Ile Glu Leu Ala Ser Ala Leu
595 600 605
Thr Val Val Ile Ala Ser Asn Ile Gly Leu Pro Ile Ser Thr Thr His
610 615 620
Cys Lys Val Gly Ser Val Val Ser Val Gly Trp Leu Arg Ser Lys Lys
625 630 635 640
Ala Val Asp Trp Arg Leu Phe Arg Asn Ile Phe Met Ala Trp Phe Val
645 650 655
Thr Val Pro Ile Ser Gly Val Ile Ser Ala Ala Ile Met Ala Ile Phe
660 665 670
Arg Tyr Val Ile Leu Arg Met
675

<210> 124
<211> 2916
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

<222> (81).. (2117)

<400> 124

tttttgatac ctcataattct gtttacacat cttgaaaggc gctcagtagt tctcttacta 60

aacaaccact actccagaga atg gca acg ctg att acc agt act aca gct gct 113

Met Ala Thr Leu Ile Thr Ser Thr Thr Ala Ala

1

5

10

acc gcc gct tct ggt cct ttg gtg gac tac cta tgg atg ctc atc ctg 161

Thr Ala Ala Ser Gly Pro Leu Val Asp Tyr Leu Trp Met Leu Ile Leu

15

20

25

ggc ttc att att gca ttt gtc ttg gca ttc tcc gtg gga gcc aat gat 209

Gly Phe Ile Ile Ala Phe Val Leu Ala Phe Ser Val Gly Ala Asn Asp

30

35

40

gta gca aat tct ttt ggt aca gct gtg ggc tca ggt gta gtg acc ctg 257

Val Ala Asn Ser Phe Gly Thr Ala Val Gly Ser Gly Val Val Thr Leu

45

50

55

aag caa gcc tgc atc cta gct agc atc ttt gaa aca gtg ggc tct gtc 305

Lys Gln Ala Cys Ile Leu Ala Ser Ile Phe Glu Thr Val Gly Ser Val

60

65

70

75

tta ctg ggg gcc aaa gtg agc gaa acc atc cgg aag ggc ttg att gac 353

Leu Leu Gly Ala Lys Val Ser Glu Thr Ile Arg Lys Gly Leu Ile Asp

80

85

90

gtg gag atg tac aac tcg act caa ggg ctg ctg atg gcc ggc tca gtc 401

Val Glu Met Tyr Asn Ser Thr Gln Gly Leu Leu Met Ala Gly Ser Val

95

100

105

agt gct atg ttt ggt tct gct gtg tgg caa ctc gtg gct tcg ttt ttg 449

Ser Ala Met Phe Gly Ser Ala Val Trp Gln Leu Val Ala Ser Phe Leu

110

115

120

aag ctc cct att tct gga acc cat tgt att gtt ggt gca act att ggt 497

Lys Leu Pro Ile Ser Gly Thr His Cys Ile Val Gly Ala Thr Ile Gly

125

130

135

ttc tcc ctc gtg gca aag ggg cag gag ggt gtc aag tgg tct gaa ctg 545

Phe Ser Leu Val Ala Lys Gly Gln Glu Gly Val Lys Trp Ser Glu Leu

140

145

150

155

ata aaa att gtg atg tct tgg ttc gtg tcc cca ctg ctt tct gga att 593

Ile Lys Ile Val Met Ser Trp Phe Val Ser Pro Leu Leu Ser Gly Ile

160

165

170

atg tct gga att tta ttc ttc ctg gtt cgt gca ttc atc ctc cat aag 641

Met Ser Gly Ile Leu Phe Phe Leu Val Arg Ala Phe Ile Leu His Lys

175

180

185

gca gat cca gtt cct aat ggt ttg cga gct ttg cca gtt ttc tat gcc 689

Ala Asp Pro Val Pro Asn Gly Leu Arg Ala Leu Pro Val Phe Tyr Ala

190

195

200

tgc_aca_gtt_gga_ata_aac_ctc_ttt_tcc_atc_atg_tat_act_gga_gca_ccg	737
Cys Thr Val Gly Ile Asn Leu Phe Ser Ile Met Tyr Thr Gly Ala Pro	
205 210 215	
ttg_ctg_ggc_ttt_gac_aaa_ctt_cct_ctg_tgg_ggt_acc_atc_ctc_atc_tcg	785
Leu Leu Gly Phe Asp Lys Leu Pro Leu Trp Gly Thr Ile Leu Ile Ser	
220 225 230 235	
gtg_gga_tgt_gca_gtt_ttc_tgt_gcc_ctt_atc_gtc_tgg_ttc_ttt_gta_tgt	833
Val Gly Cys Ala Val Phe Cys Ala Leu Ile Val Trp Phe Phe Val Cys	
240 245 250	
ccc_agg_atg_aag_aga_aaa_att_gaa_cga_gaa_ata_aag_tgt_agt_cct_tct	881
Pro Arg Met Lys Arg Lys Ile Glu Arg Glu Ile Lys Cys Ser Pro Ser	
255 260 265	
gaa_agc_ccc_tta_atg_gaa_aaa_aag_aat_agc_ttg_aaa_gaa_gac_cat_gaa	929
Glu Ser Pro Leu Met Glu Lys Lys Asn Ser Leu Lys Glu Asp His Glu	
270 275 280	
gaa_aca_aag_ttg_tct_gtt_ggt_gat_att_gaa_aac_aag_cat_cct_gtt_tct	977
Glu Thr Lys Leu Ser Val Gly Asp Ile Glu Asn Lys His Pro Val Ser	
285 290 295	
gag_gta_ggg_cct_gcc_act_gtg_ccc_ctc_cag_gct_gtg_gtg_gag_gag_aga	1025
Glu Val Gly Pro Ala Thr Val Pro Leu Gln Ala Val Val Glu Glu Arg	
300 305 310 315	
aca_gtc_tca_ttc_aaa_ctt_gga_gat_ttg_gag_gaa_gct_cca_gag_aga_gag	1073
Thr Val Ser Phe Lys Leu Gly Asp Leu Glu Glu Ala Pro Glu Arg Glu	
320 325 330	
agg_ctt_ccc_agc_gtg_gac_ttg_aaa_gag_gaa_acc_agc_ata_gat_agc_acc	1121
Arg Leu Pro Ser Val Asp Leu Lys Glu Glu Thr Ser Ile Asp Ser Thr	
335 340 345	
gtg_aat_ggt_gca_gtg_cag_ttg_cct_aat_ggg_aac_ctt_gtc_cag_ttc_agt	1169
Val Asn Gly Ala Val Gln Leu Pro Asn Gly Asn Leu Val Gln Phe Ser	
350 355 360	
caa_gcc_gtc_agc_aac_caa_ata_aac_tcc_agt_ggc_cac_tac_cag_tat_cac	1217
Gln Ala Val Ser Asn Gln Ile Asn Ser Ser Gly His Tyr Gln Tyr His	
365 370 375	
acc_gtg_cat_aag_gat_tcc_ggc_ctg_tac_aaa_gag_cta_ctc_cat_aaa_tta	1265
Thr Val His Lys Asp Ser Gly Leu Tyr Lys Glu Leu Leu His Lys Leu	
380 385 390 395	
cat_ctt_gcc_aag_gtg_gga_gat_tgc_atg_gga_gac_tcc_ggt_gac_aaa_ccc	1313
His Leu Ala Lys Val Gly Asp Cys Met Gly Asp Ser Gly Asp Lys Pro	
400 405 410	
tta_agg_cgc_aat_aat_agc_tat_act_tcc_tat_acc_atg_gca_ata_tgt_ggc	1361
Leu Arg Arg Asn Asn Ser Tyr Thr Ser Tyr Thr Met Ala Ile Cys Gly	
415 420 425	
atg_cct_ctg_gat_tca_ttc_cgt_gcc_aaa_gaa_ggt_gaa_cag_aag_ggc_gaa	1409

Met	Pro	Leu	Asp	Ser	Phe	Arg	Ala	Lys	Glu	Gly	Glu	Gln	Lys	Gly	Glu	
																430		
																435		
																440		
gaa	atg	gag	aag	ctg	aca	tgg	cct	aat	gca	gac	tcc	aag	aag	cga	att	1457		
Glu	Met	Glu	Lys	Leu	Thr	Trp	Pro	Asn	Ala	Asp	Ser	Lys	Lys	Arg	Ile			
																445		
																450		
																455		
cga	atg	gac	agt	tac	acc	agt	tac	tgc	aat	gct	gtg	tct	gac	ctt	cac	1505		
Arg	Met	Asp	Ser	Tyr	Thr	Ser	Tyr	Cys	Asn	Ala	Val	Ser	Asp	Leu	His			
																460		
																465		
																470		
																475		
tca	gca	tct	gag	ata	gac	atg	agt	gtc	aag	gca	gag	atg	ggg	cta	ggg	1553		
Ser	Ala	Ser	Glu	Ile	Asp	Met	Ser	Val	Lys	Ala	Glu	Met	Gly	Leu	Gly			
																480		
																485		
																490		
gac	aga	aaa	gga	agt	aat	ggc	tct	cta	gaa	gaa	tgg	tat	gac	cag	gat	1601		
Asp	Arg	Lys	Gly	Ser	Asn	Gly	Ser	Leu	Glu	Glu	Trp	Tyr	Asp	Gln	Asp			
																495		
																500		
																505		
aag	cct	gaa	gtc	tct	ctc	ctc	ttc	cag	ttc	ctg	cag	atc	ctt	aca	gcc	1649		
Lys	Pro	Glu	Val	Ser	Leu	Leu	Phe	Gln	Phe	Leu	Gln	Ile	Leu	Thr	Ala			
																510		
																515		
																520		
tgc	ttt	ggg	tca	ttc	gcc	cat	ggg	ggc	aat	gac	gta	agc	aat	gcc	att	1697		
Cys	Phe	Gly	Ser	Phe	Ala	His	Gly	Gly	Asn	Asp	Val	Ser	Asn	Ala	Ile			
																525		
																530		
																535		
ggg	cct	ctg	gtt	gct	tta	tat	ttg	gtt	tat	gac	aca	gga	gat	gtt	tct	1745		
Gly	Pro	Leu	Val	Ala	Leu	Tyr	Leu	Val	Tyr	Asp	Thr	Gly	Asp	Val	Ser			
																540		
																545		
																550		
																555		
tca	aaa	gtg	gca	aca	cca	ata	tgg	ctt	cta	ctc	tat	ggg	ggg	gtt	ggg	1793		
Ser	Lys	Val	Ala	Thr	Pro	Ile	Trp	Leu	Leu	Leu	Tyr	Gly	Gly	Val	Gly			
																560		
																565		
																570		
atc	tgt	gtt	ggg	ctg	tgg	gtt	tgg	gga	aga	aga	gtt	atc	cag	acc	atg	1841		
Ile	Cys	Val	Gly	Leu	Trp	Val	Trp	Gly	Arg	Arg	Val	Ile	Gln	Thr	Met			
																575		
																580		
																585		
ggg	aag	gat	ctg	aca	ccg	atc	aca	ccc	tct	agt	ggc	ttc	agt	att	gaa	1889		
Gly	Lys	Asp	Leu	Thr	Pro	Ile	Thr	Pro	Ser	Ser	Gly	Phe	Ser	Ile	Glu			
																590		
																595		
																600		
ctg	gca	tct	gcc	ctc	act	gtg	gtg	att	gca	tca	aat	att	ggc	ctt	ccc	1937		
Leu	Ala	Ser	Ala	Leu	Thr	Val	Val	Ile	Ala	Ser	Asn	Ile	Gly	Leu	Pro			
																605		
																610		
																615		
atc	agt	aca	aca	cat	tgt	aaa	gtg	ggc	tct	gtt	gtg	tct	gtt	ggc	tgg	1985		
Ile	Ser	Thr	Thr	His	Cys	Lys	Val	Gly	Ser	Val	Val	Ser	Val	Gly	Trp			
																620		
																625		
																630		
																635		
ctc																		

655 660 665
 atc atg gca atc ttc aga tat gtc atc ctc aga atg tgaagctggt 2127
 Ile Met Ala Ile Phe Arg Tyr Val Ile Leu Arg Met
 670 675
 tgagattaaa atttgtgtca atgtttggga ccatcttagg tattcctgct cccctgaaga 2187
 atgattacag tgttaacaga agactgacaa gagtcctttt atttgggagc cagaggaggg 2247
 aagtgttact tgtgctataa ctgcttttgt gctaaatatg aattgtctca aaattagctg 2307
 tgtaaaatag cccgggttcc actggctcct gctgaggtcc cctttccttc tgggctgtga 2367
 attcctgtac atatttctct actttttgta tcaggcttca attccattat gttttaatgt 2427
 tgtctctgaa gatgacttgt gatttttttt tctttttttt aaaccatgaa gagccgtttg 2487
 acagagcatg ctctgcgttg ttggtttcac cagcttctgc cctcacatgc acagggattt 2547
 aacaacaaaa atataactac aacttccctt gtagtctctt atataagtag agtccttggt 2607
 actctgcctt cctgtcagta gtggcaggat ctattggcat attcgggagc ttcttagagg 2667
 gatgaggttc tttgaacaca gtgaaaattt aaattagtaa cttttttgca agcagtttat 2727
 tgactgttat tgctaagaag aagtaagaaa gaaaaagcct gttggcaatc ttggttattt 2787
 ctttaagatt tctggcagtg tgggatggat gaatgaagtg gaatgtgaac tttgggcaag 2847
 ttaaattggga cagccttcca tgttcatttg tctacctctt aactgaataa aaaagcctac 2907
 agtttttag 2916

<210> 125
 <211> 288
 <212> PRT
 <213> Homo sapiens

<400> 125
 Met Glu Arg Pro Gln Pro Asp Ser Met Pro Gln Asp Leu Ser Glu Ala
 1 5 10 15
 Leu Lys Glu Ala Thr Lys Glu Val His Thr Gln Ala Glu Asn Ala Glu
 20 25 30
 Phe Met Arg Asn Phe Gln Lys Gly Gln Val Thr Arg Asp Gly Phe Lys
 35 40 45
 Leu Val Met Ala Ser Leu Tyr His Ile Tyr Val Ala Leu Glu Glu Glu
 50 55 60
 Ile Glu Arg Asn Lys Glu Ser Pro Val Phe Ala Pro Val Tyr Phe Pro
 65 70 75 80
 Glu Glu Leu His Arg Lys Ala Ala Leu Glu Gln Asp Leu Ala Phe Trp

	15	20	25	
gca gag aat gct gag ttc atg agg aac ttt cag aag ggc cag gtg acc				209
Ala Glu Asn Ala Glu Phe Met Arg Asn Phe Gln Lys Gly Gln Val Thr	30	35	40	
cga gac ggc ttc aag ctg gtg atg gcc tcc ctg tac cac atc tat gtg				257
Arg Asp Gly Phe Lys Leu Val Met Ala Ser Leu Tyr His Ile Tyr Val	45	50	55	
gcc ctg gag gag gag att gag cgc aac aag gag agc cca gtc ttc gcc				305
Ala Leu Glu Glu Glu Ile Glu Arg Asn Lys Glu Ser Pro Val Phe Ala	60	65	70	75
cct gtc tac ttc cca gaa gag ctg cac cgc aag gct gcc ctg gag cag				353
Pro Val Tyr Phe Pro Glu Glu Leu His Arg Lys Ala Ala Leu Glu Gln	80	85	90	
gac ctg gcc ttc tgg tac ggg ccc cgc tgg cag gag gtc atc ccc tac				401
Asp Leu Ala Phe Trp Tyr Gly Pro Arg Trp Gln Glu Val Ile Pro Tyr	95	100	105	
aca cca gcc atg cag cgc tat gtg aag cgg ctc cac gag gtg ggg cgc				449
Thr Pro Ala Met Gln Arg Tyr Val Lys Arg Leu His Glu Val Gly Arg	110	115	120	
aca gag ccc gag ctg ctg gtg gcc cac gcc tac acc cgc tac ctg ggt				497
Thr Glu Pro Glu Leu Leu Val Ala His Ala Tyr Thr Arg Tyr Leu Gly	125	130	135	
gac ctg tct ggg ggc cag gtg ctc aaa aag att gcc cag aaa gcc ctg				545
Asp Leu Ser Gly Gly Gln Val Leu Lys Lys Ile Ala Gln Lys Ala Leu	140	145	150	155
gac ctg ccc agc tct ggc gag ggc ctg gcc ttc ttc acc ttc ccc aac				593
Asp Leu Pro Ser Ser Gly Glu Gly Leu Ala Phe Phe Thr Phe Pro Asn	160	165	170	
att gcc agt gcc acc aag ttc aag cag ctc tac cgc tcc cgc atg aac				641
Ile Ala Ser Ala Thr Lys Phe Lys Gln Leu Tyr Arg Ser Arg Met Asn	175	180	185	
tcc ctg gag atg act ccc gca gtc agg cag agg gtg ata gaa gag gcc				689
Ser Leu Glu Met Thr Pro Ala Val Arg Gln Arg Val Ile Glu Glu Ala	190	195	200	
aag act gcg ttc ctg ctc aac atc cag ctc ttt gag gag ttg cag gag				737
Lys Thr Ala Phe Leu Leu Asn Ile Gln Leu Phe Glu Glu Leu Gln Glu	205	210	215	
ctg ctg acc cat gac acc aag gac cag agc ccc tca cgg gca cca ggg				785
Leu Leu Thr His Asp Thr Lys Asp Gln Ser Pro Ser Arg Ala Pro Gly	220	225	230	235
ctt cgc cag cgg gcc agc aac aaa gtg caa gat tct gcc ccc gtg gag				833
Leu Arg Gln Arg Ala Ser Asn Lys Val Gln Asp Ser Ala Pro Val Glu	240	245	250	

act ccc aga ggg aag ccc cca ctc aac acc cgc tcc cag gct ccg ctt 881
 Thr Pro Arg Gly Lys Pro Pro Leu Asn Thr Arg Ser Gln Ala Pro Leu
 255 260 265

ctc cga tgg gtc ctt aca ctc agc ttt ctg gtg gcg aca gtt gct gta 929
 Leu Arg Trp Val Leu Thr Leu Ser Phe Leu Val Ala Thr Val Ala Val
 270 275 280

ggg ctt tat gcc atg tgaatgcagg catgctggct cccagggcca tgaactttgt 984
 Gly Leu Tyr Ala Met
 285

ccggtggaag gcctttctttc tagagagggga attctcttgg ctggcttctt taccgtgggc 1044

actgaaggct ttcagggcct ccagccctct cactgtgtcc ctctctctgg aaaggaggaa 1104

ggagcctatg gcattcttccc caacgaaaag cacatccagg caatggccta aacttcagag 1164

ggggcgaagg ggtcagccct gcccttcagc atcctcagtt cctgcagcag agcctggaag 1224

acacccta at gtggcagctg tctcaaacct ccaaaagccc tgagtttcaa gtatccttgt 1284

tgacacggcc atgaccactt tccccgtggg ccatggcaat ttttacacaa acctgaaaag 1344

atgttgtgtc ttgtgttttt gtcttatttt tgttgagacc actctgttcc tggctcagcc 1404

tcaaatgcag tattttttgtt gtgttctgtt gtttttatag caggggtggg gtgggtttttg 1464

agccatgcgt ggggtggggag ggaggtgttt aacggcactg tggccttggt ctaacttttg 1524

tgtgaaataa taaacaacat tgtctg 1550

<210> 127
 <211> 135
 <212> PRT
 <213> Homo sapiens

<400> 127
 Met Ala Cys Gly Leu Val Ala Ser Asn Leu Asn Leu Lys Pro Gly Glu
 1 5 10 15

Cys Leu Arg Val Arg Gly Glu Val Ala Pro Asp Ala Lys Ser Phe Val
 20 25 30

Leu Asn Leu Gly Lys Asp Ser Asn Asn Leu Cys Leu His Phe Asn Pro
 35 40 45

Arg Phe Asn Ala His Gly Asp Ala Asn Thr Ile Val Cys Asn Ser Lys
 50 55 60

Asp Gly Gly Ala Trp Gly Thr Glu Gln Arg Glu Ala Val Phe Pro Phe
 65 70 75 80

Gln Pro Gly Ser Val Ala Glu Val Cys Ile Thr Phe Asp Gln Ala Asn
 85 90 95

Leu Thr Val Lys Leu Pro Asp Gly Tyr Glu Phe Lys Phe Pro Asn Arg
 100 105 110

Leu Asn Leu Glu Ala Ile Asn Tyr Met Ala Ala Asp Gly Asp Phe Lys
 115 120 125

Ile Lys Cys Val Ala Phe Asp
 130 135

<210> 128
 <211> 507
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (50)..(454)

<400> 128
 cttctgacag ctggtgcgcc tgcccgggaa catcctcctg gactcaatc atg gct tgt 58
 Met Ala Cys
 1

ggt ctg gtc gcc agc aac ctg aat ctc aaa cct gga gag tgc ctt cga 106
 Gly Leu Val Ala Ser Asn Leu Asn Leu Lys Pro Gly Glu Cys Leu Arg
 5 10 15

gtg cga ggc gag gtg gct cct gac gct aag agc ttc gtg ctg aac ctg 154
 Val Arg Gly Glu Val Ala Pro Asp Ala Lys Ser Phe Val Leu Asn Leu
 20 25 30 35

ggc aaa gac agc aac aac ctg tgc ctg cac ttc aac cct cgc ttc aac 202
 Gly Lys Asp Ser Asn Asn Leu Cys Leu His Phe Asn Pro Arg Phe Asn
 40 45 50

gcc cac ggc gac gcc aac acc atc gtg tgc aac agc aag gac ggc ggg 250
 Ala His Gly Asp Ala Asn Thr Ile Val Cys Asn Ser Lys Asp Gly Gly
 55 60 65

gcc tgg ggg acc gag cag cgg gag gct gtc ttt ccc ttc cag cct gga 298
 Ala Trp Gly Thr Glu Gln Arg Glu Ala Val Phe Pro Phe Gln Pro Gly
 70 75 80

agt gtt gca gag gtg tgc atc acc ttc gac cag gcc aac ctg acc gtc 346
 Ser Val Ala Glu Val Cys Ile Thr Phe Asp Gln Ala Asn Leu Thr Val
 85 90 95

aag ctg cca gat gga tac gaa ttc aag ttc ccc aac cgc ctc aac ctg 394
 Lys Leu Pro Asp Gly Tyr Glu Phe Lys Phe Pro Asn Arg Leu Asn Leu
 100 105 110 115

gag gcc atc aac tac atg gca gct gac ggt gac ttc aag atc aaa tgt 442
 Glu Ala Ile Asn Tyr Met Ala Ala Asp Gly Asp Phe Lys Ile Lys Cys
 120 125 130

gtg gcc_ttt_gac tgaaatcagc cagcccatgg cccccaataa aggcagctgc 494
 Val Ala Phe Asp
 135

ctctgctccc ctg 507

<210> 129
 <211> 662
 <212> PRT
 <213> Homo sapiens

<400> 129
 Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile Phe Asn
 1 5 10 15
 Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys Arg Val Asn Asn
 20 25 30
 Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val Cys Asp
 35 40 45
 Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu Ser Lys
 50 55 60
 Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro Gly Ser
 65 70 75 80
 Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro His Tyr
 85 90 95
 Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys Lys Leu
 100 105 110
 Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr Trp Cys
 115 120 125
 His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val Glu Ile
 130 135 140
 Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp Glu Leu
 145 150 155 160
 Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp Gln Pro
 165 170 175
 Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn Tyr Arg
 180 185 190
 Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu Leu Thr
 195 200 205
 Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu Asp Leu
 210 215 220
 Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu Leu Leu
 225 230 235 240

Asp	Lys	Gly	Val	Tyr	Gly	Leu	Leu	Tyr	Tyr	Ala	Gly	His	Gly	Tyr	Glu	245	250	255
Asn	Phe	Gly	Asn	Ser	Phe	Met	Val	Pro	Val	Asp	Ala	Pro	Asn	Pro	Tyr	260	265	270
Arg	Ser	Glu	Asn	Cys	Leu	Cys	Val	Gln	Asn	Ile	Leu	Lys	Leu	Met	Gln	275	280	285
Glu	Lys	Glu	Thr	Gly	Leu	Asn	Val	Phe	Leu	Leu	Asp	Met	Cys	Arg	Lys	290	295	300
Arg	Asn	Asp	Tyr	Asp	Asp	Thr	Ile	Pro	Ile	Leu	Asp	Ala	Leu	Lys	Val	305	310	315
Thr	Ala	Asn	Ile	Val	Phe	Gly	Tyr	Ala	Thr	Cys	Gln	Gly	Ala	Glu	Ala	325	330	335
Phe	Glu	Ile	Gln	His	Ser	Gly	Leu	Ala	Asn	Gly	Ile	Phe	Met	Lys	Phe	340	345	350
Leu	Lys	Asp	Arg	Leu	Leu	Glu	Asp	Lys	Lys	Ile	Thr	Val	Leu	Leu	Asp	355	360	365
Glu	Val	Ala	Glu	Asp	Met	Gly	Lys	Cys	His	Leu	Thr	Lys	Gly	Lys	Gln	370	375	380
Ala	Leu	Glu	Ile	Arg	Ser	Ser	Leu	Ser	Glu	Lys	Arg	Ala	Leu	Thr	Asp	385	390	395
Pro	Ile	Gln	Gly	Thr	Glu	Tyr	Ser	Ala	Glu	Ser	Leu	Val	Arg	Asn	Leu	405	410	415
Gln	Trp	Ala	Lys	Ala	His	Glu	Leu	Pro	Glu	Ser	Met	Cys	Leu	Lys	Phe	420	425	430
Asp	Cys	Gly	Val	Gln	Ile	Gln	Leu	Gly	Phe	Ala	Ala	Glu	Phe	Ser	Asn	435	440	445
Val	Met	Ile	Ile	Tyr	Thr	Ser	Ile	Val	Tyr	Lys	Pro	Pro	Glu	Ile	Ile	450	455	460
Met	Cys	Asp	Ala	Tyr	Val	Thr	Asp	Phe	Pro	Leu	Asp	Leu	Asp	Ile	Asp	465	470	475
Pro	Lys	Asp	Ala	Asn	Lys	Gly	Thr	Pro	Glu	Glu	Thr	Gly	Ser	Tyr	Leu	485	490	495
Val	Ser	Lys	Asp	Leu	Pro	Lys	His	Cys	Leu	Tyr	Thr	Arg	Leu	Ser	Ser	500	505	510
Leu	Gln	Lys	Leu	Lys	Glu	His	Leu	Val	Phe	Thr	Val	Cys	Leu	Ser	Tyr	515	520	525
Gln	Tyr	Ser	Gly	Leu	Glu	Asp	Thr	Val	Glu	Asp	Lys	Gln	Glu	Val	Asn	530	535	540

Val	Gly	Lys	Pro	Leu	Ile	Ala	Lys	Leu	Asp	Met	His	Arg	Gly	Leu	Gly
545					550					555					560
Arg	Lys	Thr	Cys	Phe	Gln	Thr	Cys	Leu	Met	Ser	Asn	Gly	Pro	Tyr	Gln
				565					570					575	
Ser	Ser	Ala	Ala	Thr	Ser	Gly	Gly	Ala	Gly	His	Tyr	His	Ser	Leu	Gln
			580					585					590		
Asp	Pro	Phe	His	Gly	Val	Tyr	His	Ser	His	Pro	Gly	Asn	Pro	Ser	Asn
		595					600					605			
Val	Thr	Pro	Ala	Asp	Ser	Cys	His	Cys	Ser	Arg	Thr	Pro	Asp	Ala	Phe
	610					615					620				
Ile	Ser	Ser	Phe	Ala	His	His	Ala	Ser	Cys	His	Phe	Ser	Arg	Ser	Asn
625					630					635					640
Val	Pro	Val	Glu	Thr	Thr	Asp	Glu	Ile	Pro	Phe	Ser	Phe	Ser	Asp	Arg
				645					650					655	
Leu	Arg	Ile	Ser	Glu	Lys										
			660												

<210> 130
 <211> 2251
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (74)..(2059)

<400> 130
 cttggctgga cagtttgtga aactgtgttg ccgggcaact ggacatcctt ttgttcaata 60

tcagtggttc	aaa	atg	aat	aaa	gag	att	cca	aat	gga	aat	aca	tca	gag		109
	Met	Asn	Lys	Glu	Ile	Pro	Asn	Gly	Asn	Thr	Ser	Glu			
	1				5					10					

ctt	att	ttt	aat	gca	gtg	cat	gta	aaa	gat	gca	ggc	ttt	tat	gtc	tgt	157
Leu	Ile	Phe	Asn	Ala	Val	His	Val	Lys	Asp	Ala	Gly	Phe	Tyr	Val	Cys	
	15					20					25					

cga	gtt	aat	aac	aat	ttc	acc	ttt	gaa	ttc	agc	cag	tgg	tca	cag	ctg	205
Arg	Val	Asn	Asn	Asn	Phe	Thr	Phe	Glu	Phe	Ser	Gln	Trp	Ser	Gln	Leu	
	30				35					40						

gat	gtt	tgc	gac	atc	cca	gag	agc	ttc	cag	aga	agt	gtt	gat	ggc	gtc	253
Asp	Val	Cys	Asp	Ile	Pro	Glu	Ser	Phe	Gln	Arg	Ser	Val	Asp	Gly	Val	
	45			50				55						60		

tct	gaa	tcc	aag	ttg	caa	atc	tgt	gtt	gaa	cca	act	tcc	caa	aag	ctg	301
Ser	Glu	Ser	Lys	Leu	Gln	Ile	Cys	Val	Glu	Pro	Thr	Ser	Gln	Lys	Leu	
				65				70						75		

atg cca ggc agc aca ttg gtt tta cag tgt gtt gct gtt gga agc cct	349
Met Pro Gly Ser Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro	
80 85 90	
att cct cac tac cag tgg ttc aaa aat gaa tta cca tta aca cat gag	397
Ile Pro His Tyr Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu	
95 100 105	
acc aaa aag cta tac atg gtg cct tat gtg gat ttg gaa cac caa gga	445
Thr Lys Lys Leu Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly	
110 115 120	
acc tac tgg tgt cat gta tat aat gat cga gac agt caa gat agc aag	493
Thr Tyr Trp Cys His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys	
125 130 135 140	
aag gta gaa atc atc ata gga aga aca gat gag gca gtg gag tgc act	541
Lys Val Glu Ile Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr	
145 150 155	
gaa gat gaa tta aat aat ctt ggt cat cct gat aat aaa gag caa aca	589
Glu Asp Glu Leu Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr	
160 165 170	
act gac cag cct ttg gcg aag gac aag gtt gcc ctt ttg ata gga aat	637
Thr Asp Gln Pro Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn	
175 180 185	
atg aat tac cgg gag cac ccc aag ctc aaa gct cct ttg gtg gat gtg	685
Met Asn Tyr Arg Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val	
190 195 200	
tac gaa ttg act aac tta ctg aga cag ctg gac ttc aaa gtg gtt tca	733
Tyr Glu Leu Thr Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser	
205 210 215 220	
ctg ttg gat ctt act gaa tat gag atg cgt aat gct gtg gat gag ttt	781
Leu Leu Asp Leu Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe	
225 230 235	
tta ctc ctt tta gac aag gga gta tat ggg tta tta tat tat gca gga	829
Leu Leu Leu Leu Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly	
240 245 250	
cat ggt tat gaa aat ttt ggg aac agc ttc atg gtc ccc gtt gat gct	877
His Gly Tyr Glu Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala	
255 260 265	
cca aat cca tat agg tct gaa aat tgt ctg tgt gta caa aat ata ctg	925
Pro Asn Pro Tyr Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu	
270 275 280	
aaa ttg atg caa gaa aaa gaa act gga ctt aat gtg ttc tta ttg gat	973
Lys Leu Met Gln Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp	
285 290 295 300	

atg tgt-agg aaa aga aat-gac tac gat gat-acc-att cca atc ttg-gat	1021
Met Cys Arg Lys Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp	
305 310 315	
gca cta aaa gtc acc gcc aat att gtg ttt gga tat gcc acg tgt caa	1069
Ala Leu Lys Val Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln	
320 325 330	
gga gca gaa gct ttt gaa atc cag cat tct gga ttg gca aat gga atc	1117
Gly Ala Glu Ala Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile	
335 340 345	
ttt atg aaa ttt tta aaa gac aga tta tta gaa gat aag aaa atc act	1165
Phe Met Lys Phe Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr	
350 355 360	
gtg tta ctg gat gaa gtt gca gaa gat atg ggt aag tgt cac ctt acc	1213
Val Leu Leu Asp Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr	
365 370 375 380	
aaa ggc aaa cag gct cta gag att cga agt agt tta tct gag aag aga	1261
Lys Gly Lys Gln Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg	
385 390 395	
gca ctt act gat cca ata cag gga aca gaa tat tct gct gaa tct ctt	1309
Ala Leu Thr Asp Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu	
400 405 410	
gtg cgg aat cta cag tgg gcc aag gct cat gaa ctt cca gaa agt atg	1357
Val Arg Asn Leu Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met	
415 420 425	
tgt ctt aag ttt gac tgt ggt gtt cag att caa tta gga ttt gca gct	1405
Cys Leu Lys Phe Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala	
430 435 440	
gag ttt tcc aat gtc atg atc atc tat aca agt ata gtt tac aaa cca	1453
Glu Phe Ser Asn Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro	
445 450 455 460	
ccg gag ata ata atg tgt gat gcc tac gtt act gat ttt cca ctt gat	1501
Pro Glu Ile Ile Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp	
465 470 475	
cta gat att gat cca aaa gat gca aat aaa ggc aca cct gaa gaa act	1549
Leu Asp Ile Asp Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr	
480 485 490	
ggc agc tac ttg gta tca aag gat ctt ccc aag cat tgc ctc tat acc	1597
Gly Ser Tyr Leu Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr	
495 500 505	
aga ctc agt tca ctg caa aaa tta aag gaa cat cta gtc ttc aca gta	1645
Arg Leu Ser Ser Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val	
510 515 520	
tgt tta tca tat cag tac tca gga ttg gaa gat act gta gag gac aag	1693

Cys	Leu	Ser	Tyr	Gln	Tyr	Ser	Gly	Leu	Glu	Asp	Thr	Val	Glu	Asp	Lys	
525					530					535					540	
cag	gaa	gtg	aat	gtt	ggg	aaa	cct	ctc	att	gct	aaa	tta	gac	atg	cat	1741
Gln	Glu	Val	Asn	Val	Gly	Lys	Pro	Leu	Ile	Ala	Lys	Leu	Asp	Met	His	
				545					550					555		
cga	ggt	ttg	gga	agg	aag	act	tgc	ttt	caa	act	tgt	ctt	atg	tct	aat	1789
Arg	Gly	Leu	Gly	Arg	Lys	Thr	Cys	Phe	Gln	Thr	Cys	Leu	Met	Ser	Asn	
			560					565					570			
ggt	cct	tac	cag	agt	tct	gca	gcc	acc	tca	gga	gga	gca	ggg	cat	tat	1837
Gly	Pro	Tyr	Gln	Ser	Ser	Ala	Ala	Thr	Ser	Gly	Gly	Ala	Gly	His	Tyr	
		575					580					585				
cac	tca	ttg	caa	gac	cca	ttc	cat	ggt	gtt	tac	cat	tca	cat	cct	ggt	1885
His	Ser	Leu	Gln	Asp	Pro	Phe	His	Gly	Val	Tyr	His	Ser	His	Pro	Gly	
		590				595				600						
aat	cca	agt	aat	gtt	aca	cca	gca	gat	agc	tgt	cat	tgc	agc	cgg	act	1933
Asn	Pro	Ser	Asn	Val	Thr	Pro	Ala	Asp	Ser	Cys	His	Cys	Ser	Arg	Thr	
605					610				615					620		
cca	gat	gca	ttt	att	tca	agt	ttc	gct	cac	cat	gct	tca	tgt	cat	ttt	1981
Pro	Asp	Ala	Phe	Ile	Ser	Ser	Phe	Ala	His	His	Ala	Ser	Cys	His	Phe	
			625					630					635			
agt	aga	agt	aat	gtg	cca	gta	gag	aca	act	gat	gaa	ata	cca	ttt	agt	2029
Ser	Arg	Ser	Asn	Val	Pro	Val	Glu	Thr	Thr	Asp	Glu	Ile	Pro	Phe	Ser	
			640				645					650				
ttc	tct	gac	agg	ctc	aga	att	tct	gaa	aaa	tgacctcctt	gtttttgaaa					2079
Phe	Ser	Asp	Arg	Leu	Arg	Ile	Ser	Glu	Lys							
		655				660										
gtagcataa	tttagatgc	ctgtgaaata	gtactgcact	tacataaagt	gagacattgt											2139
gaaaaggcaa	atttgtatat	gtagagaaag	aatagtagta	actgtttcat	agcaaacttc											2199
aggactttga	gatgttgaaa	ttacattatt	taattacaga	cttctctttt	ct											2251

<210> 131
 <211> 824
 <212> PRT
 <213> Homo sapiens

<400> 131
 Met Ser Leu Leu Gly Asp Pro Leu Gln Ala Leu Pro Pro Ser Ala Ala
 1 5 10 15
 Pro Thr Gly Pro Leu Leu Ala Pro Pro Ala Gly Ala Thr Leu Asn Arg
 20 25 30
 Leu Arg Glu Pro Leu Leu Arg Arg Leu Ser Glu Leu Leu Asp Gln Ala
 35 40 45


```

-----Pro-Glu-Gly-Arg-Gly-Trp-Arg-Arg-Leu-Ala-Glu-Leu-Ala-Gly-Ser-Arg-----
          50                      55                      60

Gly Arg Leu Arg Leu Ser Cys Leu Asp Leu Glu Gln Cys Ser Leu Lys
 65                      70                      75                      80

Val Leu Glu Pro Glu Gly Ser Pro Ser Leu Cys Leu Leu Lys Leu Met
                      85                      90                      95

Gly Glu Lys Gly Cys Thr Val Thr Glu Leu Ser Asp Phe Leu Gln Ala
 100                      105                      110

Met Glu His Thr Glu Val Leu Gln Leu Leu Ser Pro Pro Gly Ile Lys
 115                      120                      125

Ile Thr Val Asn Pro Glu Ser Lys Ala Val Leu Ala Gly Gln Phe Val
 130                      135                      140

Lys Leu Cys Cys Arg Ala Thr Gly His Pro Phe Val Gln Tyr Gln Trp
 145                      150                      155                      160

Phe Lys Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile
                      165                      170                      175

Phe Asn Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys Arg Val
 180                      185                      190

Asn Asn Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val
 195                      200                      205

Cys Asp Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu
 210                      215                      220

Ser Lys Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro
 225                      230                      235                      240

Gly Ser Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro
 245                      250                      255

His Tyr Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys
 260                      265                      270

Lys Leu Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr
 275                      280                      285

Trp Cys His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val
 290                      295                      300

Glu Ile Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp
 305                      310                      315                      320

Glu Leu Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp
 325                      330                      335

Gln Pro Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn
 340                      345                      350

```

~~Tyr Arg Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu~~
355 360 365

Leu Thr Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu
370 375 380

Asp Leu Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu
385 390 395 400

Leu Leu Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly His Gly
405 410 415

Tyr Glu Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala Pro Asn
420 425 430

Pro Tyr Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu Lys Leu
435 440 445

Met Gln Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys
450 455 460

Arg Lys Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu
465 470 475 480

Lys Val Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala
485 490 495

Glu Ala Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met
500 505 510

Lys Phe Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr Val Leu
515 520 525

Leu Asp Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr Lys Gly
530 535 540

Lys Gln Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu
545 550 555 560

Thr Asp Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg
565 570 575

Asn Leu Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu
580 585 590

Lys Phe Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe
595 600 605

Ser Asn Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu
610 615 620

Ile Ile Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp
625 630 635 640

Ile Asp Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser
645 650 655

Tyr Leu Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu
 660 665 670
 Ser Ser Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu
 675 680 685
 Ser Tyr Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu
 690 695 700
 Val Asn Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly
 705 710 715 720
 Leu Gly Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro
 725 730 735
 Tyr Gln Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser
 740 745 750
 Leu Gln Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro
 755 760 765
 Ser Asn Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp
 770 775 780
 Ala Phe Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg
 785 790 795 800
 Ser Asn Val Pro Val Glu Thr Thr Asp Glu Ile Pro Phe Ser Phe Ser
 805 810 815
 Asp Arg Leu Arg Ile Ser Glu Lys
 820

<210> 132
 <211> 2828
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (165)..(2636)

<400> 132
 ggggcgggga gcggaacttcc tcctctgagg gccgtgccgc gctgccagat ttgttcttcc 60
 gcccttgcct ccgcggctcg gaggcgagcg gaaggtgcc cggggccgag gcccgtagcg 120
 gggcgggagg gagccccggc agtcgggggt cgccggcgag ggcc atg tcg ctg ttg 176
 Met Ser Leu Leu
 1
 ggg gac ccg cta cag gcc ctg ccg ccc tcg gcc gcc ccc acg ggg ccg 224
 Gly Asp Pro Leu Gln Ala Leu Pro Pro Ser Ala Ala Pro Thr Gly Pro
 5 10 15 20
 ctg ctc gcc cct ccg gcc ggc gcg acc ctc aac cgc ctg cgg gag ccg 272

Leu	Leu	Ala	Pro	Pro	Ala	Gly	Ala	Thr	Leu	Asn	Arg	Leu	Arg	Glu	Pro				
				25					30					35					
ctg	ctg	cgg	agg	ctc	agc	gag	ctc	ctg	gat	cag	gcg	ccc	gag	ggc	cgg	320			
Leu	Leu	Arg	Arg	Leu	Ser	Glu	Leu	Leu	Asp	Gln	Ala	Pro	Glu	Gly	Arg				
			40					45					50						
ggc	tgg	agg	aga	ctg	gcg	gag	ctg	gcg	ggg	agt	cgc	ggg	cgc	ctc	cgc	368			
Gly	Trp	Arg	Arg	Leu	Ala	Glu	Leu	Ala	Gly	Ser	Arg	Gly	Arg	Leu	Arg				
		55					60					65							
ctc	agt	tgc	cta	gac	ctg	gag	cag	tgt	tct	ctt	aag	gta	ctg	gag	cct	416			
Leu	Ser	Cys	Leu	Asp	Leu	Glu	Gln	Cys	Ser	Leu	Lys	Val	Leu	Glu	Pro				
	70					75					80								
gaa	gga	agc	ccc	agc	ctg	tgt	ctg	ctg	aag	tta	atg	ggg	gaa	aaa	ggg	464			
Glu	Gly	Ser	Pro	Ser	Leu	Cys	Leu	Leu	Lys	Leu	Met	Gly	Glu	Lys	Gly				
	85				90				95						100				
tgc	aca	gtc	aca	gaa	ttg	agt	gat	ttc	ctg	cag	gct	atg	gaa	cac	act	512			
Cys	Thr	Val	Thr	Glu	Leu	Ser	Asp	Phe	Leu	Gln	Ala	Met	Glu	His	Thr				
				105					110					115					
gaa	gtt	ctt	cag	ctt	ctc	agc	ccc	cca	gga	ata	aag	att	act	gta	aac	560			
Glu	Val	Leu	Gln	Leu	Leu	Ser	Pro	Pro	Gly	Ile	Lys	Ile	Thr	Val	Asn				
			120					125					130						
cca	gag	tca	aag	gca	gtc	ttg	gct	gga	cag	ttt	gtg	aaa	ctg	tgt	tgc	608			
Pro	Glu	Ser	Lys	Ala	Val	Leu	Ala	Gly	Gln	Phe	Val	Lys	Leu	Cys	Cys				
		135					140					145							
cgg	gca	act	gga	cat	cct	ttt	gtt	caa	tat	cag	tgg	ttc	aaa	atg	aat	656			
Arg	Ala	Thr	Gly	His	Pro	Phe	Val	Gln	Tyr	Gln	Trp	Phe	Lys	Met	Asn				
	150					155					160								
aaa	gag	att	cca	aat	gga	aat	aca	tca	gag	ctt	att	ttt	aat	gca	gtg	704			
Lys	Glu	Ile	Pro	Asn	Gly	Asn	Thr	Ser	Glu	Leu	Ile	Phe	Asn	Ala	Val				
	165				170				175					180					
cat	gta	aaa	gat	gca	ggc	ttt	tat	gtc	tgt	cga	gtt	aat	aac	aat	ttc	752			
His	Val	Lys	Asp	Ala	Gly	Phe	Tyr	Val	Cys	Arg	Val	Asn	Asn	Asn	Phe				
				185				190						195					
acc	ttt	gaa	ttc	agc	cag	tgg	tca	cag	ctg	gat	gtt	tgc	gac	atc	cca	800			
Thr	Phe	Glu	Phe	Ser	Gln	Trp	Ser	Gln	Leu	Asp	Val	Cys	Asp	Ile	Pro				
			200					205					210						
gag	agc	ttc	cag	aga	agt	gtt	gat	ggc	gtc	tct	gaa	tcc	aag	ttg	caa	848			
Glu	Ser	Phe	Gln	Arg	Ser	Val	Asp	Gly	Val	Ser	Glu	Ser	Lys	Leu	Gln				
		215					220					225							
atc	tgt	gtt	gaa	cca	act	tcc	caa	aag	ctg	atg	cca	ggc	agc	aca	ttg	896			
Ile	Cys	Val	Glu	Pro	Thr	Ser	Gln	Lys	Leu	Met	Pro	Gly	Ser	Thr	Leu				
	230					235					240								
gtt	tta	cag	tgt	gtt	gct	gtt	gga	agc	cct	att	cct	cac	tac	cag	tgg	944			
Val	Leu	Gln	Cys	Val	Ala	Val	Gly	Ser	Pro	Ile	Pro	His	Tyr	Gln	Trp				

245		250		255		260	
ttc aaa aat gaa tta cca tta aca cat gag acc aaa aag cta tac atg	992						
Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys Lys Leu Tyr Met							
		265		270		275	
gtg cct tat gtg gat ttg gaa cac caa gga acc tac tgg tgt cat gta	1040						
Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr Trp Cys His Val							
		280		285		290	
tat aat gat cga gac agt caa gat agc aag aag gta gaa atc atc ata	1088						
Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val Glu Ile Ile Ile							
		295		300		305	
gga aga aca gat gag gca gtg gag tgc act gaa gat gaa tta aat aat	1136						
Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp Glu Leu Asn Asn							
		310		315		320	
ctt ggt cat cct gat aat aaa gag caa aca act gac cag cct ttg gcg	1184						
Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp Gln Pro Leu Ala							
		325		330		335	340
aag gac aag gtt gcc ctt ttg ata gga aat atg aat tac cgg gag cac	1232						
Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn Tyr Arg Glu His							
		345		350		355	
ccc aag ctc aaa gct cct ttg gtg gat gtg tac gaa ttg act aac tta	1280						
Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu Leu Thr Asn Leu							
		360		365		370	
ctg aga cag ctg gac ttc aaa gtg gtt tca ctg ttg gat ctt act gaa	1328						
Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu Asp Leu Thr Glu							
		375		380		385	
tat gag atg cgt aat gct gtg gat gag ttt tta ctc ctt tta gac aag	1376						
Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu Leu Leu Asp Lys							
		390		395		400	
gga gta tat ggg tta tta tat tat gca gga cat ggt tat gaa aat ttt	1424						
Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly His Gly Tyr Glu Asn Phe							
		405		410		415	420
ggg aac agc ttc atg gtc ccc gtt gat gct cca aat cca tat agg tct	1472						
Gly Asn Ser Phe Met Val Pro Val Asp Ala Pro Asn Pro Tyr Arg Ser							
		425		430		435	
gaa aat tgt ctg tgt gta caa aat ata ctg aaa ttg atg caa gaa aaa	1520						
Glu Asn Cys Leu Cys Val Gln Asn Ile Leu Lys Leu Met Gln Glu Lys							
		440		445		450	
gaa act gga ctt aat gtg ttc tta ttg gat atg tgt agg aaa aga aat	1568						
Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys Arg Lys Arg Asn							
		455		460		465	
gac tac gat gat acc att cca atc ttg gat gca cta aaa gtc acc gcc	1616						
Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu Lys Val Thr Ala							
		470		475		480	

aat att gtg ttt gga tat gcc acg tgt caa gga gca gaa gct ttt gaa	1664
Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala Glu Ala Phe Glu	
485 490 495 500	
atc cag cat tct gga ttg gca aat gga atc ttt atg aaa ttt tta aaa	1712
Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met Lys Phe Leu Lys	
505 510 515	
gac aga tta tta gaa gat aag aaa atc act gtg tta ctg gat gaa gtt	1760
Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr Val Leu Leu Asp Glu Val	
520 525 530	
gca gaa gat atg ggt aag tgt cac ctt acc aaa ggc aaa cag gct cta	1808
Ala Glu Asp Met Gly Lys Cys His Leu Thr Lys Gly Lys Gln Ala Leu	
535 540 545	
gag att cga agt agt tta tct gag aag aga gca ctt act gat cca ata	1856
Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu Thr Asp Pro Ile	
550 555 560	
cag gga aca gaa tat tct gct gaa tct ctt gtg cgg aat cta cag tgg	1904
Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg Asn Leu Gln Trp	
565 570 575 580	
gcc aag gct cat gaa ctt cca gaa agt atg tgt ctt aag ttt gac tgt	1952
Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu Lys Phe Asp Cys	
585 590 595	
ggt gtt cag att caa tta gga ttt gca gct gag ttt tcc aat gtc atg	2000
Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe Ser Asn Val Met	
600 605 610	
atc atc tat aca agt ata gtt tac aaa cca ccg gag ata ata atg tgt	2048
Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu Ile Ile Met Cys	
615 620 625	
gat gcc tac gtt act gat ttt cca ctt gat cta gat att gat cca aaa	2096
Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp Ile Asp Pro Lys	
630 635 640	
gat gca aat aaa ggc aca cct gaa gaa act ggc agc tac ttg gta tca	2144
Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser Tyr Leu Val Ser	
645 650 655 660	
aag gat ctt ccc aag cat tgc ctc tat acc aga ctc agt tca ctg caa	2192
Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu Ser Ser Leu Gln	
665 670 675	
aaa tta aag gaa cat cta gtc ttc aca gta tgt tta tca tat cag tac	2240
Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu Ser Tyr Gln Tyr	
680 685 690	
tca gga ttg gaa gat act gta gag gac aag cag gaa gtg aat gtt ggg	2288
Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu Val Asn Val Gly	
695 700 705	

```

aaa cct ctc att gct aaa tta gac atg cat cga-ggt ttg gga-agg aag 2336
Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly Leu Gly Arg Lys
710 715 720

act tgc ttt caa act tgt ctt atg tct aat ggt cct tac cag agt tct 2384
Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro Tyr Gln Ser Ser
725 730 735 740

gca gcc acc tca gga gga gca ggg cat tat cac tca ttg caa gac cca 2432
Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser Leu Gln Asp Pro
745 750 755

ttc cat ggt gtt tac cat tca cat cct ggt aat cca agt aat gtt aca 2480
Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro Ser Asn Val Thr
760 765 770

cca gca gat agc tgt cat tgc agc cgg act cca gat gca ttt att tca 2528
Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp Ala Phe Ile Ser
775 780 785

agt ttc gct cac cat gct tca tgt cat ttt agt aga agt aat gtg cca 2576
Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg Ser Asn Val Pro
790 795 800

gta gag aca act gat gaa ata cca ttt agt ttc tct gac agg ctc aga 2624
Val Glu Thr Thr Asp Glu Ile Pro Phe Ser Phe Ser Asp Arg Leu Arg
805 810 815 820

att tct gaa aaa tgacctcctt gtttttgaaa gtttagcataa ttttagatgc 2676
Ile Ser Glu Lys

ctgtgaaata gtactgcact tacataaagt gagacattgt gaaaaggcaa atttgtatat 2736

gtagagaaag aatagtagta actgtttcat agcaaacttc aggactttga gatgttgaaa 2796

ttacattatt taattacaga cttcctcttt ct 2828

```

```

<210> 133
<211> 919
<212> PRT
<213> Homo sapiens

```

```

<400> 133
Met Lys Val Ala Arg Phe Gln Lys Ile Pro Asn Gly Glu Asn Glu Thr
 1 5 10 15

Met Ile Pro Val Leu Thr Ser Lys Lys Ala Ser Glu Leu Pro Val Ser
20 25 30

Glu Val Ala Ser Ile Leu Gln Ala Asp Leu Gln Asn Gly Leu Asn Lys
35 40 45

Cys Glu Val Ser His Arg Arg Ala Phe His Gly Trp Asn Glu Phe Asp
50 55 60

Ile Ser Glu Asp Glu Pro Leu Trp Lys Lys Tyr Ile Ser Gln Phe Lys

```

65					70					75					80
Asn	Pro	Leu	Ile	Met	Leu	Leu	Leu	Ala	Ser	Ala	Val	Ile	Ser	Val	Leu
				85					90					95	
Met	His	Gln	Phe	Asp	Asp	Ala	Val	Ser	Ile	Thr	Val	Ala	Ile	Leu	Ile
			100					105					110		
Val	Val	Thr	Val	Ala	Phe	Val	Gln	Glu	Tyr	Arg	Ser	Glu	Lys	Ser	Leu
		115					120					125			
Glu	Glu	Leu	Ser	Lys	Leu	Val	Pro	Pro	Glu	Cys	His	Cys	Val	Arg	Glu
	130					135					140				
Gly	Lys	Leu	Glu	His	Thr	Leu	Ala	Arg	Asp	Leu	Val	Pro	Gly	Asp	Thr
145					150					155					160
Val	Cys	Leu	Ser	Val	Gly	Asp	Arg	Val	Pro	Ala	Asp	Leu	Arg	Leu	Phe
				165					170					175	
Glu	Ala	Val	Asp	Leu	Ser	Ile	Asp	Glu	Ser	Ser	Leu	Thr	Gly	Glu	Thr
			180					185					190		
Thr	Pro	Cys	Ser	Lys	Val	Thr	Ala	Pro	Gln	Pro	Ala	Ala	Thr	Asn	Gly
		195					200					205			
Asp	Leu	Ala	Ser	Arg	Ser	Asn	Ile	Ala	Phe	Met	Gly	Thr	Leu	Val	Arg
	210					215					220				
Cys	Gly	Lys	Ala	Lys	Gly	Val	Val	Ile	Gly	Thr	Gly	Glu	Asn	Ser	Glu
225					230					235					240
Phe	Gly	Glu	Val	Phe	Lys	Met	Met	Gln	Ala	Glu	Glu	Ala	Pro	Lys	Thr
				245					250					255	
Pro	Leu	Gln	Lys	Ser	Met	Asp	Leu	Leu	Gly	Lys	Gln	Leu	Ser	Phe	Tyr
			260					265					270		
Ser	Phe	Gly	Ile	Ile	Gly	Ile	Ile	Met	Leu	Val	Gly	Trp	Leu	Leu	Gly
		275					280					285			
Lys	Asp	Ile	Leu	Glu	Met	Phe	Thr	Ile	Ser	Val	Ser	Leu	Ala	Val	Ala
	290					295					300				
Ala	Ile	Pro	Glu	Gly	Leu	Pro	Ile	Val	Val	Thr	Val	Thr	Leu	Ala	Leu
305					310					315					320
Gly	Val	Met	Arg	Met	Val	Lys	Lys	Arg	Ala	Ile	Val	Lys	Lys	Leu	Pro
				325					330					335	
Ile	Val	Glu	Thr	Leu	Gly	Cys	Cys	Asn	Val	Ile	Cys	Ser	Asp	Lys	Thr
			340					345					350		
Gly	Thr	Leu	Thr	Lys	Asn	Glu	Met	Thr	Val	Thr	His	Ile	Phe	Thr	Ser
	355						360					365			
Asp	Gly	Leu	His	Ala	Glu	Val	Thr	Gly	Val	Gly	Tyr	Asn	Gln	Phe	Gly

370 375 380
 Glu Val Ile Val Asp Gly Asp Val Val His Gly Phe Tyr Asn Pro Ala
 385 390 395 400
 Val Ser Arg Ile Val Glu Ala Gly Cys Val Cys Asn Asp Ala Val Ile
 405 410 415
 Arg Asn Asn Thr Leu Met Gly Lys Pro Thr Glu Gly Ala Leu Ile Ala
 420 425 430
 Leu Ala Met Lys Met Gly Leu Asp Gly Leu Gln Gln Asp Tyr Ile Arg
 435 440 445
 Lys Ala Glu Tyr Pro Phe Ser Ser Glu Gln Lys Trp Met Ala Val Lys
 450 455 460
 Cys Val His Arg Thr Gln Gln Asp Arg Pro Glu Ile Cys Phe Met Lys
 465 470 475 480
 Gly Ala Tyr Glu Gln Val Ile Lys Tyr Cys Thr Thr Tyr Gln Ser Lys
 485 490 495
 Gly Gln Thr Leu Thr Leu Thr Gln Gln Gln Arg Asp Val Tyr Gln Gln
 500 505 510
 Glu Lys Ala Arg Met Gly Ser Ala Gly Leu Arg Val Leu Ala Leu Ala
 515 520 525
 Ser Gly Pro Glu Leu Gly Gln Leu Thr Phe Leu Gly Leu Val Gly Ile
 530 535 540
 Ile Asp Pro Pro Arg Thr Gly Val Lys Glu Ala Val Thr Thr Leu Ile
 545 550 555 560
 Ala Ser Gly Val Ser Ile Lys Met Ile Thr Gly Asp Ser Gln Glu Thr
 565 570 575
 Ala Val Ala Ile Ala Ser Arg Leu Gly Leu Tyr Ser Lys Thr Ser Gln
 580 585 590
 Ser Val Ser Gly Glu Glu Ile Asp Ala Met Asp Val Gln Gln Leu Ser
 595 600 605
 Gln Ile Val Pro Lys Val Ala Val Phe Tyr Arg Ala Ser Pro Arg His
 610 615 620
 Lys Met Lys Ile Ile Lys Ser Leu Gln Lys Asn Gly Ser Val Val Ala
 625 630 635 640
 Met Thr Gly Asp Gly Val Asn Asp Ala Val Ala Leu Lys Ala Ala Asp
 645 650 655
 Ile Gly Val Ala Met Gly Gln Thr Gly Thr Asp Val Cys Lys Glu Ala
 660 665 670
 Ala Asp Met Ile Leu Val Asp Asp Asp Phe Gln Thr Ile Met Ser Ala

```

-- 675 -- 680 -- 685 --
Ile Glu Glu Gly Lys Gly Ile Tyr Asn Asn Ile Lys Asn Phe Val Arg
690 695 700
Phe Gln Leu Ser Thr Ser Ile Ala Ala Leu Thr Leu Ile Ser Leu Ala
705 710 715 720
Thr Leu Met Asn Phe Pro Asn Pro Leu Asn Ala Met Gln Ile Leu Trp
725 730 735
Ile Asn Ile Ile Met Asp Gly Pro Pro Ala Gln Ser Leu Gly Val Glu
740 745 750
Pro Val Asp Lys Asp Val Ile Arg Lys Pro Pro Arg Asn Trp Lys Asp
755 760 765
Ser Ile Leu Thr Lys Asn Leu Ile Leu Lys Ile Leu Val Ser Ser Ile
770 775 780
Ile Ile Val Cys Gly Thr Leu Phe Val Phe Trp Arg Glu Leu Arg Asp
785 790 795 800
Asn Val Ile Thr Pro Arg Asp Thr Thr Met Thr Phe Thr Cys Phe Val
805 810 815
Phe Phe Asp Met Phe Asn Ala Leu Ser Ser Arg Ser Gln Thr Lys Ser
820 825 830
Val Phe Glu Ile Gly Leu Cys Ser Asn Arg Met Phe Cys Tyr Ala Val
835 840 845
Leu Gly Ser Ile Met Gly Gln Leu Leu Val Ile Tyr Phe Pro Pro Leu
850 855 860
Gln Lys Val Phe Gln Thr Glu Ser Leu Ser Ile Leu Asp Leu Leu Phe
865 870 875 880
Leu Leu Gly Leu Thr Ser Ser Val Cys Ile Val Ala Glu Ile Ile Lys
885 890 895
Lys Val Glu Arg Ser Arg Glu Lys Ile Gln Lys His Val Ser Ser Thr
900 905 910
Ser Ser Ser Phe Leu Glu Val
915

```

```

<210> 134
<211> 3612
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (427)..(3183)

```

```

<400> 134
acggcctcgc ggagccggcc cggcggaccg tgacgggtcc cctcacctcc tcttctctcc 60
cctccccgcc cgccctctct cctcccttc ctcctcccg ctcgtttctt ctcacgccgg 120
gagcaggctc ccgcctcgca ccgctgcccc gcgagcagct cctcttctcc cgaggcgcg 180
ggggcgcccc cgcgagcccc gcggctgaga ccccgagcc tggaggaggg ctgtccgggg 240
ctttggatgc tgctgctagg ggtggtggga gcagcgtgg gacgctggc cgggagcggg 300
ggtgacagcc tgggattccg ggggcttctc ttccttgtcc tctcctctc ctctctattc 360
ccagtgtggc cgtggctgac actaaagact ttgtagccat caacccgagt gcagtttcga 420

tggaaa atg aag gtt gca cgt ttt caa aaa ata cct aat ggt gaa aat 468
Met Lys Val Ala Arg Phe Gln Lys Ile Pro Asn Gly Glu Asn
1 5 10

gag aca atg att cct gta ttg aca tca aaa aaa gca agt gaa tta cca 516
Glu Thr Met Ile Pro Val Leu Thr Ser Lys Lys Ala Ser Glu Leu Pro
15 20 25 30

gtc agt gaa gtt gca agc att ctc caa gct gat ctt cag aat ggt cta 564
Val Ser Glu Val Ala Ser Ile Leu Gln Ala Asp Leu Gln Asn Gly Leu
35 40 45

aac aaa tgt gaa gtt agt cat agg cga gcc ttt cat ggc tgg aat gag 612
Asn Lys Cys Glu Val Ser His Arg Arg Ala Phe His Gly Trp Asn Glu
50 55 60

ttt gat att agt gaa gat gag cca ctg tgg aag aag tat att tct cag 660
Phe Asp Ile Ser Glu Asp Glu Pro Leu Trp Lys Lys Tyr Ile Ser Gln
65 70 75

ttt aaa aat ccc ctt att atg ctg ctt ctg gct tct gca gtc atc agt 708
Phe Lys Asn Pro Leu Ile Met Leu Leu Leu Ala Ser Ala Val Ile Ser
80 85 90

gtt tta atg cat cag ttt gat gat gcc gtc agt atc act gtg gca ata 756
Val Leu Met His Gln Phe Asp Asp Ala Val Ser Ile Thr Val Ala Ile
95 100 105 110

ctt atc gtt gtt aca gtt gcc ttt gtt cag gaa tat cgt tca gaa aaa 804
Leu Ile Val Val Thr Val Ala Phe Val Gln Glu Tyr Arg Ser Glu Lys
115 120 125

tct ctt gaa gaa ttg agt aaa ctt gtg cca cca gaa tgc cat tgt gtg 852
Ser Leu Glu Glu Leu Ser Lys Leu Val Pro Pro Glu Cys His Cys Val
130 135 140

cgt gaa gga aaa ttg gag cat aca ctt gcc cga gac ttg gtt cca ggt 900
Arg Glu Gly Lys Leu Glu His Thr Leu Ala Arg Asp Leu Val Pro Gly
145 150 155

gat aca gtt tgc ctt tct gtt ggg gat aga gtt cct gct gac tta cgc 948
Asp Thr Val Cys Leu Ser Val Gly Asp Arg Val Pro Ala Asp Leu Arg

```

160	165	170	
ttg ttt gag gct gtg gat ctt tcc att gat gag tcc agc ttg aca ggt	996		
Leu Phe Glu Ala Val Asp Leu Ser Ile Asp Glu Ser Ser Leu Thr Gly			
175	180	185	190
gag aca acg cct tgt tct aag gtg aca gct cct cag cca gct gca act	1044		
Glu Thr Thr Pro Cys Ser Lys Val Thr Ala Pro Gln Pro Ala Ala Thr			
	195	200	205
aat gga gat ctt gca tcg aga agt aac att gcc ttt atg gga aca ctg	1092		
Asn Gly Asp Leu Ala Ser Arg Ser Asn Ile Ala Phe Met Gly Thr Leu			
	210	215	220
gtc aga tgt ggc aaa gca aag ggt gtt gtc att gga aca gga gaa aat	1140		
Val Arg Cys Gly Lys Ala Lys Gly Val Val Ile Gly Thr Gly Glu Asn			
	225	230	235
tct gaa ttt ggg gag gtt ttt aaa atg atg caa gca gaa gag gca cca	1188		
Ser Glu Phe Gly Glu Val Phe Lys Met Met Gln Ala Glu Glu Ala Pro			
	240	245	250
aaa acc cct ctg cag aag agc atg gac ctc tta gga aaa caa ctt tcc	1236		
Lys Thr Pro Leu Gln Lys Ser Met Asp Leu Leu Gly Lys Gln Leu Ser			
	255	260	265
ttt tac tcc ttt ggt ata ata gga atc atc atg ttg gtt ggc tgg tta	1284		
Phe Tyr Ser Phe Gly Ile Ile Gly Ile Ile Met Leu Val Gly Trp Leu			
	275	280	285
ctg gga aaa gat atc ctg gaa atg ttt act att agt gta agt ttg gct	1332		
Leu Gly Lys Asp Ile Leu Glu Met Phe Thr Ile Ser Val Ser Leu Ala			
	290	295	300
gta gca gca att cct gaa ggt ctc ccc att gtg gtc aca gtg acg cta	1380		
Val Ala Ala Ile Pro Glu Gly Leu Pro Ile Val Val Thr Val Thr Leu			
	305	310	315
gct ctt ggt gtt atg aga atg gtg aag aaa agg gcc att gtg aaa aag	1428		
Ala Leu Gly Val Met Arg Met Val Lys Lys Arg Ala Ile Val Lys Lys			
	320	325	330
ctg cct att gtt gaa act ctg ggc tgc tgt aat gtg att tgt tca gat	1476		
Leu Pro Ile Val Glu Thr Leu Gly Cys Cys Asn Val Ile Cys Ser Asp			
	335	340	345
aaa act gga aca ctg acg aag aat gaa atg act gtt act cac ata ttt	1524		
Lys Thr Gly Thr Leu Thr Lys Asn Glu Met Thr Val Thr His Ile Phe			
	355	360	365
act tca gat ggt ctg cat gct gag gtt act gga gtt ggc tat aat caa	1572		
Thr Ser Asp Gly Leu His Ala Glu Val Thr Gly Val Gly Tyr Asn Gln			
	370	375	380
ttt ggg gaa gtg att gtt gat ggt gat gtt gtt cat gga ttc tat aac	1620		
Phe Gly Glu Val Ile Val Asp Gly Asp Val Val His Gly Phe Tyr Asn			
	385	390	395

cca gct gtt agc aga att gtt gag gcg ggc tgt gtg tgc aat gat gct	1668
Pro Ala Val Ser Arg Ile Val Glu Ala Gly Cys Val Cys Asn Asp Ala	
400 405 410	
gta att aga aac aat act cta atg ggg aag cca aca gaa ggg gcc tta	1716
Val Ile Arg Asn Asn Thr Leu Met Gly Lys Pro Thr Glu Gly Ala Leu	
415 420 425 430	
att gct ctt gca atg aag atg ggt ctt gat gga ctt caa caa gac tac	1764
Ile Ala Leu Ala Met Lys Met Gly Leu Asp Gly Leu Gln Gln Asp Tyr	
435 440 445	
atc aga aaa gct gaa tac cct ttt agc tct gag caa aag tgg atg gct	1812
Ile Arg Lys Ala Glu Tyr Pro Phe Ser Ser Glu Gln Lys Trp Met Ala	
450 455 460	
gtt aag tgt gta cac cga aca cag cag gac aga cca gag att tgt ttt	1860
Val Lys Cys Val His Arg Thr Gln Gln Asp Arg Pro Glu Ile Cys Phe	
465 470 475	
atg aaa ggt gct tac gaa caa gta att aag tac tgt act aca tac cag	1908
Met Lys Gly Ala Tyr Glu Gln Val Ile Lys Tyr Cys Thr Thr Tyr Gln	
480 485 490	
agc aaa ggg cag acc ttg aca ctt act cag cag cag aga gat gtg tac	1956
Ser Lys Gly Gln Thr Leu Thr Leu Thr Gln Gln Gln Arg Asp Val Tyr	
495 500 505 510	
caa caa gag aag gca cgc atg ggc tca gcg gga ctc aga gtt ctt gct	2004
Gln Gln Glu Lys Ala Arg Met Gly Ser Ala Gly Leu Arg Val Leu Ala	
515 520 525	
ttg gct tct ggt cct gaa ctg gga cag ctg aca ttt ctt ggc ttg gtg	2052
Leu Ala Ser Gly Pro Glu Leu Gly Gln Leu Thr Phe Leu Gly Leu Val	
530 535 540	
gga atc att gat cca cct aga act ggt gtg aaa gaa gct gtt aca aca	2100
Gly Ile Ile Asp Pro Pro Arg Thr Gly Val Lys Glu Ala Val Thr Thr	
545 550 555	
ctc att gcc tca gga gta tca ata aaa atg att act gga gat tca cag	2148
Leu Ile Ala Ser Gly Val Ser Ile Lys Met Ile Thr Gly Asp Ser Gln	
560 565 570	
gag act gca gtt gca atc gcc agt cgt ctg gga ttg tat tcc aaa act	2196
Glu Thr Ala Val Ala Ile Ala Ser Arg Leu Gly Leu Tyr Ser Lys Thr	
575 580 585 590	
tcc cag tca gtc tca gga gaa gaa ata gat gca atg gat gtt cag cag	2244
Ser Gln Ser Val Ser Gly Glu Glu Ile Asp Ala Met Asp Val Gln Gln	
595 600 605	
ctt tca caa ata gta cca aag gtt gca gta ttt tac aga gct agc cca	2292
Leu Ser Gln Ile Val Pro Lys Val Ala Val Phe Tyr Arg Ala Ser Pro	
610 615 620	

agg_cac_aag_atg_aaa_att_att_aag_tcg_cta_cag_aag_aac_ggt_tca_gtt	2340
Arg His Lys Met Lys Ile Ile Lys Ser Leu Gln Lys Asn Gly Ser Val	
625 630 635	
gta_gcc_atg_aca_gga_gat_gga_gta_aat_gat_gca_gtt_gct_ctg_aag_gct	2388
Val Ala Met Thr Gly Asp Gly Val Asn Asp Ala Val Ala Leu Lys Ala	
640 645 650	
gca_gac_att_gga_gtt_gcg_atg_ggc_cag_act_ggt_aca_gat_gtt_tgc_aaa	2436
Ala Asp Ile Gly Val Ala Met Gly Gln Thr Gly Thr Asp Val Cys Lys	
655 660 665 670	
gag_gca_gca_gac_atg_atc_cta_gtg_gat_gat_gat_ttt_caa_acc_ata_atg	2484
Glu Ala Ala Asp Met Ile Leu Val Asp Asp Asp Phe Gln Thr Ile Met	
675 680 685	
tct_gca_atc_gaa_gag_ggt_aaa_ggg_att_tat_aat_aac_att_aaa_aat_ttc	2532
Ser Ala Ile Glu Glu Gly Lys Gly Ile Tyr Asn Asn Ile Lys Asn Phe	
690 695 700	
gtt_aga_ttc_cag_ctg_agc_acg_agt_ata_gca_gca_tta_act_tta_atc_tca	2580
Val Arg Phe Gln Leu Ser Thr Ser Ile Ala Ala Leu Thr Leu Ile Ser	
705 710 715	
ttg_gct_aca_tta_atg_aac_ttt_cct_aat_cct_ctc_aat_gcc_atg_cag_att	2628
Leu Ala Thr Leu Met Asn Phe Pro Asn Pro Leu Asn Ala Met Gln Ile	
720 725 730	
ttg_tgg_atc_aat_att_att_atg_gat_gga_ccc_cca_gct_cag_agc_ctt_gga	2676
Leu Trp Ile Asn Ile Ile Met Asp Gly Pro Pro Ala Gln Ser Leu Gly	
735 740 745 750	
gta_gaa_cca_gtg_gat_aaa_gat_gtc_att_cgt_aaa_cct_cct_cgc_aac_tgg	2724
Val Glu Pro Val Asp Lys Asp Val Ile Arg Lys Pro Pro Arg Asn Trp	
755 760 765	
aaa_gac_agc_att_ttg_act_aaa_aac_ttg_ata_ctt_aaa_ata_ctt_gtt_tca	2772
Lys Asp Ser Ile Leu Thr Lys Asn Leu Ile Leu Lys Ile Leu Val Ser	
770 775 780	
tca_ata_atc_att_gtt_tgt_ggg_act_ttg_ttt_gtc_ttc_tgg_cgt_gag_cta	2820
Ser Ile Ile Ile Val Cys Gly Thr Leu Phe Val Phe Trp Arg Glu Leu	
785 790 795	
cga_gac_aat_gtg_att_aca_cct_cga_gac_aca_aca_atg_acc_ttc_aca_tgc	2868
Arg Asp Asn Val Ile Thr Pro Arg Asp Thr Thr Met Thr Phe Thr Cys	
800 805 810	
ttt_gtg_ttt_ttt_gac_atg_ttc_aat_gca_cta_agt_tcc_aga_tcc_cag_acc	2916
Phe Val Phe Phe Asp Met Phe Asn Ala Leu Ser Ser Arg Ser Gln Thr	
815 820 825 830	
aag_tct_gtg_ttt_gag_att_gga_ctc_tgc_agt_aat_aga_atg_ttt_tgc_tat	2964
Lys Ser Val Phe Glu Ile Gly Leu Cys Ser Asn Arg Met Phe Cys Tyr	
835 840 845	
gca_gtt_ctt_gga_tcc_atc_atg_gga_caa_tta_cta_gtt_att_tac_ttt_cct	3012

Ala Val Leu Gly Ser Ile Met Gly Gln Leu Leu Val Ile Tyr Phe Pro	850	855	860	
ccg ctt cag aag gtt ttt cag act gag agc cta agc ata ctg gat ctg				3060
Pro Leu Gln Lys Val Phe Gln Thr Glu Ser Leu Ser Ile Leu Asp Leu	865	870	875	
ttg ttt ctt ttg ggt ctc acc tca tca gtg tgc ata gtg gca gaa att				3108
Leu Phe Leu Leu Gly Leu Thr Ser Ser Val Cys Ile Val Ala Glu Ile	880	885	890	
ata aag aag gtt gaa agg agc agg gaa aag atc cag aag cat gtt agt				3156
Ile Lys Lys Val Glu Arg Ser Arg Glu Lys Ile Gln Lys His Val Ser	895	900	905	910
tcg aca tca tca tct ttt ctt gaa gta tgatgcatat tgcattattt				3203
Ser Thr Ser Ser Ser Phe Leu Glu Val	915			

tatttgcaaa ctaggaattg cagtctgagg atcatttaga agggcaagtt caagaggata 3263

tgaagatttg agaacttttt aactattcat tgactaaaaa tgaacattaa tgtaaagac 3323

ttaagacttt aacctgctgg cagtcccaaa tgaaattatg caactttgat atcatattcc 3383

ttgatttaaa ttggcttttg tgattgagtg aaactttata aagcatatgg tcagttattt 3443

aattaaaaag gcaaaacctg aaccaccttc tgcacttaaa gaagtctaac agtacaaata 3503

cactatctat cttagataga tatatttttt tttattttta aatattgtac tatttatggg 3563

gggtggggcctt tcttactaat acacaaataa atttaatcat ttcaaaggc 3612

<210> 135
 <211> 382
 <212> PRT
 <213> Homo sapiens

<400> 135

Met Gly Ala Phe Leu Asp Lys Pro Lys Met Glu Lys His Asn Ala Gln	1	5	10	15
Gly Gln Gly Asn Gly Leu Arg Tyr Gly Leu Ser Ser Met Gln Gly Trp	20	25	30	
Arg Val Glu Met Glu Asp Ala His Thr Ala Val Ile Gly Leu Pro Ser	35	40	45	
Gly Leu Glu Ser Trp Ser Phe Phe Ala Val Tyr Asp Gly His Ala Gly	50	55	60	
Ser Gln Val Ala Lys Tyr Cys Cys Glu His Leu Leu Asp His Ile Thr	65	70	75	80
Asn Asn Gln Asp Phe Lys Gly Ser Ala Gly Ala Pro Ser Val Glu Asn	85	90	95	

Val	Lys	Asn	Gly	Ile	Arg	Thr	Gly	Phe	Leu	Glu	Ile	Asp	Glu	His	Met	
			100					105					110			
Arg	Val	Met	Ser	Glu	Lys	Lys	His	Gly	Ala	Asp	Arg	Ser	Gly	Ser	Thr	
		115					120					125				
Ala	Val	Gly	Val	Leu	Ile	Ser	Pro	Gln	His	Thr	Tyr	Phe	Ile	Asn	Cys	
		130				135					140					
Gly	Asp	Ser	Arg	Gly	Leu	Leu	Cys	Arg	Asn	Arg	Lys	Val	His	Phe	Phe	
145					150					155					160	
Thr	Gln	Asp	His	Lys	Pro	Ser	Asn	Pro	Leu	Glu	Lys	Glu	Arg	Ile	Gln	
				165					170					175		
Asn	Ala	Gly	Gly	Ser	Val	Met	Ile	Gln	Arg	Val	Asn	Gly	Ser	Leu	Ala	
			180					185					190			
Val	Ser	Arg	Ala	Leu	Gly	Asp	Phe	Asp	Tyr	Lys	Cys	Val	His	Gly	Lys	
		195					200					205				
Gly	Pro	Thr	Glu	Gln	Leu	Val	Ser	Pro	Glu	Pro	Glu	Val	His	Asp	Ile	
	210					215					220					
Glu	Arg	Ser	Glu	Glu	Asp	Asp	Gln	Phe	Ile	Ile	Leu	Ala	Cys	Asp	Gly	
225					230					235					240	
Ile	Trp	Asp	Val	Met	Gly	Asn	Glu	Glu	Leu	Cys	Asp	Phe	Val	Arg	Ser	
				245					250					255		
Arg	Leu	Glu	Val	Thr	Asp	Asp	Leu	Glu	Lys	Val	Cys	Asn	Glu	Val	Val	
			260					265					270			
Asp	Thr	Cys	Leu	Tyr	Lys	Gly	Ser	Arg	Asp	Asn	Met	Ser	Val	Ile	Leu	
		275					280					285				
Ile	Cys	Phe	Pro	Asn	Ala	Pro	Lys	Val	Ser	Pro	Glu	Ala	Val	Lys	Lys	
	290					295					300					
Glu	Ala	Glu	Leu	Asp	Lys	Tyr	Leu	Glu	Cys	Arg	Val	Glu	Glu	Ile	Ile	
305					310					315					320	
Lys	Lys	Gln	Gly	Glu	Gly	Val	Pro	Asp	Leu	Val	His	Val	Met	Arg	Thr	
				325					330					335		
Leu	Ala	Ser	Glu	Asn	Ile	Pro	Ser	Leu	Pro	Pro	Gly	Gly	Glu	Leu	Ala	
			340					345					350			
Ser	Lys	Arg	Asn	Val	Ile	Glu	Ala	Val	Tyr	Asn	Arg	Leu	Asn	Pro	Tyr	
		355					360					365				
Lys	Asn	Asp	Asp	Thr	Asp	Ser	Thr	Ser	Thr	Asp	Asp	Met	Trp			
	370					375						380				

<210> 136

125	130	135	
act tat ttc att aac tgt gga gac tca aga ggt tta ctt tgt agg aac Thr Tyr Phe Ile Asn Cys Gly Asp Ser Arg Gly Leu Leu Cys Arg Asn 140 145 150			905
agg aaa gtt cat ttc ttc aca caa gat cac aaa cca agt aat ccg ctg Arg Lys Val His Phe Phe Thr Gln Asp His Lys Pro Ser Asn Pro Leu 155 160 165 170			953
gag aaa gaa cga att cag aat gca ggt ggc tct gta atg att cag cgt Glu Lys Glu Arg Ile Gln Asn Ala Gly Gly Ser Val Met Ile Gln Arg 175 180 185			1001
gtg aat ggc tct ctg gct gta tcg agg gcc ctt ggg gat ttt gat tac Val Asn Gly Ser Leu Ala Val Ser Arg Ala Leu Gly Asp Phe Asp Tyr 190 195 200			1049
aaa tgt gtc cat gga aaa ggt cct act gag cag ctt gtc tca cca gag Lys Cys Val His Gly Lys Gly Pro Thr Glu Gln Leu Val Ser Pro Glu 205 210 215			1097
cct gaa gtc cat gat att gaa aga tct gaa gaa gat gat cag ttc att Pro Glu Val His Asp Ile Glu Arg Ser Glu Glu Asp Asp Gln Phe Ile 220 225 230			1145
atc ctt gca tgt gat ggt atc tgg gat gtt atg gga aat gaa gag ctc Ile Leu Ala Cys Asp Gly Ile Trp Asp Val Met Gly Asn Glu Glu Leu 235 240 245 250			1193
tgt gat ttt gta aga tcc aga ctt gaa gtc act gat gac ctt gag aaa Cys Asp Phe Val Arg Ser Arg Leu Glu Val Thr Asp Asp Leu Glu Lys 255 260 265			1241
gtt tgc aat gaa gta gtc gac acc tgt ttg tat aag gga agt cga gac Val Cys Asn Glu Val Val Asp Thr Cys Leu Tyr Lys Gly Ser Arg Asp 270 275 280			1289
aac atg agt gtg att ttg atc tgt ttt cca aat gca ccc aaa gta tcg Asn Met Ser Val Ile Leu Ile Cys Phe Pro Asn Ala Pro Lys Val Ser 285 290 295			1337
cca gaa gca gtg aag aag gag gca gag ttg gac aag tac ctg gaa tgc Pro Glu Ala Val Lys Lys Glu Ala Glu Leu Asp Lys Tyr Leu Glu Cys 300 305 310			1385
aga gta gaa gaa atc ata aag aag cag ggg gaa ggc gtc ccc gac tta Arg Val Glu Glu Ile Ile Lys Lys Gln Gly Glu Gly Val Pro Asp Leu 315 320 325 330			1433
gtc cat gtg atg cgc aca tta gcg agt gag aac atc ccc agc ctc cca Val His Val Met Arg Thr Leu Ala Ser Glu Asn Ile Pro Ser Leu Pro 335 340 345			1481
cca ggg ggt gaa ttg gca agc aag agg aat gtt att gaa gcc gtt tac Pro Gly Gly Glu Leu Ala Ser Lys Arg Asn Val Ile Glu Ala Val Tyr 350 355 360			1529

aat aga ctg aat cct tac aaa aat gac gac act gac tct aca tca aca 1577
 Asn Arg Leu Asn Pro Tyr Lys Asn Asp Asp Thr Asp Ser Thr Ser Thr
 365 370 375

gat gat atg tgg taaaactgct catctagcca tggagtttac cttcacctcc 1629
 Asp Asp Met Trp
 380

aaaggagagt acagctcaac tttgttgaaa cttttaacat ccatcctcaa ctttaaggaa 1689
 ggggatatga catgggtgag aatgattaca tcagagaact tcagcagtac aacagctagc 1749
 ccagaactga tttttttttt ttttttgtaa atttgagact tatgtaagcg tgatttcaaa 1809
 ccataattcg tgttgtaa at cagactccag caatttttgt tgtatgattt tgtttttttg 1869
 taaagtgtaa ttgtccttgt acaaaatgct catattta at tatgaactgc tttaaatcac 1929
 tatcaaagtt acaagaaatg tttggcttat tgtgtgatgc aacagatata tagccctttc 1989
 aagtcatggt gtgtttggac ttgggggttg aacagggaga gcagcagcca tgtcagctac 2049
 acgctcaa at gtgcagatga ttatggaaaa taacctcaaa atcttacaaa gctgaacatc 2109
 caaggagtta ttgaaaacta tcttaaatgt tcttggtagg ggagttggca ttgttgataa 2169
 agccagtccc ttcatttaac tgtctttcag gatgttccct cgttggtttcc atgagtattg 2229
 caggtaataa tacagtgtat tcataagaat ctcaatcttg gggctaaatg ccttgtttct 2289
 ttgcacctct tttcaagtcc ttacatttaa ttactaattg ataagcagca gcttcctaca 2349
 tatagtagga aactgccaca tttttgctat catgattggc tgggcctgct gctgttcccta 2409
 gtaagatatt ctgaattcca ttttatcaat aaagcttgat ttaacaaaca agaaactt 2467

<210> 137
 <211> 358
 <212> PRT
 <213> Homo sapiens

<400> 137
 Met Met Gln Arg Val Phe Arg Gly Lys Leu Leu Ser Asn Asp Glu Val
 1 5 10 15
 Thr Ile Lys Tyr Lys Asp Glu Asp Gly Asp Leu Ile Thr Ile Phe Asp
 20 25 30
 Ser Ser Asp Leu Ser Phe Ala Ile Gln Cys Ser Arg Ile Leu Lys Leu
 35 40 45
 Thr Leu Phe Val Asn Gly Gln Pro Arg Pro Leu Glu Ser Ser Gln Val
 50 55 60
 Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu Arg Asn Lys Val Asn Arg

65		70		75		80									
Leu	Leu	Asp	Ser	Leu	Glu	Pro	Pro	Gly	Glu	Pro	Gly	Pro	Ser	Thr	Asn
				85					90					95	
Ile	Pro	Glu	Asn	Asp	Thr	Val	Asp	Gly	Arg	Glu	Glu	Lys	Ser	Ala	Ser
			100					105					110		
Asp	Ser	Ser	Gly	Lys	Gln	Ser	Thr	Gln	Val	Met	Ala	Ala	Ser	Met	Ser
		115					120						125		
Ala	Phe	Asp	Pro	Leu	Lys	Asn	Gln	Asp	Glu	Ile	Asn	Lys	Asn	Val	Met
	130					135					140				
Ser	Ala	Phe	Gly	Leu	Thr	Asp	Asp	Gln	Val	Ser	Gly	Pro	Pro	Ser	Ala
145					150					155					160
Pro	Ala	Glu	Asp	Arg	Ser	Gly	Thr	Pro	Asp	Ser	Ile	Ala	Ser	Ser	Ser
				165					170					175	
Ser	Ala	Ala	His	Pro	Pro	Gly	Val	Gln	Pro	Gln	Gln	Pro	Pro	Tyr	Thr
			180					185					190		
Gly	Ala	Gln	Thr	Gln	Ala	Gly	Gln	Met	Tyr	Gln	Gln	Tyr	Gln	Gln	Gln
		195					200					205			
Ala	Gly	Tyr	Gly	Ala	Gln	Gln	Pro	Gln	Ala	Pro	Pro	Gln	Gln	Pro	Gln
	210					215					220				
Gln	Tyr	Gly	Ile	Gln	Tyr	Ser	Ala	Ser	Tyr	Ser	Gln	Gln	Thr	Gly	Pro
225				230						235					240
Gln	Gln	Pro	Gln	Gln	Phe	Gln	Gly	Tyr	Gly	Gln	Gln	Pro	Thr	Ser	Gln
			245					250						255	
Ala	Pro	Ala	Pro	Ala	Phe	Ser	Gly	Gln	Pro	Gln	Gln	Leu	Pro	Ala	Gln
			260					265					270		
Pro	Pro	Gln	Gln	Tyr	Gln	Ala	Ser	Asn	Tyr	Pro	Ala	Gln	Thr	Tyr	Thr
		275					280					285			
Ala	Gln	Thr	Ser	Gln	Pro	Thr	Asn	Tyr	Thr	Val	Ala	Pro	Ala	Ser	Gln
	290					295					300				
Pro	Gly	Met	Ala	Pro	Ser	Gln	Pro	Gly	Ala	Tyr	Gln	Pro	Arg	Pro	Gly
305				310						315					320
Phe	Thr	Ser	Leu	Pro	Gly	Ser	Thr	Met	Thr	Pro	Pro	Pro	Ser	Gly	Pro
				325					330					335	
Asn	Pro	Tyr	Ala	Arg	Asn	Arg	Pro	Pro	Phe	Gly	Gln	Gly	Tyr	Thr	Gln
			340				345						350		
Pro	Gly	Pro	Gly	Tyr	Arg										
		355													

<210> 138
 <211> 1519
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (11)..(1084)

```

<400> 138
attagtgcta atg atg caa cga gtt ttc aga gga aaa ctt ctg agt aat      49
      Met Met Gln Arg Val Phe Arg Gly Lys Leu Leu Ser Asn
            1              5              10

gat gaa gta aca ata aag tat aaa gat gaa gat gga gat ctt ata aca      97
Asp Glu Val Thr Ile Lys Tyr Lys Asp Glu Asp Gly Asp Leu Ile Thr
      15              20              25

att ttt gat agt tct gac ctt tcc ttt gca att cag tgc agt agg ata      145
Ile Phe Asp Ser Ser Asp Leu Ser Phe Ala Ile Gln Cys Ser Arg Ile
      30              35              40              45

ctg aaa ctg aca tta ttt gtt aat ggc cag cca aga ccc ctt gaa tca      193
Leu Lys Leu Thr Leu Phe Val Asn Gly Gln Pro Arg Pro Leu Glu Ser
            50              55              60

agt cag gtg aaa tat ctc cgt cga gaa ctg ata gaa ctt cga aat aaa      241
Ser Gln Val Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu Arg Asn Lys
            65              70              75

gtg aat cgt tta ttg gat agc ttg gaa cca cct gga gaa cca gga cct      289
Val Asn Arg Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu Pro Gly Pro
            80              85              90

tcc acc aat att cct gaa aat gat act gtg gat ggt agg gaa gaa aag      337
Ser Thr Asn Ile Pro Glu Asn Asp Thr Val Asp Gly Arg Glu Glu Lys
            95              100             105

tct gct tct gat tct tct gga aaa cag tct act cag gtt atg gca gca      385
Ser Ala Ser Asp Ser Ser Gly Lys Gln Ser Thr Gln Val Met Ala Ala
      110              115              120              125

agt atg tct gct ttt gat cct tta aaa aac caa gat gaa atc aat aaa      433
Ser Met Ser Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu Ile Asn Lys
            130              135              140

aat gtt atg tca gcg ttt ggc tta aca gat gat cag gtt tca ggg cca      481
Asn Val Met Ser Ala Phe Gly Leu Thr Asp Asp Gln Val Ser Gly Pro
            145              150              155

ccc agt gct cct gca gaa gat cgt tca gga aca ccc gac agc att gct      529
Pro Ser Ala Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp Ser Ile Ala
            160              165              170

tcc tcc tcc tca gca gct cac cca cca ggc gtt cag cca cag cag cca      577
Ser Ser Ser Ser Ala Ala His Pro Pro Gly Val Gln Pro Gln Gln Pro
            175              180              185

```

cca tat aca gga gct cag act caa gca ggt cag atg tac caa cag tac	625
Pro Tyr Thr Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr Gln Gln Tyr	
190 195 200 205	
cag caa cag gcc ggc tat ggt gca cag cag ccg cag gct cca cct cag	673
Gln Gln Gln Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala Pro Pro Gln	
210 215 220	
cag cct caa cag tat ggt att cag tat tca gca agc tat agt cag cag	721
Gln Pro Gln Gln Tyr Gly Ile Gln Tyr Ser Ala Ser Tyr Ser Gln Gln	
225 230 235	
act gga ccc caa caa cct cag cag ttc cag gga tat ggc cag caa cca	769
Thr Gly Pro Gln Gln Pro Gln Gln Phe Gln Gly Tyr Gly Gln Gln Pro	
240 245 250	
act tcc cag gca cca gct cct gcc ttt tct ggt cag cct caa caa ctg	817
Thr Ser Gln Ala Pro Ala Pro Ala Phe Ser Gly Gln Pro Gln Gln Leu	
255 260 265	
cct gct cag ccg cca cag cag tac cag gcg agc aat tat cct gca caa	865
Pro Ala Gln Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr Pro Ala Gln	
270 275 280 285	
act tac act gcc caa act tct cag cct act aat tat act gtg gct cct	913
Thr Tyr Thr Ala Gln Thr Ser Gln Pro Thr Asn Tyr Thr Val Ala Pro	
290 295 300	
gcc tct caa cct gga atg gct cca agc caa cct ggg gcc tat caa cca	961
Ala Ser Gln Pro Gly Met Ala Pro Ser Gln Pro Gly Ala Tyr Gln Pro	
305 310 315	
aga cca ggt ttt act tca ctt cct gga agt acc atg acc cct cct cca	1009
Arg Pro Gly Phe Thr Ser Leu Pro Gly Ser Thr Met Thr Pro Pro Pro	
320 325 330	
agt ggg cct aat cct tat gcg cgt aac cgt cct ccc ttt ggt cag ggc	1057
Ser Gly Pro Asn Pro Tyr Ala Arg Asn Arg Pro Pro Phe Gly Gln Gly	
335 340 345	
tat acc caa cct gga cct ggt tat cga taaggaggct cctctacacc	1104
Tyr Thr Gln Pro Gly Pro Gly Tyr Arg	
350 355	
aattaatgta gctgctagct attggcctcc caaaagactc cagtactatt ttaatttgta	1164
ttgaagaagt tcagaaattht aaaagcagag ctttttttat gatattcattg ttggtgttaa	1224
ttgaaagtat aatttgctgg aacacaaaga ccaaaatgaa agtttttttcc tccctgctta	1284
aaaatgtagc agcttcttag ttacttttga acactactct tacatgtata aagtgattga	1344
cttgactttc tagcttccct tgtccggagg atattaaaat gctaggggtga ggtttagcca	1404
tcttacttgg ctttttacta ttaacatgat gtactaaagt agagcccttt gagaatacaa	1464

gatattatgt ataaaatgta acactgatga taggttaata-aagatgattg aatcc

1519

<210> 139
 <211> 396
 <212> PRT
 <213> Homo sapiens

<400> 139
 Met Asn Gly Gln Leu Asp Leu Ser Gly Lys Leu Ile Val Lys Ala Gln
 1 5 10 15
 Leu Gly Glu Asp Ile Arg Arg Ile Pro Ile His Asn Glu Asp Ile Thr
 20 25 30
 Tyr Asp Glu Leu Val Leu Met Met Gln Arg Val Phe Arg Gly Lys Leu
 35 40 45
 Leu Ser Asn Asp Glu Val Thr Ile Lys Tyr Lys Asp Glu Asp Gly Asp
 50 55 60
 Leu Ile Thr Ile Phe Asp Ser Ser Asp Leu Ser Phe Ala Ile Gln Cys
 65 70 75 80
 Ser Arg Ile Leu Lys Leu Thr Leu Phe Val Asn Gly Gln Pro Arg Pro
 85 90 95
 Leu Glu Ser Ser Gln Val Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu
 100 105 110
 Arg Asn Lys Val Asn Arg Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu
 115 120 125
 Pro Gly Pro Ser Thr Asn Ile Pro Glu Asn Asp Thr Val Asp Gly Arg
 130 135 140
 Glu Glu Lys Ser Ala Ser Asp Ser Ser Gly Lys Gln Ser Thr Gln Val
 145 150 155 160
 Met Ala Ala Ser Met Ser Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu
 165 170 175
 Ile Asn Lys Asn Val Met Ser Ala Phe Gly Leu Thr Asp Asp Gln Val
 180 185 190
 Ser Gly Pro Pro Ser Ala Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp
 195 200 205
 Ser Ile Ala Ser Ser Ser Ser Ala Ala His Pro Pro Gly Val Gln Pro
 210 215 220
 Gln Gln Pro Pro Tyr Thr Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr
 225 230 235 240
 Gln Gln Tyr Gln Gln Gln Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala
 245 250 255

Pro Pro Gln Gln Pro Gln Gln Tyr Gly Ile Gln Tyr Ser Ala Ser Tyr
 260 265 270
 Ser Gln Gln Thr Gly Pro Gln Gln Pro Gln Gln Phe Gln Gly Tyr Gly
 275 280 285
 Gln Gln Pro Thr Ser Gln Ala Pro Ala Pro Ala Phe Ser Gly Gln Pro
 290 295 300
 Gln Gln Leu Pro Ala Gln Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr
 305 310 315 320
 Pro Ala Gln Thr Tyr Thr Ala Gln Thr Ser Gln Pro Thr Asn Tyr Thr
 325 330 335
 Val Ala Pro Ala Ser Gln Pro Gly Met Ala Pro Ser Gln Pro Gly Ala
 340 345 350
 Tyr Gln Pro Arg Pro Gly Phe Thr Ser Leu Pro Gly Ser Thr Met Thr
 355 360 365
 Pro Pro Pro Ser Gly Pro Asn Pro Tyr Ala Arg Asn Arg Pro Pro Phe
 370 375 380
 Gly Gln Gly Tyr Thr Gln Pro Gly Pro Gly Tyr Arg
 385 390 395

<210> 140
 <211> 1641
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (19)..(1206)

<400> 140
 aacatcctgg agtccacc atg aac gga cag ttg gat cta agt ggg aag cta 51
 Met Asn Gly Gln Leu Asp Leu Ser Gly Lys Leu
 1 5 10
 atc gtc aaa gct caa ctt ggg gag gat att cgg cga att cct att cat 99
 Ile Val Lys Ala Gln Leu Gly Glu Asp Ile Arg Arg Ile Pro Ile His
 15 20 25
 aat gaa gat att act tat gat gaa tta gtg cta atg atg caa cga gtt 147
 Asn Glu Asp Ile Thr Tyr Asp Glu Leu Val Leu Met Met Gln Arg Val
 30 35 40
 ttc aga gga aaa ctt ctg agt aat gat gaa gta aca ata aag tat aaa 195
 Phe Arg Gly Lys Leu Leu Ser Asn Asp Glu Val Thr Ile Lys Tyr Lys
 45 50 55
 gat gaa gat gga gat ctt ata aca att ttt gat agt tct gac ctt tcc 243
 Asp Glu Asp Gly Asp Leu Ile Thr Ile Phe Asp Ser Ser Asp Leu Ser
 60 65 70 75

ttt gca att cag tgc agt agg ata ctg aaa ctg aca tta ttt gtt aat	291
Phe Ala Ile Gln Cys Ser Arg Ile Leu Lys Leu Thr Leu Phe Val Asn	
80 85 90	
ggc cag cca aga ccc ctt gaa tca agt cag gtg aaa tat ctc cgt cga	339
Gly Gln Pro Arg Pro Leu Glu Ser Ser Gln Val Lys Tyr Leu Arg Arg	
95 100 105	
gaa ctg ata gaa ctt cga aat aaa gtg aat cgt tta ttg gat agc ttg	387
Glu Leu Ile Glu Leu Arg Asn Lys Val Asn Arg Leu Leu Asp Ser Leu	
110 115 120	
gaa cca cct gga gaa cca gga cct tcc acc aat att cct gaa aat gat	435
Glu Pro Pro Gly Glu Pro Gly Pro Ser Thr Asn Ile Pro Glu Asn Asp	
125 130 135	
act gtg gat ggt agg gaa gaa aag tct gct tct gat tct tct gga aaa	483
Thr Val Asp Gly Arg Glu Glu Lys Ser Ala Ser Asp Ser Ser Gly Lys	
140 145 150 155	
cag tct act cag gtt atg gca gca agt atg tct gct ttt gat cct tta	531
Gln Ser Thr Gln Val Met Ala Ala Ser Met Ser Ala Phe Asp Pro Leu	
160 165 170	
aaa aac caa gat gaa atc aat aaa aat gtt atg tca gcg ttt ggc tta	579
Lys Asn Gln Asp Glu Ile Asn Lys Asn Val Met Ser Ala Phe Gly Leu	
175 180 185	
aca gat gat cag gtt tca ggg cca ccc agt gct cct gca gaa gat cgt	627
Thr Asp Asp Gln Val Ser Gly Pro Pro Ser Ala Pro Ala Glu Asp Arg	
190 195 200	
tca gga aca ccc gac agc att gct tcc tcc tcc tca gca gct cac cca	675
Ser Gly Thr Pro Asp Ser Ile Ala Ser Ser Ser Ser Ala Ala His Pro	
205 210 215	
cca ggc gtt cag cca cag cag cca cca tat aca gga gct cag act caa	723
Pro Gly Val Gln Pro Gln Gln Pro Pro Tyr Thr Gly Ala Gln Thr Gln	
220 225 230 235	
gca ggt cag atg tac caa cag tac cag caa cag gcc ggc tat ggt gca	771
Ala Gly Gln Met Tyr Gln Gln Tyr Gln Gln Gln Ala Gly Tyr Gly Ala	
240 245 250	
cag cag ccg cag gct cca cct cag cag cct caa cag tat ggt att cag	819
Gln Gln Pro Gln Ala Pro Pro Gln Gln Pro Gln Gln Tyr Gly Ile Gln	
255 260 265	
tat tca gca agc tat agt cag cag act gga ccc caa caa cct cag cag	867
Tyr Ser Ala Ser Tyr Ser Gln Gln Thr Gly Pro Gln Gln Pro Gln Gln	
270 275 280	
ttc cag gga tat ggc cag caa cca act tcc cag gca cca gct cct gcc	915
Phe Gln Gly Tyr Gly Gln Gln Pro Thr Ser Gln Ala Pro Ala Pro Ala	
285 290 295	

ttt_tct ggt cag_cct caa caa ctg cct gct cag ccg-cca cag cag-tac 963
Phe Ser Gly Gln Pro Gln Gln Leu Pro Ala Gln Pro Pro Gln Gln Tyr
300 305 310 315

cag gcg agc aat tat cct gca caa act tac act gcc caa act tct cag 1011
Gln Ala Ser Asn Tyr Pro Ala Gln Thr Tyr Thr Ala Gln Thr Ser Gln
320 325 330

cct act aat tat act gtg gct cct gcc tct caa cct gga atg gct cca 1059
Pro Thr Asn Tyr Thr Val Ala Pro Ala Ser Gln Pro Gly Met Ala Pro
335 340 345

agc caa cct ggg gcc tat caa cca aga cca ggt ttt act tca ctt cct 1107
Ser Gln Pro Gly Ala Tyr Gln Pro Arg Pro Gly Phe Thr Ser Leu Pro
350 355 360

gga agt acc atg acc cct cct cca agt ggg cct aat cct tat gcg cgt 1155
Gly Ser Thr Met Thr Pro Pro Pro Ser Gly Pro Asn Pro Tyr Ala Arg
365 370 375

aac cgt cct ccc ttt ggt cag ggc tat acc caa cct gga cct ggt tat 1203
Asn Arg Pro Pro Phe Gly Gln Gly Tyr Thr Gln Pro Gly Pro Gly Tyr
380 385 390 395

cga taaggaggct cctctacacc aattaatgta gctgctagct attggcctcc 1256
Arg

caaaagactc cagtactatt ttaatttgta ttgaagaagt tcagaaattt aaaagcagag 1316

catttttttat gatatacattg ttggtgttaa ttgaaagtat aatttgctgg aacacaaaga 1376

ccaaaatgaa agttttttcc tccctgctta aaaatgtagc agcttcttag ttactttgga 1436

acactactct tacatgtata aagtgattga cttgactttc tagcttccct tgtccggagg 1496

atattaaaat gctaggggtga ggttttagcca tcttacttgg ctttttacta ttaacatgat 1556

gtactaaagt agagcccttt gagaatacaa gatattatgt ataaaatgta aactgatga 1616

taggttaata aagatgattg aatcc 1641

<210> 141

<211> 323

<212> PRT

<213> Homo sapiens

<400> 141

Met Ala Phe Ser Gly Ser Gln Ala Pro Tyr Leu Ser Pro Ala Val Pro
1 5 10 15

Phe Ser Gly Thr Ile Gln Gly Gly Leu Gln Asp Gly Leu Gln Ile Thr
20 25 30

Val Asn Gly Thr Val Leu Ser Ser Ser Gly Thr Arg Phe Ala Val Asn
35 40 45

```

Phe_Gln Thr Gly_Phe Ser Gly Asn Asp_Ile Ala Phe_His Phe Asn_Pro
50 55 60
Arg Phe Glu Asp Gly Gly Tyr Val Val Cys Asn Thr Arg Gln Asn Gly
65 70 75 80
Ser Trp Gly Pro Glu Glu Arg Lys Thr His Met Pro Phe Gln Lys Gly
85 90 95
Met Pro Phe Asp Leu Cys Phe Leu Val Gln Ser Ser Asp Phe Lys Val
100 105 110
Met Val Asn Gly Ile Leu Phe Val Gln Tyr Phe His Arg Val Pro Phe
115 120 125
His Arg Val Asp Thr Ile Ser Val Asn Gly Ser Val Gln Leu Ser Tyr
130 135 140
Ile Ser Phe Gln Pro Pro Gly Val Trp Pro Ala Asn Pro Ala Pro Ile
145 150 155 160
Thr Gln Thr Val Ile His Thr Val Gln Ser Ala Pro Gly Gln Met Phe
165 170 175
Ser Thr Pro Ala Ile Pro Pro Met Met Tyr Pro His Pro Ala Tyr Pro
180 185 190
Met Pro Phe Ile Thr Thr Ile Leu Gly Gly Leu Tyr Pro Ser Lys Ser
195 200 205
Ile Leu Leu Ser Gly Thr Val Leu Pro Ser Ala Gln Arg Phe His Ile
210 215 220
Asn Leu Cys Ser Gly Asn His Ile Ala Phe His Leu Asn Pro Arg Phe
225 230 235 240
Asp Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asp Asn Ser Trp Gly
245 250 255
Ser Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe Val Arg Gly Gln
260 265 270
Ser Phe Ser Val Trp Ile Leu Cys Glu Ala His Cys Leu Lys Val Ala
275 280 285
Val Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg Leu Arg Asn Leu
290 295 300
Pro Thr Ile Asn Arg Leu Glu Val Gly Gly Asp Ile Gln Leu Thr His
305 310 315 320
Val Gln Thr

```

<210> 142
 <211> 1616

<212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (72)..(1040)

<400> 142
 aagtcgttcc ctctacaaag gacttcctag tgggtgtgaa aggcagcggg ggccacagag 60
 gcggcggaga g atg gcc ttc agc ggt tcc cag gct ccc tac ctg agt cca 110
 Met Ala Phe Ser Gly Ser Gln Ala Pro Tyr Leu Ser Pro
 1 5 10
 gct gtc ccc ttt tct ggg act att caa gga ggt ctc cag gac gga ctt 158
 Ala Val Pro Phe Ser Gly Thr Ile Gln Gly Gly Leu Gln Asp Gly Leu
 15 20 25
 cag atc act gtc aat ggg acc gtt ctc agc tcc agt gga acc agg ttt 206
 Gln Ile Thr Val Asn Gly Thr Val Leu Ser Ser Ser Gly Thr Arg Phe
 30 35 40 45
 gct gtg aac ttt cag act ggc ttc agt gga aat gac att gcc ttc cac 254
 Ala Val Asn Phe Gln Thr Gly Phe Ser Gly Asn Asp Ile Ala Phe His
 50 55 60
 ttc aac cct cgg ttt gaa gat gga ggg tac gtg gtg tgc aac acg agg 302
 Phe Asn Pro Arg Phe Glu Asp Gly Gly Tyr Val Val Cys Asn Thr Arg
 65 70 75
 cag aac gga agc tgg ggg ccc gag gag agg aag aca cac atg cct ttc 350
 Gln Asn Gly Ser Trp Gly Pro Glu Glu Arg Lys Thr His Met Pro Phe
 80 85 90
 cag aag ggg atg ccc ttt gac ctc tgc ttc ctg gtg cag agc tca gat 398
 Gln Lys Gly Met Pro Phe Asp Leu Cys Phe Leu Val Gln Ser Ser Asp
 95 100 105
 ttc aag gtg atg gtg aac ggg atc ctc ttc gtg cag tac ttc cac cgc 446
 Phe Lys Val Met Val Asn Gly Ile Leu Phe Val Gln Tyr Phe His Arg
 110 115 120 125
 gtg ccc ttc cac cgt gtg gac acc atc tcc gtc aat ggc tct gtg cag 494
 Val Pro Phe His Arg Val Asp Thr Ile Ser Val Asn Gly Ser Val Gln
 130 135 140
 ctg tcc tac atc agc ttc cag cct ccc ggc gtg tgg cct gcc aac ccg 542
 Leu Ser Tyr Ile Ser Phe Gln Pro Pro Gly Val Trp Pro Ala Asn Pro
 145 150 155
 gct ccc att acc cag aca gtc atc cac aca gtg cag agc gcc cct gga 590
 Ala Pro Ile Thr Gln Thr Val Ile His Thr Val Gln Ser Ala Pro Gly
 160 165 170
 cag atg ttc tct act ccc gcc atc cca cct atg atg tac ccc cac ccc 638
 Gln Met Phe Ser Thr Pro Ala Ile Pro Pro Met Met Tyr Pro His Pro
 175 180 185

gcc tat ccg atg cct ttc atc acc acc att ctg gga ggg ctg tac cca	686
Ala Tyr Pro Met Pro Phe Ile Thr Thr Ile Leu Gly Gly Leu Tyr Pro	
190 195 200 205	
tcc aag tcc atc ctc ctg tca ggc act gtc ctg ccc agt gct cag agg	734
Ser Lys Ser Ile Leu Leu Ser Gly Thr Val Leu Pro Ser Ala Gln Arg	
210 215 220	
ttc cac atc aac ctg tgc tct ggg aac cac atc gcc ttc cac ctg aac	782
Phe His Ile Asn Leu Cys Ser Gly Asn His Ile Ala Phe His Leu Asn	
225 230 235	
ccc cgt ttt gat gag aat gct gtg gtc cgc aac acc cag atc gac aac	830
Pro Arg Phe Asp Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asp Asn	
240 245 250	
tcc tgg ggg tct gag gag cga agt ctg ccc cga aaa atg ccc ttc gtc	878
Ser Trp Gly Ser Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe Val	
255 260 265	
cgt ggc cag agc ttc tca gtg tgg atc ttg tgt gaa gct cac tgc ctc	926
Arg Gly Gln Ser Phe Ser Val Trp Ile Leu Cys Glu Ala His Cys Leu	
270 275 280 285	
aag gtg gcc gtg gat ggt cag cac ctg ttt gaa tac tac cat cgc ctg	974
Lys Val Ala Val Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg Leu	
290 295 300	
agg aac ctg ccc acc atc aac aga ctg gaa gtg ggg ggc gac atc cag	1022
Arg Asn Leu Pro Thr Ile Asn Arg Leu Glu Val Gly Gly Asp Ile Gln	
305 310 315	
ctg acc cat gtg cag aca taggcggcctt cctggccctg gggccggggg	1070
Leu Thr His Val Gln Thr	
320	
ctggggtgtg gggcagtctg ggtcctctca tcatccccac ttcccaggcc cagcctttcc	1130
aacctgcct gggatctggg ctttaatgca gaggccatgt ccttgtctgg tctgctttct	1190
ggctacagcc acctggaac ggagaaggca gctgacgggg attgccttcc tcagccgcag	1250
cagcacctgg ggctccagct gctggaatcc taccatccca ggaggcaggc acagccaggg	1310
agaggggagg agtgggcagt gaagatgaag ccccatgctc agtccccctcc catccccccac	1370
gcagctccac cccagtccca agccaccagc tgtctgctcc tgggtgggagg tggcctctc	1430
agccccctct ctctgacctt taacctcact ctcaccttgc accgtgcacc aaccttcac	1490
ccctcctgga aagcaggcct gatggcttcc cactggcctc caccacctga ccagagtgtt	1550
ctcttcagag gactggctcc tttcccagtg tccttaaaat aaagaaatga aaatgcttgt	1610
tggcac	1616

```

<210> 143
<211> 136
<212> PRT
<213> Homo sapiens

<400> 143
Met Ala Gly Ala Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile
  1             5             10             15

Val Gly Gly Ile Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly
      20             25             30

Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val
      35             40             45

Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val
      50             55             60

Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala
      65             70             75             80

Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile
      85             90             95

Pro Leu Pro His Met Ala Leu Ser Cys Gly Phe Leu Asp Gln Arg His
      100            105            110

Gly His Leu Ser Val Cys Leu Leu Thr Val Ala Phe Gly Gly Arg Phe
      115            120            125

Leu Gln Pro Leu Met His Cys Val
      130            135

```

```

<210> 144
<211> 1252
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (225)..(632)

```

```

<400> 144
acaatcacag ctccgggcat tgggggaacc cgagccggct gcgccggggg aatccgtgcg 60
ggcgccttcc gtcccggtcc catcctcgcc gcgctcagc acctctgaag ttttgcagcg 120
cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcaccct 180
aaaacattta tttcaaggag aaaagaaaaa gggggggcgc aaaa atg gct ggg gca 236
                                   Met Ala Gly Ala
                                   1

att ata gaa aac atg agc acc aag aag ctg tgc att gtt ggt ggg att 284
Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile

```

5	10	15	20	
ctg ctc gtg ttc caa atc atc gcc ttt ctg gtg gga ggc ttg att gct	332			
Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala				
25 30 35				
cca ggg ccc aca acg gca gtg tcc tac atg tcg gtg aaa tgt gtg gat	380			
Pro Gly Pro Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp				
40 45 50				
gcc cgt aag aac cat cac aag aca aaa tgg ttc gtg cct tgg gga ccc	428			
Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro				
55 60 65				
aat cat tgt gac aag atc cga gac att gaa gag gca att cca agg gaa	476			
Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu				
70 75 80				
att gaa gcc aat gac atc gtg ttt tct gtt cac att ccc ctc ccc cac	524			
Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His				
85 90 95 100				
atg gct ctt agc tgt ggt ttc ttg gac cag cgg cat gga cat ttg tca	572			
Met Ala Leu Ser Cys Gly Phe Leu Asp Gln Arg His Gly His Leu Ser				
105 110 115				
gtt tgc ctt ctg acg gta gct ttt gga gga aga ttc ctg cag cca cta	620			
Val Cys Leu Leu Thr Val Ala Phe Gly Gly Arg Phe Leu Gln Pro Leu				
120 125 130				
atg cat tgt gta tgataacaaa aactctggta tgacacattt tctgtgatca	672			
Met His Cys Val				
135				
ttgttaatta gtgacatagt aacatctgta gcagctgggt agtaaaccctc atgtgggggt	732			
gggggtggggg tgtattcctt gggggatggt ttggggccgaa tggggagtggt aatatttgac	792			
atcttttctg ttttaaattc taggatagat tttaacatcc tttgcgggtcc cagtccaagg	852			
taggctggtg tcatagtctt ctactccta atccatgacc actgtttttt tctattttat	912			
atcaccaggt agcctactga gttaatatatt aagttgtcaa tagataagtg tccctgtttt	972			
gtggcataat ataactgaat ttcattgagaa gattttattcc accaggggta tttcagcttt	1032			
gaaaccaaact ctgtgtatct aataactaacc aatctgtttg atgtggggtt taaaaaatgt	1092			
ttgctaaact acccaagtaa gattttactgt attaaatggc cttcgggtct gaaaagcttt	1152			
tttaacctct tgcttaaaat gcgtttttatt ttgataagat acttcaaata gcctccaaaa	1212			
gtgtagatcc aatcacttaa ataaacctgt atgtatatgc	1252			

<210> 145

<211> 468

<212> PRT

<213> Homo sapiens

<400> 145

Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser Cys Leu Gly Asp
1 5 10 15

Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys Arg Gln Phe Gln Phe
20 25 30

Met Leu Phe Ile Leu Gln Leu Asp Ile Ala Phe Lys Leu Asn Asn Gln
35 40 45

Ile Arg Glu Asn Ala Glu Val Ser Met Asp Val Ser Leu Ala Tyr Arg
50 55 60

Asp Asp Ala Phe Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro
65 70 75 80

Arg Lys Leu Lys Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu
85 90 95

Gly Arg Tyr Tyr Glu Cys Asp Val Leu Pro Phe Met Glu Ile Gly Ser
100 105 110

Val Ala His Lys Phe Tyr Leu Leu Asn Ile Arg Leu Pro Val Asn Glu
115 120 125

Lys Lys Lys Ile Asn Val Gly Ile Gly Glu Ile Lys Asp Ile Arg Leu
130 135 140

Val Gly Ile His Gln Asn Gly Gly Phe Thr Lys Val Trp Phe Ala Met
145 150 155 160

Lys Thr Phe Leu Thr Pro Ser Ile Phe Ile Ile Met Val Trp Tyr Trp
165 170 175

Arg Arg Ile Thr Met Met Ser Arg Pro Pro Val Leu Leu Glu Lys Val
180 185 190

Ile Phe Ala Leu Gly Ile Ser Met Thr Phe Ile Asn Ile Pro Val Glu
195 200 205

Trp Phe Ser Ile Gly Phe Asp Trp Thr Trp Met Leu Leu Phe Gly Asp
210 215 220

Ile Arg Gln Gly Ile Phe Tyr Ala Met Leu Leu Ser Phe Trp Ile Ile
225 230 235 240

Phe Cys Gly Glu His Met Met Asp Gln His Glu Arg Asn His Ile Ala
245 250 255

Gly Tyr Trp Lys Gln Val Gly Pro Ile Ala Val Gly Ser Phe Cys Leu
260 265 270

Phe Ile Phe Asp Met Cys Glu Arg Gly Val Gln Leu Thr Asn Pro Phe
275 280 285

Tyr Ser Ile Trp Thr Thr Asp Ile Gly Thr Glu Leu Ala Met Ala Phe
 290 295 300
 Ile Ile Val Ala Gly Ile Cys Leu Cys Leu Tyr Phe Leu Phe Leu Cys
 305 310 315 320
 Phe Met Val Phe Gln Val Phe Arg Asn Ile Ser Gly Lys Gln Ser Ser
 325 330 335
 Leu Pro Ala Met Ser Lys Val Arg Arg Leu His Tyr Glu Gly Leu Ile
 340 345 350
 Phe Arg Phe Lys Phe Leu Met Leu Ile Thr Leu Ala Cys Ala Ala Met
 355 360 365
 Thr Val Ile Phe Phe Ile Val Ser Gln Val Thr Glu Gly His Trp Lys
 370 375 380
 Trp Gly Gly Val Thr Val Gln Val Asn Ser Ala Phe Phe Thr Gly Ile
 385 390 395 400
 Tyr Gly Met Trp Asn Leu Tyr Val Phe Ala Leu Met Phe Leu Tyr Ala
 405 410 415
 Pro Ser His Lys Asn Tyr Gly Glu Asp Gln Ser Asn Gly Met Gln Leu
 420 425 430
 Pro Cys Lys Ser Arg Glu Asp Cys Ala Leu Phe Val Ser Glu Leu Tyr
 435 440 445
 Gln Glu Leu Phe Ser Ala Ser Lys Tyr Ser Phe Ile Asn Asp Asn Ala
 450 455 460
 Ala Ser Gly Ile
 465

<210> 146
 <211> 1943
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (379)..(1782)

<400> 146
 acaatcacag ctccgggcat tgggggaacc cgagccggct gcgccggggg aatccgtgcg 60
 ggcgccttcc gtcccggtcc catcctcgcc gcgctccagc acctctgaag ttttgcagcg 120
 cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcaccct 180
 aaaacattta tttcaaggag aaaagaaaaa gggggggcgc aaaaatggct ggggcaatta 240
 tagaaaacat gagcaccaag aagctgtgca ttgttggtgg gattctgctc gtgttccaaa 300

tcacgcctt tctggtggga ggcttgattg ctccagggcc cacaacggca gtgtcctaca 360

tgctcggtgaa atgtgtgg atg ccc gta aga acc atc aca aga caa aat ggt 411
Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly
1 5 10

tcg tgc ctt ggg gac cca atc att gtg aca aga tcc gag aca ttg aag 459
Ser Cys Leu Gly Asp Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys
15 20 25

agg caa ttc caa ttc atg ctg ttt atc ctg cag ctg gac att gcc ttc 507
Arg Gln Phe Gln Phe Met Leu Phe Ile Leu Gln Leu Asp Ile Ala Phe
30 35 40

aag cta aac aac caa atc aga gaa aat gca gaa gtc tcc atg gac gtt 555
Lys Leu Asn Asn Gln Ile Arg Glu Asn Ala Glu Val Ser Met Asp Val
45 50 55

tcc ctg gct tac cgt gat gac gcg ttt gct gag tgg act gaa atg gcc 603
Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp Thr Glu Met Ala
60 65 70 75

cat gaa aga gta cca cgg aaa ctc aaa tgc acc ttc aca tct ccc aag 651
His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe Thr Ser Pro Lys
80 85 90

act cca gag cat gag ggc cgt tac tat gaa tgt gat gtc ctt cct ttc 699
Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp Val Leu Pro Phe
95 100 105

atg gaa att ggg tct gtg gcc cat aag ttt tac ctt tta aac atc cgg 747
Met Glu Ile Gly Ser Val Ala His Lys Phe Tyr Leu Leu Asn Ile Arg
110 115 120

ctg cct gtg aat gag aag aag aaa atc aat gtg gga att ggg gag ata 795
Leu Pro Val Asn Glu Lys Lys Lys Ile Asn Val Gly Ile Gly Glu Ile
125 130 135

aag gat atc cgg ttg gtg ggg atc cac caa aat gga ggc ttc acc aag 843
Lys Asp Ile Arg Leu Val Gly Ile His Gln Asn Gly Gly Phe Thr Lys
140 145 150 155

gtg tgg ttt gcc atg aag acc ttc ctt acg ccc agc atc ttc atc att 891
Val Trp Phe Ala Met Lys Thr Phe Leu Thr Pro Ser Ile Phe Ile Ile
160 165 170

atg gtg tgg tat tgg agg agg atc acc atg atg tcc cga ccc cca gtg 939
Met Val Trp Tyr Trp Arg Arg Ile Thr Met Met Ser Arg Pro Pro Val
175 180 185

ctt ctg gaa aaa gtc atc ttt gcc ctt ggg att tcc atg acc ttt atc 987
Leu Leu Glu Lys Val Ile Phe Ala Leu Gly Ile Ser Met Thr Phe Ile
190 195 200

aat atc cca gtg gaa tgg ttt tcc atc ggg ttt gac tgg acc tgg atg 1035
Asn Ile Pro Val Glu Trp Phe Ser Ile Gly Phe Asp Trp Thr Trp Met

205	210	215	
ctg ctg ttt ggt gac atc cga cag ggc atc ttc tat gcg atg ctt ctg Leu Leu Phe Gly Asp Ile Arg Gln Gly Ile Phe Tyr Ala Met Leu Leu 220 225 230 235			1083
tcc ttc tgg atc atc ttc tgt ggc gag cac atg atg gat cag cac gag Ser Phe Trp Ile Ile Phe Cys Gly Glu His Met Met Asp Gln His Glu 240 245 250			1131
cgg aac cac atc gca ggg tat tgg aag caa gtc gga ccc att gcc gtt Arg Asn His Ile Ala Gly Tyr Trp Lys Gln Val Gly Pro Ile Ala Val 255 260 265			1179
ggc tcc ttc tgc ctc ttc ata ttt gac atg tgt gag aga ggg gta caa Gly Ser Phe Cys Leu Phe Ile Phe Asp Met Cys Glu Arg Gly Val Gln 270 275 280			1227
ctc acg aat ccc ttc tac agt atc tgg act aca gac att gga aca gag Leu Thr Asn Pro Phe Tyr Ser Ile Trp Thr Thr Asp Ile Gly Thr Glu 285 290 295			1275
ctg gcc atg gcc ttc atc atc gtg gct gga atc tgc ctc tgc ctc tac Leu Ala Met Ala Phe Ile Ile Val Ala Gly Ile Cys Leu Cys Leu Tyr 300 305 310 315			1323
ttc ctg ttt cta tgc ttc atg gta ttt cag gtg ttt cgg aac atc agt Phe Leu Phe Leu Cys Phe Met Val Phe Gln Val Phe Arg Asn Ile Ser 320 325 330			1371
ggg aag cag tcc agc ctg cca gct atg agc aaa gtc cgg cgg cta cac Gly Lys Gln Ser Ser Leu Pro Ala Met Ser Lys Val Arg Arg Leu His 335 340 345			1419
tat gag ggg cta att ttt agg ttc aag ttc ctc atg ctt atc acc ttg Tyr Glu Gly Leu Ile Phe Arg Phe Lys Phe Leu Met Leu Ile Thr Leu 350 355 360			1467
gcc tgc gct gcc atg act gtc atc ttc ttc atc gtt agt cag gta acg Ala Cys Ala Ala Met Thr Val Ile Phe Phe Ile Val Ser Gln Val Thr 365 370 375			1515
gaa ggc cat tgg aaa tgg ggc ggc gtc aca gtc caa gtg aac agt gcc Glu Gly His Trp Lys Trp Gly Gly Val Thr Val Gln Val Asn Ser Ala 380 385 390 395			1563
ttt ttc aca ggc atc tat ggg atg tgg aat ctg tat gtc ttt gct ctg Phe Phe Thr Gly Ile Tyr Gly Met Trp Asn Leu Tyr Val Phe Ala Leu 400 405 410			1611
atg ttc ttg tat gca cca tcc cat aaa aac tat gga gaa gac cag tcc Met Phe Leu Tyr Ala Pro Ser His Lys Asn Tyr Gly Glu Asp Gln Ser 415 420 425			1659
aat gga atg caa ctc cca tgt aaa tcg agg gaa gat tgt gct ttg ttt Asn Gly Met Gln Leu Pro Cys Lys Ser Arg Glu Asp Cys Ala Leu Phe 430 435 440			1707

gtt tcg gaa ctt tat caa gaa ttg ttc agc gct tcg aaa tat tcc ttc 1755
 Val Ser Glu Leu Tyr Gln Glu Leu Phe Ser Ala Ser Lys Tyr Ser Phe
 445 450 455

atc aat gac aac gca gct tct ggt att tgagtcaaca aggcaacaca 1802
 Ile Asn Asp Asn Ala Ala Ser Gly Ile
 460 465

tgtttatcag ctttgcattt gcagttgtca cagtcacatt gattgtactt gtatacgcac 1862
 acaaatacac tcatttagcc tttatctcaa aatgttaaata ataaggaaaa aagcgtcaac 1922
 aataaatatt ctttgagtat t 1943

<210> 147
 <211> 460
 <212> PRT
 <213> Homo sapiens

<400> 147
 Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser Cys Leu Gly Asp
 1 5 10 15

Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys Arg Gln Phe Gln Gly
 20 25 30

Lys Leu Lys Pro Met Thr Ser Cys Phe Leu Phe Thr Phe Pro Ser Pro
 35 40 45

Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp Thr
 50 55 60

Glu Met Ala His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe Thr
 65 70 75 80

Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp Val
 85 90 95

Leu Pro Phe Met Glu Ile Gly Ser Val Ala His Lys Phe Tyr Leu Leu
 100 105 110

Asn Ile Arg Leu Pro Val Asn Glu Lys Lys Lys Ile Asn Val Gly Ile
 115 120 125

Gly Glu Ile Lys Asp Ile Arg Leu Val Gly Ile His Gln Asn Gly Gly
 130 135 140

Phe Thr Lys Val Trp Phe Ala Met Lys Thr Phe Leu Thr Pro Ser Ile
 145 150 155 160

Phe Ile Ile Met Val Trp Tyr Trp Arg Arg Ile Thr Met Met Ser Arg
 165 170 175

Pro Pro Val Leu Leu Glu Lys Val Ile Phe Ala Leu Gly Ile Ser Met
 180 185 190

Thr	Phe	Ile	Asn	Ile	Pro	Val	Glu	Trp	Phe	Ser	Ile	Gly	Phe	Asp	Trp			
		195					200					205						
Thr	Trp	Met	Leu	Leu	Phe	Gly	Asp	Ile	Arg	Gln	Gly	Ile	Phe	Tyr	Ala			
	210					215					220							
Met	Leu	Leu	Ser	Phe	Trp	Ile	Ile	Phe	Cys	Gly	Glu	His	Met	Met	Asp			
225					230					235					240			
Gln	His	Glu	Arg	Asn	His	Ile	Ala	Gly	Tyr	Trp	Lys	Gln	Val	Gly	Pro			
				245					250					255				
Ile	Ala	Val	Gly	Ser	Phe	Cys	Leu	Phe	Ile	Phe	Asp	Met	Cys	Glu	Arg			
			260					265					270					
Gly	Val	Gln	Leu	Thr	Asn	Pro	Phe	Tyr	Ser	Ile	Trp	Thr	Thr	Asp	Ile			
		275					280					285						
Gly	Thr	Glu	Leu	Ala	Met	Ala	Phe	Ile	Ile	Val	Ala	Gly	Ile	Cys	Leu			
	290					295					300							
Cys	Leu	Tyr	Phe	Leu	Phe	Leu	Cys	Phe	Met	Val	Phe	Gln	Val	Phe	Arg			
305					310					315					320			
Asn	Ile	Ser	Gly	Lys	Gln	Ser	Ser	Leu	Pro	Ala	Met	Ser	Lys	Val	Arg			
				325					330					335				
Arg	Leu	His	Tyr	Glu	Gly	Leu	Ile	Phe	Arg	Phe	Lys	Phe	Leu	Met	Leu			
			340					345					350					
Ile	Thr	Leu	Ala	Cys	Ala	Ala	Met	Thr	Val	Ile	Phe	Phe	Ile	Val	Ser			
		355					360					365						
Gln	Val	Thr	Glu	Gly	His	Trp	Lys	Trp	Gly	Gly	Ile	Thr	Val	Gln	Val			
	370					375					380							
Asn	Ser	Ala	Phe	Phe	Thr	Gly	Ile	Tyr	Gly	Met	Trp	Asn	Leu	Tyr	Val			
385					390					395					400			
Phe	Ala	Leu	Met	Phe	Leu	Tyr	Ala	Pro	Ser	His	Lys	Asn	Tyr	Gly	Glu			
			405					410						415				
Asp	Gln	Ser	Asn	Gly	Met	Gln	Leu	Pro	Cys	Lys	Ser	Arg	Glu	Asp	Cys			
			420					425					430					
Ala	Leu	Phe	Val	Ser	Glu	Leu	Tyr	Gln	Glu	Leu	Phe	Ser	Ala	Ser	Lys			
		435					440					445						
Tyr	Ser	Phe	Ile	Asn	Asp	Asn	Ala	Ala	Ser	Gly	Ile							
	450					455					460							

<210> 148
 <211> 1919
 <212> DNA
 <213> Homo sapiens

```

<220>
<221> CDS
<222> (376)..(1755)

<400> 148
atcacagctc cgggcattgg gggaacccga gccggctgcg ccgggggaat ccgtgcgggc 60
gccttcgcgc cgggtcccat cctgcgcgcg ctccagcacc tctgaagttt tgcagcgccc 120
agaaaggagg cgaggaagga gggagtgtat gagaggaggg agcaaaaagc tcaccctaaa 180
acatttattt caaggagaaa agaaaaaggg ggggcgcgaaa aatggctggg gcaattatag 240
aaaacatgag caccaagaag ctgtgcattg ttggtgggat tctgctcgtg ttccaaatca 300
tcgcctttct ggtgggaggg ttgattgctc cagggcccac aacggcagtg tcctacatgt 360
cggtgaaatg tgtgg atg ccc gta aga acc atc aca aga caa aat ggt tcg 411
      Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser
              1              5              10

tgc ctt ggg gac cca atc att gtg aca aga tcc gag aca ttg aag agg 459
Cys Leu Gly Asp Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys Arg
      15              20              25

caa ttc caa ggg aaa ttg aag cca atg aca tcg tgt ttt ctg ttc aca 507
Gln Phe Gln Gly Lys Leu Lys Pro Met Thr Ser Cys Phe Leu Phe Thr
      30              35              40

ttc ccc tcc ccc atg gac gtt tcc ctg gct tac cgt gat gac gcg ttt 555
Phe Pro Ser Pro Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala Phe
      45              50              55              60

gct gag tgg act gaa atg gcc cat gaa aga gta cca cgg aaa ctc aaa 603
Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro Arg Lys Leu Lys
      65              70              75

tgc acc ttc aca tct ccc aag act cca gag cat gag ggc cgt tac tat 651
Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr Tyr
      80              85              90

gaa tgt gat gtc ctt cct ttc atg gaa att ggg tct gtg gcc cat aag 699
Glu Cys Asp Val Leu Pro Phe Met Glu Ile Gly Ser Val Ala His Lys
      95              100              105

ttt tac ctt tta aac atc cgg ctg cct gtg aat gag aag aag aaa atc 747
Phe Tyr Leu Leu Asn Ile Arg Leu Pro Val Asn Glu Lys Lys Lys Ile
      110              115              120

aat gtg gga att ggg gag ata aag gat atc cgg ttg gtg ggg atc cac 795
Asn Val Gly Ile Gly Glu Ile Lys Asp Ile Arg Leu Val Gly Ile His
      125              130              135              140

caa aat gga ggc ttc acc aag gtg tgg ttt gcc atg aag acc ttc ctt 843
Gln Asn Gly Gly Phe Thr Lys Val Trp Phe Ala Met Lys Thr Phe Leu
      145              150              155

```

acg ccc agc atc ttc atc att atg gtg tgg tat tgg agg agg atc acc	891
Thr Pro Ser Ile Phe Ile Ile Met Val Trp Tyr Trp Arg Arg Ile Thr	
160 165 170	
atg atg tcc cga ccc cca gtg ctt ctg gaa aaa gtc atc ttt gcc ctt	939
Met Met Ser Arg Pro Pro Val Leu Leu Glu Lys Val Ile Phe Ala Leu	
175 180 185	
ggg att tcc atg acc ttt atc aat atc cca gtg gaa tgg ttt tcc atc	987
Gly Ile Ser Met Thr Phe Ile Asn Ile Pro Val Glu Trp Phe Ser Ile	
190 195 200	
ggg ttt gac tgg acc tgg atg ctg ctg ttt ggt gac atc cga cag ggc	1035
Gly Phe Asp Trp Thr Trp Met Leu Leu Phe Gly Asp Ile Arg Gln Gly	
205 210 215 220	
atc ttc tat gcg atg ctt ctg tcc ttc tgg atc atc ttc tgt ggc gag	1083
Ile Phe Tyr Ala Met Leu Leu Ser Phe Trp Ile Ile Phe Cys Gly Glu	
225 230 235	
cac atg atg gat cag cac gag cgg aac cac atc gca ggg tat tgg aag	1131
His Met Met Asp Gln His Glu Arg Asn His Ile Ala Gly Tyr Trp Lys	
240 245 250	
caa gtc gga ccc att gcc gtt ggc tcc ttc tgc ctc ttc ata ttt gac	1179
Gln Val Gly Pro Ile Ala Val Gly Ser Phe Cys Leu Phe Ile Phe Asp	
255 260 265	
atg tgt gag aga ggg gta caa ctc acg aat ccc ttc tac agt atc tgg	1227
Met Cys Glu Arg Gly Val Gln Leu Thr Asn Pro Phe Tyr Ser Ile Trp	
270 275 280	
act aca gac att gga aca gag ctg gcc atg gcc ttc atc atc gtg gct	1275
Thr Thr Asp Ile Gly Thr Glu Leu Ala Met Ala Phe Ile Ile Val Ala	
285 290 295 300	
gga atc tgc ctc tgc ctc tac ttc ctg ttt cta tgc ttc atg gta ttt	1323
Gly Ile Cys Leu Cys Leu Tyr Phe Leu Phe Leu Cys Phe Met Val Phe	
305 310 315	
cag gtg ttt cgg aac atc agt ggg aag cag tcc agc ctg cca gct atg	1371
Gln Val Phe Arg Asn Ile Ser Gly Lys Gln Ser Ser Leu Pro Ala Met	
320 325 330	
agc aaa gtc cgg cgg cta cac tat gag ggg cta att ttt agg ttc aag	1419
Ser Lys Val Arg Arg Leu His Tyr Glu Gly Leu Ile Phe Arg Phe Lys	
335 340 345	
ttc ctc atg ctt atc acc ttg gcc tgc gct gcc atg act gtc atc ttc	1467
Phe Leu Met Leu Ile Thr Leu Ala Cys Ala Ala Met Thr Val Ile Phe	
350 355 360	
ttc atc gtt agt cag gta acg gaa ggc cat tgg aaa tgg ggc ggc atc	1515
Phe Ile Val Ser Gln Val Thr Glu Gly His Trp Lys Trp Gly Gly Ile	
365 370 375 380	

aca gtc caa gtg aac agt gcc ttt ttc aca ggc atc tat ggg atg tgg 1563
 Thr Val Gln Val Asn Ser Ala Phe Phe Thr Gly Ile Tyr Gly Met Trp
 385 390 395

aat ctg tat gtc ttt gct ctg atg ttc ttg tat gca cca tcc cat aaa 1611
 Asn Leu Tyr Val Phe Ala Leu Met Phe Leu Tyr Ala Pro Ser His Lys
 400 405 410

aac tat gga gaa gac cag tcc aat gga atg caa ctc cca tgt aaa tcg 1659
 Asn Tyr Gly Glu Asp Gln Ser Asn Gly Met Gln Leu Pro Cys Lys Ser
 415 420 425

agg gaa gat tgt gct ttg ttt gtt tcg gaa ctt tat caa gaa ttg ttc 1707
 Arg Glu Asp Cys Ala Leu Phe Val Ser Glu Leu Tyr Gln Glu Leu Phe
 430 435 440

agc gct tcg aaa tat tcc ttc atc aat gac aac gca gct tct ggt att 1755
 Ser Ala Ser Lys Tyr Ser Phe Ile Asn Asp Asn Ala Ala Ser Gly Ile
 445 450 455 460

tgagtcaaca aggcaacaca tgtttatcag ctttgcat ttc gcagttgtca cagtcacatt 1815

gattgtactt gtatacgcac acaaatacac tcatttagcc tttatctcaa aatgttaa at 1875

ataaggaaaa aagcgtcaac aataaatatt ctttgagtat tgtc 1919

<210> 149
 <211> 183
 <212> PRT
 <213> Homo sapiens

<400> 149
 Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro
 1 5 10 15

Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile
 20 25 30

Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val
 35 40 45

Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val
 50 55 60

Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr
 65 70 75 80

Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu
 85 90 95

Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val
 100 105 110

Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn
 115 120 125


```

---
Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ala Ser
  130                      135                      140
Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala
 145                      150                      155                      160
Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe
      165                      170                      175
Asp Arg His Lys Met Leu Ser
      180

```

```

<210> 150
<211> 1562
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (120)..(668)

```

```

<400> 150
tacggctgcg agaagacgac agaaggggat taagaggag ggcggggaca actgggtctt 60
ttgcggctgc agcgggcttg taggtgtccg gctttgctgg cccagcaagc ctgataagc 119
atg aag ctc tta tct ttg gtg gct gtg gtc ggg tgt ttg ctg gtg ccc 167
Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro
  1                      5                      10                      15
cca gct gaa gcc aac aag agt tct gaa gat atc cgg tgc aaa tgc atc 215
Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile
      20                      25                      30
tgt cca cct tat aga aac atc agt ggg cac att tac aac cag aat gta 263
Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val
      35                      40                      45
tcc cag aag gac tgc aac tgc ctg cac gtg gtg gag ccc atg cca gtg 311
Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val
      50                      55                      60
cct ggc cat gac gtg gag gcc tac tgc ctg ctg tgc gag tgc agg tac 359
Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr
      65                      70                      75                      80
gag gag cgc agc acc acc acc atc aag gtc atc att gtc atc tac ctg 407
Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu
      85                      90                      95
tcc gtg gtg ggt gcc ctg ttg ctc tac atg gcc ttc ctg atg ctg gtg 455
Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val
      100                      105                      110
gac cct ctg atc cga aag ccg gat gca tat act gag caa ctg cac aat 503
Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn

```

```

----- 115 ----- 120 ----- 125 -----
gag gag gag aat gag gat gct cgc tct atg gca gca gct gct gca tcc 551
Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ser
      130              135              140

ctc ggg gga ccc cga gca aac aca gtc ctg gag cgt gtg gaa ggt gcc 599
Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala
145              150              155              160

cag cag cgg tgg aag ctg cag gtg cag gag cag cgg aag aca gtc ttc 647
Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe
              165              170              175

gat cgg cac aag atg ctc agc tagatgggct ggtgtggttg ggtcaaggcc 698
Asp Arg His Lys Met Leu Ser
              180

ccaacacccat ggctgccagc ttccaggctg gacaaagcag ggggctactt ctcccttccc 758

tcggttccag tcttcccttt aaaagcctgt ggcatttttc ctcccttctcc ctaacttttag 818

aaatgttgta cttggctatt ttgattaggg aagaggggatg tggctctctga tctccgttgt 878

cttcttgggt ctttgggggt gaagggaggg ggaaggcagg ccagaaggga atggagacat 938

tcgaggcggc ctcaggagtg gatgcgatct gtctctcctg gctccactct tgccgccttc 998

cagctctgag tcttggaat gttgttacct ttggaagata aagctgggtc ttcaggaact 1058

cagtgtctgg gaggaagca tggcccagca ttcagcatgt gttcctttct gcagtgggtc 1118

tttatcacca cctccctccc agccccagcg cctcagcccc agccccagct ccagccctga 1178

ggacagctct gatgggagag ctgggcccc tgagccact gggctctcag ggtgcactgg 1238

aagctggtgt tcgctgtccc ctgtgcactt ctgcactgg ggcattggagt gcccatgcat 1298

actctgctgc cggccccctc acctgcactt gaggggtctg ggcagtcct cctctcccca 1358

gtgtccacag tcaactgagc agacggtcgg ttggaacatg agactcgagg ctgagcgtgg 1418

atctgaacac cacagcccct gtacttgggt tgccctttgt cctgaactt cgttgtacca 1478

gtgcatggag agaaaatttt gtcctcttgt cttagagttg tgtgtaaatc aaggaagcca 1538

tcattaaatt gttttatttc tctc 1562

```

```

<210> 151
<211> 2815
<212> DNA
<213> Mus musculus

```

```

<220>
<221> CDS
<222> (192)..(2387)

```

<400> 151
tctctctctcc tctctccagca gccaccaggg accgggagat ctaccagctc aagacccta 60
cagccagggtc tgtgctgccc ccctccagca tctttgcagc aggggacgag gctgtgtggg 120
aggctgtcgg ttccgaacat gtctccaccc accccaccct ctgtggctcc aggcttcatt 180
ctcccccatc c atg gat aac cca ggg cct tcg ctc cgt ggt gcc ttt ggc 230
Met Asp Asn Pro Gly Pro Ser Leu Arg Gly Ala Phe Gly
1 5 10
att cta ggt gcc ttg gaa agg gac agg ctg acc cac ctg aaa cac aag 278
Ile Leu Gly Ala Leu Glu Arg Asp Arg Leu Thr His Leu Lys His Lys
15 20 25
ctg ggg agt ctg tgt tca ggc agc cag gag tca aag ctt ctc cat gcc 326
Leu Gly Ser Leu Cys Ser Gly Ser Gln Glu Ser Lys Leu Leu His Ala
30 35 40 45
atg gta ctc ctg gct ctg ggc cag gac acg gag gcc agg gtc tct ctg 374
Met Val Leu Leu Ala Leu Gly Gln Asp Thr Glu Ala Arg Val Ser Leu
50 55 60
gag tcc ttg aag atg aac aca gta gcc cag ctg gta gcc cac cag tgg 422
Glu Ser Leu Lys Met Asn Thr Val Ala Gln Leu Val Ala His Gln Trp
65 70 75
gca gac atg gag acc aca gag ggc cct gag gag cct cca gac ttg tcc 470
Ala Asp Met Glu Thr Thr Glu Gly Pro Glu Glu Pro Pro Asp Leu Ser
80 85 90
tgg acg gtg gct cgc ctg tac cac ctg ctg gct gag gag aac ctg tgt 518
Trp Thr Val Ala Arg Leu Tyr His Leu Leu Ala Glu Glu Asn Leu Cys
95 100 105
ccg gcc tct aca agg gac atg gct tac cag gtg gcc ctt cgt gac ttt 566
Pro Ala Ser Thr Arg Asp Met Ala Tyr Gln Val Ala Leu Arg Asp Phe
110 115 120 125
gcc tcc cag ggt gac cac cag ctg ggc caa ctc cag aat gag gcc tgg 614
Ala Ser Gln Gly Asp His Gln Leu Gly Gln Leu Gln Asn Glu Ala Trp
130 135 140
gat cgg tgc agt tca gat atc aag ggg gac ccc agt ggt ttc cag cca 662
Asp Arg Cys Ser Ser Asp Ile Lys Gly Asp Pro Ser Gly Phe Gln Pro
145 150 155
ctc cat tct cat cag ggt tcc ctg cag cca cct tca gca tcc cct gca 710
Leu His Ser His Gln Gly Ser Leu Gln Pro Pro Ser Ala Ser Pro Ala
160 165 170
gtg acc aga agc cag cct cgt ccc att gac aca cca gac tgg agt tgg 758
Val Thr Arg Ser Gln Pro Arg Pro Ile Asp Thr Pro Asp Trp Ser Trp
175 180 185
gga cat acg tta cac tcc acc aac agc act gcc tca ctg gcc agc cac 806

Gly	His	Thr	Leu	His	Ser	Thr	Asn	Ser	Thr	Ala	Ser	Leu	Ala	Ser	His	
190					195					200					205	
cta	gag	atc	agc	cag	tca	ccc	act	ctt	gcc	ttt	ctc	tct	tca	cac	cat	854
Leu	Glu	Ile	Ser	Gln	Ser	Pro	Thr	Leu	Ala	Phe	Leu	Ser	Ser	His	His	
				210					215					220		
gga	acc	cat	ggg	ccc	agc	aag	cta	tgt	aac	aca	ccg	ctg	gac	act	cag	902
Gly	Thr	His	Gly	Pro	Ser	Lys	Leu	Cys	Asn	Thr	Pro	Leu	Asp	Thr	Gln	
			225					230					235			
gag	cct	cag	ctt	gtc	cct	gaa	ggc	tgc	caa	gaa	cct	gag	gag	ata	agc	950
Glu	Pro	Gln	Leu	Val	Pro	Glu	Gly	Cys	Gln	Glu	Pro	Glu	Glu	Ile	Ser	
		240					245					250				
tgg	cct	cca	tca	gtg	gag	acc	agt	gtc	tcc	tta	ggg	tta	cca	cac	gaa	998
Trp	Pro	Pro	Ser	Val	Glu	Thr	Ser	Val	Ser	Leu	Gly	Leu	Pro	His	Glu	
	255					260					265					
att	agc	gtt	cca	gag	gtg	tct	cca	gag	gag	gct	tcg	ccc	atc	ctc	cct	1046
Ile	Ser	Val	Pro	Glu	Val	Ser	Pro	Glu	Glu	Ala	Ser	Pro	Ile	Leu	Pro	
270					275					280					285	
gac	gcc	ctg	gct	gct	cca	gac	aca	agt	gtc	cac	tgt	ccc	att	gaa	tgc	1094
Asp	Ala	Leu	Ala	Ala	Pro	Asp	Thr	Ser	Val	His	Cys	Pro	Ile	Glu	Cys	
				290					295					300		
aca	gag	ttg	tct	aca	aac	tcc	agg	tct	ccc	ctg	acg	tcc	acc	aca	gaa	1142
Thr	Glu	Leu	Ser	Thr	Asn	Ser	Arg	Ser	Pro	Leu	Thr	Ser	Thr	Thr	Glu	
			305					310					315			
agt	gtt	gga	aag	cag	tgg	cct	att	aca	agt	cag	agg	tca	cct	cag	gtt	1190
Ser	Val	Gly	Lys	Gln	Trp	Pro	Ile	Thr	Ser	Gln	Arg	Ser	Pro	Gln	Val	
		320					325					330				
cct	gta	gga	gat	gat	tct	ctg	cag	aac	acc	acg	tca	tcc	agc	cct	cct	1238
Pro	Val	Gly	Asp	Asp	Ser	Leu	Gln	Asn	Thr	Thr	Ser	Ser	Ser	Pro	Pro	
		335				340					345					
gcc	cag	cca	cca	tcc	ctc	caa	gcc	tcc	cct	aag	ctg	cct	cct	tcc	cct	1286
Ala	Gln	Pro	Pro	Ser	Leu	Gln	Ala	Ser	Pro	Lys	Leu	Pro	Pro	Ser	Pro	
350					355					360					365	
ctg	tcc	tct	gct	tcc	tcc	ccg	agc	agc	tac	cct	gct	cct	cca	acc	tcc	1334
Leu	Ser	Ser	Ala	Ser	Ser	Pro	Ser	Ser	Tyr	Pro	Ala	Pro	Pro	Thr	Ser	
				370					375					380		
aca	tcc	cct	gtt	ttg	gac	cac	tca	gaa	aca	tct	gat	cag	aaa	ttc	tat	1382
Thr	Ser	Pro	Val	Leu	Asp	His	Ser	Glu	Thr	Ser	Asp	Gln	Lys	Phe	Tyr	
			385					390					395			
aac	ttt	gtg	gtt	atc	cat	gcc	agg	gct	gat	gaa	cag	gtg	gcc	cta	cgt	1430
Asn	Phe	Val	Val	Ile	His	Ala	Arg	Ala	Asp	Glu	Gln	Val	Ala	Leu	Arg	
		400					405					410				
att	cgg	gag	aag	ctg	gag	acc	ctc	ggg	gta	cct	gac	ggg	gcc	acc	ttc	1478
Ile	Arg	Glu	Lys	Leu	Glu	Thr	Leu	Gly	Val	Pro	Asp	Gly	Ala	Thr	Phe	

415	420	425	
tgt gag gaa ttt cag gtg ccc ggg cgt ggt gag ctg cac tgt ctc caa			1526
Cys Glu Glu Phe Gln Val Pro Gly Arg Gly Glu Leu His Cys Leu Gln			
430	435	440	445
gat gcc atc gat cac tcg ggg ttc acg atc ctg ctc ctg act gct agc			1574
Asp Ala Ile Asp His Ser Gly Phe Thr Ile Leu Leu Leu Thr Ala Ser			
	450	455	460
ttt gat tgc agc ctg agc ctg cat caa atc aac cat gct ctc atg aac			1622
Phe Asp Cys Ser Leu Ser Leu His Gln Ile Asn His Ala Leu Met Asn			
	465	470	475
agc ctt aca cag tct ggg agg cag gac tgt gtg atc ccc ctc ctc cca			1670
Ser Leu Thr Gln Ser Gly Arg Gln Asp Cys Val Ile Pro Leu Leu Pro			
	480	485	490
ctt gag tgt tcc cag gcc cag ctc agc cca gat aca acc aga ctg ctc			1718
Leu Glu Cys Ser Gln Ala Gln Leu Ser Pro Asp Thr Thr Arg Leu Leu			
	495	500	505
cac agc att gtg tgg ctg gat gaa cac tcc cca atc ttc gcc aga aag			1766
His Ser Ile Val Trp Leu Asp Glu His Ser Pro Ile Phe Ala Arg Lys			
510	515	520	525
gtg gca aac acc ttc aag aca cag aag ctc cag gca cag cgg gta cgc			1814
Val Ala Asn Thr Phe Lys Thr Gln Lys Leu Gln Ala Gln Arg Val Arg			
	530	535	540
tgg aag aaa gcg cag gag gcc aga acc ctc aag gag cag agc ata cag			1862
Trp Lys Lys Ala Gln Glu Ala Arg Thr Leu Lys Glu Gln Ser Ile Gln			
	545	550	555
ctg gag gca gag cgg caa aac gtg gca gcc ata tct gct gcc tac aca			1910
Leu Glu Ala Glu Arg Gln Asn Val Ala Ala Ile Ser Ala Ala Tyr Thr			
	560	565	570
gcc tat gtc cat agc tat agg gcc tgg caa gca gag atg aac aaa ctt			1958
Ala Tyr Val His Ser Tyr Arg Ala Trp Gln Ala Glu Met Asn Lys Leu			
	575	580	585
ggg gtg gct ttt ggg aag aac ttg tca ctg ggg act cca aca ccc agc			2006
Gly Val Ala Phe Gly Lys Asn Leu Ser Leu Gly Thr Pro Thr Pro Ser			
590	595	600	605
tgg ccc gga tgt cca cag cca ata cct tct cat cct cag ggt ggt act			2054
Trp Pro Gly Cys Pro Gln Pro Ile Pro Ser His Pro Gln Gly Gly Thr			
	610	615	620
cca gtt ttc ccc tat tcc cca cag cct cca tcc ttc cct cag cct cca			2102
Pro Val Phe Pro Tyr Ser Pro Gln Pro Pro Ser Phe Pro Gln Pro Pro			
	625	630	635
tgc ttc cct cag cct cca tcc ttc cct cag cct cca tcc ttc cca ctg			2150
Cys Phe Pro Gln Pro Pro Ser Phe Pro Gln Pro Pro Ser Phe Pro Leu			
	640	645	650

cct cca gtc tct tcc cca cag tcc caa tcc ttt cca tca gcc tcc tcc 2198
Pro Pro Val Ser Ser Pro Gln Ser Gln Ser Phe Pro Ser Ala Ser Ser
655 660 665

cca gcc cca cag act cca gga cct cag cct ctc att att cac cat gcc 2246
Pro Ala Pro Gln Thr Pro Gly Pro Gln Pro Leu Ile Ile His His Ala
670 675 680 685

cag atg gtt cag ctg ggt gtc aac aat cac atg tgg ggc cac aca ggg 2294
Gln Met Val Gln Leu Gly Val Asn Asn His Met Trp Gly His Thr Gly
690 695 700

gcc cag tca tct gat gac aag act gag tgt tgc gag aac ccc tgt atg 2342
Ala Gln Ser Ser Asp Asp Lys Thr Glu Cys Ser Glu Asn Pro Cys Met
705 710 715

ggc cct ctg act gat cag ggc gaa ccc ctt ctt gag act cca gag 2387
Gly Pro Leu Thr Asp Gln Gly Glu Pro Leu Leu Glu Thr Pro Glu
720 725 730

tgaccagggtt ggaccccacc tagatggcta gagtgacaag attggacttc acctgggtcc 2447
ttaaagtat agtggaggaa gggaacctcg cctgggtccc cagagtagcc agaggactta 2507
gcttgggctc ccacagtggc tattagttgg acccagcttg agaccccaga ggcaggggaag 2567
accacaccta taaatcaggc ctgggaaaca tgcagaaacc ccatttgaac agactgtggg 2627
actccaatct gaatcctcta tgtggacaga ggatgatggg gccagaggca cctctgaggt 2687
gccctcagcg cagcctcgta aacttcattc actgtgacac atgctgttca taggggtctct 2747
ctggggagga tgcgggtccg gggcacatag ggagggctct gtttttataa taaagttatt 2807
gacaactg 2815

<210> 152
<211> 732
<212> PRT
<213> Mus musculus

<400> 152
Met Asp Asn Pro Gly Pro Ser Leu Arg Gly Ala Phe Gly Ile Leu Gly
1 5 10 15
Ala Leu Glu Arg Asp Arg Leu Thr His Leu Lys His Lys Leu Gly Ser
20 25 30
Leu Cys Ser Gly Ser Gln Glu Ser Lys Leu Leu His Ala Met Val Leu
35 40 45
Leu Ala Leu Gly Gln Asp Thr Glu Ala Arg Val Ser Leu Glu Ser Leu
50 55 60
Lys Met Asn Thr Val Ala Gln Leu Val Ala His Gln Trp Ala Asp Met

370	375	380
Val Leu Asp His Ser Glu Thr Ser Asp Gln Lys Phe Tyr Asn Phe Val		
385	390	395 400
Val Ile His Ala Arg Ala Asp Glu Gln Val Ala Leu Arg Ile Arg Glu		
	405	410 415
Lys Leu Glu Thr Leu Gly Val Pro Asp Gly Ala Thr Phe Cys Glu Glu		
	420	425 430
Phe Gln Val Pro Gly Arg Gly Glu Leu His Cys Leu Gln Asp Ala Ile		
	435	440 445
Asp His Ser Gly Phe Thr Ile Leu Leu Leu Thr Ala Ser Phe Asp Cys		
	450	455 460
Ser Leu Ser Leu His Gln Ile Asn His Ala Leu Met Asn Ser Leu Thr		
465	470	475 480
Gln Ser Gly Arg Gln Asp Cys Val Ile Pro Leu Leu Pro Leu Glu Cys		
	485	490 495
Ser Gln Ala Gln Leu Ser Pro Asp Thr Thr Arg Leu Leu His Ser Ile		
	500	505 510
Val Trp Leu Asp Glu His Ser Pro Ile Phe Ala Arg Lys Val Ala Asn		
	515	520 525
Thr Phe Lys Thr Gln Lys Leu Gln Ala Gln Arg Val Arg Trp Lys Lys		
	530	535 540
Ala Gln Glu Ala Arg Thr Leu Lys Glu Gln Ser Ile Gln Leu Glu Ala		
545	550	555 560
Glu Arg Gln Asn Val Ala Ala Ile Ser Ala Ala Tyr Thr Ala Tyr Val		
	565	570 575
His Ser Tyr Arg Ala Trp Gln Ala Glu Met Asn Lys Leu Gly Val Ala		
	580	585 590
Phe Gly Lys Asn Leu Ser Leu Gly Thr Pro Thr Pro Ser Trp Pro Gly		
	595	600 605
Cys Pro Gln Pro Ile Pro Ser His Pro Gln Gly Gly Thr Pro Val Phe		
610	615	620
Pro Tyr Ser Pro Gln Pro Pro Ser Phe Pro Gln Pro Pro Cys Phe Pro		
625	630	635 640
Gln Pro Pro Ser Phe Pro Gln Pro Pro Ser Phe Pro Leu Pro Pro Val		
	645	650 655
Ser Ser Pro Gln Ser Gln Ser Phe Pro Ser Ala Ser Ser Pro Ala Pro		
	660	665 670
Gln Thr Pro Gly Pro Gln Pro Leu Ile Ile His His Ala Gln Met Val		

675	680	685
Gln Leu Gly Val Asn Asn His Met Trp Gly His Thr Gly Ala Gln Ser		
690	695	700
Ser Asp Asp Lys Thr Glu Cys Ser Glu Asn Pro Cys Met Gly Pro Leu		
705	710	715
		720
Thr Asp Gln Gly Glu Pro Leu Leu Glu Thr Pro Glu		
	725	730

<210> 153
 <211> 2544
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (97)..(2232)

<400> 153
 taggggacac tgggcgtgca gaaggcgggg ggcagtgtgg aacatgcctt caccacctcc 60
 agcttctgct gccggaggct gcacccacct gtgccc atg gcc tgc aca ggc cca 114
 Met Ala Cys Thr Gly Pro
 1 5
 tca ctt cct agc gcc ttc gac att cta ggt gca gca ggc cag gac aag 162
 Ser Leu Pro Ser Ala Phe Asp Ile Leu Gly Ala Ala Gly Gln Asp Lys
 10 15 20
 ctc ttg tat ctg aag cac aaa ctg aag acc cca cgc cca ggc tgc cag 210
 Leu Leu Tyr Leu Lys His Lys Leu Lys Thr Pro Arg Pro Gly Cys Gln
 25 30 35
 ggg cag gac ctc ctg cat gcc atg gtt ctc ctg aag ctg ggc cag gaa 258
 Gly Gln Asp Leu Leu His Ala Met Val Leu Leu Lys Leu Gly Gln Glu
 40 45 50
 act gag gcc agg atc tct cta gag gca ttg aag gcc gat gcg gtg gcc 306
 Thr Glu Ala Arg Ile Ser Leu Glu Ala Leu Lys Ala Asp Ala Val Ala
 55 60 65 70
 cgg ctg gtg gcc cgc cag tgg gct ggc gtg gac agc acc gag gac cca 354
 Arg Leu Val Ala Arg Gln Trp Ala Gly Val Asp Ser Thr Glu Asp Pro
 75 80 85
 gag gag ccc cca gat gtg tcc tgg gct gtg gcc cgc ttg tac cac ctg 402
 Glu Glu Pro Pro Asp Val Ser Trp Ala Val Ala Arg Leu Tyr His Leu
 90 95 100
 ctg gct gag gag aag ctg tgc ccc gcc tcg ctg cgg gac gtg gcc tac 450
 Leu Ala Glu Glu Lys Leu Cys Pro Ala Ser Leu Arg Asp Val Ala Tyr
 105 110 115
 cag gaa gcc gtc cgc acc ctc agc tcc agg gac gac cac cgg ctg ggg 498

Gln	Glu	Ala	Val	Arg	Thr	Leu	Ser	Ser	Arg	Asp	Asp	His	Arg	Leu	Gly		
120						125					130						
gaa	ctt	cag	gat	gag	gcc	cga	aac	cgg	tgt	ggg	tgg	gac	att	gct	ggg	546	
Glu	Leu	Gln	Asp	Glu	Ala	Arg	Asn	Arg	Cys	Gly	Trp	Asp	Ile	Ala	Gly		
135					140					145					150		
gat	cca	ggg	agc	atc	cgg	acg	ctc	cag	tcc	aat	ctg	ggc	tgc	ctc	cca	594	
Asp	Pro	Gly	Ser	Ile	Arg	Thr	Leu	Gln	Ser	Asn	Leu	Gly	Cys	Leu	Pro		
				155					160						165		
cca	tcc	tcg	gct	ttg	ccc	tct	ggg	acc	agg	agc	ctc	cca	cgc	ccc	att	642	
Pro	Ser	Ser	Ala	Leu	Pro	Ser	Gly	Thr	Arg	Ser	Leu	Pro	Arg	Pro	Ile		
			170					175					180				
gac	ggt	gtt	tcg	gac	tgg	agc	caa	ggg	tgc	tcc	ctg	cga	tcc	act	ggc	690	
Asp	Gly	Val	Ser	Asp	Trp	Ser	Gln	Gly	Cys	Ser	Leu	Arg	Ser	Thr	Gly		
		185					190					195					
agc	cct	gcc	tcc	ctg	gcc	agc	aac	ttg	gaa	atc	agc	cag	tcc	cct	acc	738	
Ser	Pro	Ala	Ser	Leu	Ala	Ser	Asn	Leu	Glu	Ile	Ser	Gln	Ser	Pro	Thr		
	200					205					210						
atg	ccc	ttc	ctc	agc	ctg	cac	cgc	agc	cca	cat	ggg	ccc	agc	aag	ctc	786	
Met	Pro	Phe	Leu	Ser	Leu	His	Arg	Ser	Pro	His	Gly	Pro	Ser	Lys	Leu		
215					220					225					230		
tgt	gac	gac	ccc	cag	gcc	agc	ttg	gtg	ccc	gag	cct	gtc	ccc	ggt	ggc	834	
Cys	Asp	Asp	Pro	Gln	Ala	Ser	Leu	Val	Pro	Glu	Pro	Val	Pro	Gly	Gly		
				235					240					245			
tgc	cag	gag	cct	gag	gag	atg	agc	tgg	ccg	cca	tcg	ggg	gag	att	gcc	882	
Cys	Gln	Glu	Pro	Glu	Glu	Met	Ser	Trp	Pro	Pro	Ser	Gly	Glu	Ile	Ala		
			250					255					260				
agc	cca	cca	gag	ctg	cca	agc	agc	cca	cct	cct	ggg	ctt	ccc	gaa	gtg	930	
Ser	Pro	Pro	Glu	Leu	Pro	Ser	Ser	Pro	Pro	Pro	Gly	Leu	Pro	Glu	Val		
		265					270					275					
gcc	cca	gat	gca	acc	tcc	act	ggc	ctc	cct	gat	acc	ccc	gca	gct	cca	978	
Ala	Pro	Asp	Ala	Thr	Ser	Thr	Gly	Leu	Pro	Asp	Thr	Pro	Ala	Ala	Pro		
	280					285					290						
gaa	acc	agc	acc	aac	tac	cca	gtg	gag	tgc	acc	gag	ggg	tct	gca	ggc	1026	
Glu	Thr	Ser	Thr	Asn	Tyr	Pro	Val	Glu	Cys	Thr	Glu	Gly	Ser	Ala	Gly		
295				300						305					310		
ccc	cag	tct	ctc	ccc	ttg	cct	att	ctg	gag	ccg	gtc	aaa	aac	ccc	tgc	1074	
Pro	Gln	Ser	Leu	Pro	Leu	Pro	Ile	Leu	Glu	Pro	Val	Lys	Asn	Pro	Cys		
				315					320					325			
tct	gtc	aaa	gac	cag	acg	cca	ctc	caa	ctt	tct	gta	gaa	gat	acc	acc	1122	
Ser	Val	Lys	Asp	Gln	Thr	Pro	Leu	Gln	Leu	Ser	Val	Glu	Asp	Thr	Thr		
			330					335					340				
tct	cca	aat	acc	aag	ccg	tgc	cca	cct	act	ccc	acc	acc	cca	gaa	aca	1170	
Ser	Pro	Asn	Thr	Lys	Pro	Cys	Pro	Pro	Thr	Pro	Thr	Thr	Pro	Glu	Thr		

	345		350		355		
tcc cct cct cct cct cct cct cct cct tca tct act cct tgt tca gct	1218						
Ser Pro Pro Pro Pro Pro Pro Pro Pro Ser Ser Thr Pro Cys Ser Ala							
360		365		370			
cac ctg acc ccc tcc tcc ctg ttc cct tcc tcc ctg gaa tca tca tcg	1266						
His Leu Thr Pro Ser Ser Leu Phe Pro Ser Ser Leu Glu Ser Ser Ser							
375		380		385			390
gaa cag aaa ttc tat aac ttt gtg atc ctc cac gcc agg gca gac gaa	1314						
Glu Gln Lys Phe Tyr Asn Phe Val Ile Leu His Ala Arg Ala Asp Glu							
	395		400			405	
cac atc gcc ctg cgg gtt cgg gag aag ctg gag gcc ctt ggc gtg ccc	1362						
His Ile Ala Leu Arg Val Arg Glu Lys Leu Glu Ala Leu Gly Val Pro							
	410		415			420	
gac ggg gcc acc ttc tgc gag gat ttc cag gtg ccg ggg cgc ggg gag	1410						
Asp Gly Ala Thr Phe Cys Glu Asp Phe Gln Val Pro Gly Arg Gly Glu							
	425		430			435	
ctg agc tgc ctg cag gac gcc ata gac cac tca gct ttc atc atc cta	1458						
Leu Ser Cys Leu Gln Asp Ala Ile Asp His Ser Ala Phe Ile Ile Leu							
	440		445			450	
ctt ctc acc tcc aac ttc gac tgt cgc ctg agc ctg cac cag gtg aac	1506						
Leu Leu Thr Ser Asn Phe Asp Cys Arg Leu Ser Leu His Gln Val Asn							
455		460		465		470	
caa gcc atg atg agc aac ctc acg cga cag ggg tcg cca gac tgt gtc	1554						
Gln Ala Met Met Ser Asn Leu Thr Arg Gln Gly Ser Pro Asp Cys Val							
	475		480			485	
atc ccc ttc ctg ccc ctg gag agc tcc ccg gcc cag ctc agc tcc gac	1602						
Ile Pro Phe Leu Pro Leu Glu Ser Ser Pro Ala Gln Leu Ser Ser Asp							
	490		495			500	
acg gcc agc ctg ctc tcc ggg ctg gtg cgg ctg gac gaa cac tcc cag	1650						
Thr Ala Ser Leu Leu Ser Gly Leu Val Arg Leu Asp Glu His Ser Gln							
	505		510			515	
atc ttc gcc agg aag gtg gcc aac acc ttc aag ccc cac agg ctt cag	1698						
Ile Phe Ala Arg Lys Val Ala Asn Thr Phe Lys Pro His Arg Leu Gln							
	520		525			530	
gcc cga aag gcc atg tgg agg aag gaa cag gac acc cga gcc ctg cgg	1746						
Ala Arg Lys Ala Met Trp Arg Lys Glu Gln Asp Thr Arg Ala Leu Arg							
535		540		545		550	
gaa cag agc caa cac ctg gac ggt gag cgg atg cag gcg gcg gca ctg	1794						
Glu Gln Ser Gln His Leu Asp Gly Glu Arg Met Gln Ala Ala Ala Leu							
	555		560			565	
aac gca gcc tac tca gcc tac ctc cag agc tac ttg tcc tac cag gca	1842						
Asn Ala Ala Tyr Ser Ala Tyr Leu Gln Ser Tyr Leu Ser Tyr Gln Ala							
	570		575			580	

cag atg gag cag ctc cag gtg gct ttt ggg agc cac atg tca ttt ggg	1890
Gln Met Glu Gln Leu Gln Val Ala Phe Gly Ser His Met Ser Phe Gly	
585 590 595	
act ggg gcg ccc tat ggg gct cga atg ccc ttt ggg ggc cag gtg ccc	1938
Thr Gly Ala Pro Tyr Gly Ala Arg Met Pro Phe Gly Gly Gln Val Pro	
600 605 610	
ctg gga gcc ccg cca ccc ttt ccc act tgg ccg ggg tgc ccg cag ccg	1986
Leu Gly Ala Pro Pro Phe Pro Thr Trp Pro Gly Cys Pro Gln Pro	
615 620 625 630	
cca ccc ctg cac gca tgg cag gct ggc acc ccc cca ccg ccc tcc cca	2034
Pro Pro Leu His Ala Trp Gln Ala Gly Thr Pro Pro Pro Pro Ser Pro	
635 640 645	
cag cca gca gcc ttt cca cag tca ctg ccc ttc ccg cag tcc cca gcc	2082
Gln Pro Ala Ala Phe Pro Gln Ser Leu Pro Phe Pro Gln Ser Pro Ala	
650 655 660	
ttc cct acg gcc tca ccc gca ccc cct cag agc cca ggg ctg caa ccc	2130
Phe Pro Thr Ala Ser Pro Ala Pro Pro Gln Ser Pro Gly Leu Gln Pro	
665 670 675	
ctc att atc cac cac gca cag atg gta cag ctg ggg ctg aac aac cac	2178
Leu Ile Ile His His Ala Gln Met Val Gln Leu Gly Leu Asn Asn His	
680 685 690	
atg tgg aac cag aga ggg tcc cag gcg ccc gag gac aag acg cag gag	2226
Met Trp Asn Gln Arg Gly Ser Gln Ala Pro Glu Asp Lys Thr Gln Glu	
695 700 705 710	
gca gaa tgaccgcgtg tccttgccctg accacctggg gaacacccct ggacccaggc	2282
Ala Glu	
atcggccagg accccataga gcaccccggt ctgccctgtg ccctgtggac agtggaagat	2342
gaggtcacatc gccactttca ggacattgtc cgggagccct tcatttagga caaaacgggc	2402
gcgatgatgc cctggctttc aggggtggtca gaactggata cgggtgtttac aattccaatc	2462
tctctatttc tgggtgaagg gtcttggtgg tgggggtatt gctacggtct tttaattata	2522
ataaatattt attgaatgct tc	2544

<210> 154
 <211> 712
 <212> PRT
 <213> Homo sapiens

<400> 154
 Met Ala Cys Thr Gly Pro Ser Leu Pro Ser Ala Phe Asp Ile Leu Gly
 1 5 10 15
 Ala Ala Gly Gln Asp Lys Leu Leu Tyr Leu Lys His Lys Leu Lys Thr

			20				25				30				
Pro	Arg	Pro	Gly	Cys	Gln	Gly	Gln	Asp	Leu	Leu	His	Ala	Met	Val	Leu
		35					40					45			
Leu	Lys	Leu	Gly	Gln	Glu	Thr	Glu	Ala	Arg	Ile	Ser	Leu	Glu	Ala	Leu
		50					55					60			
Lys	Ala	Asp	Ala	Val	Ala	Arg	Leu	Val	Ala	Arg	Gln	Trp	Ala	Gly	Val
		65					70					75			
Asp	Ser	Thr	Glu	Asp	Pro	Glu	Glu	Pro	Pro	Asp	Val	Ser	Trp	Ala	Val
					85					90					95
Ala	Arg	Leu	Tyr	His	Leu	Leu	Ala	Glu	Glu	Lys	Leu	Cys	Pro	Ala	Ser
			100							105					110
Leu	Arg	Asp	Val	Ala	Tyr	Gln	Glu	Ala	Val	Arg	Thr	Leu	Ser	Ser	Arg
		115					120					125			
Asp	Asp	His	Arg	Leu	Gly	Glu	Leu	Gln	Asp	Glu	Ala	Arg	Asn	Arg	Cys
		130					135					140			
Gly	Trp	Asp	Ile	Ala	Gly	Asp	Pro	Gly	Ser	Ile	Arg	Thr	Leu	Gln	Ser
		145					150					155			
Asn	Leu	Gly	Cys	Leu	Pro	Pro	Ser	Ser	Ala	Leu	Pro	Ser	Gly	Thr	Arg
					165					170					175
Ser	Leu	Pro	Arg	Pro	Ile	Asp	Gly	Val	Ser	Asp	Trp	Ser	Gln	Gly	Cys
			180							185					190
Ser	Leu	Arg	Ser	Thr	Gly	Ser	Pro	Ala	Ser	Leu	Ala	Ser	Asn	Leu	Glu
		195					200					205			
Ile	Ser	Gln	Ser	Pro	Thr	Met	Pro	Phe	Leu	Ser	Leu	His	Arg	Ser	Pro
		210					215					220			
His	Gly	Pro	Ser	Lys	Leu	Cys	Asp	Asp	Pro	Gln	Ala	Ser	Leu	Val	Pro
		225					230					235			
Glu	Pro	Val	Pro	Gly	Gly	Cys	Gln	Glu	Pro	Glu	Glu	Met	Ser	Trp	Pro
					245					250					255
Pro	Ser	Gly	Glu	Ile	Ala	Ser	Pro	Pro	Glu	Leu	Pro	Ser	Ser	Pro	Pro
			260							265					270
Pro	Gly	Leu	Pro	Glu	Val	Ala	Pro	Asp	Ala	Thr	Ser	Thr	Gly	Leu	Pro
		275					280					285			
Asp	Thr	Pro	Ala	Ala	Pro	Glu	Thr	Ser	Thr	Asn	Tyr	Pro	Val	Glu	Cys
		290					295					300			
Thr	Glu	Gly	Ser	Ala	Gly	Pro	Gln	Ser	Leu	Pro	Leu	Pro	Ile	Leu	Glu
		305					310					315			
Pro	Val	Lys	Asn	Pro	Cys	Ser	Val	Lys	Asp	Gln	Thr	Pro	Leu	Gln	Leu

Pro	Pro	Pro	Pro	Ser 645	Pro	Gln	Pro	Ala	Ala 650	Phe	Pro	Gln	Ser	Leu 655	Pro
Phe	Pro	Gln	Ser 660	Pro	Ala	Phe	Pro	Thr 665	Ala	Ser	Pro	Ala	Pro 670	Pro	Gln
Ser	Pro	Gly 675	Leu	Gln	Pro	Leu	Ile 680	Ile	His	His	Ala	Gln 685	Met	Val	Gln
Leu	Gly 690	Leu	Asn	Asn	His	Met 695	Trp	Asn	Gln	Arg	Gly 700	Ser	Gln	Ala	Pro
Glu 705	Asp	Lys	Thr	Gln	Glu 710	Ala	Glu								

```
<210> 155
<211> 3456
<212> DNA
<213> Homo sapiens
```

```
<220>  
<221> CDS  
<222> (281)..(3016)
```

<400> 155																
agcattcaag	gagctcccca	ggagaaagag	caagttctga	ggagccctct	gagcccggaa	60										
cgtgtccacc	cggtcatgcc	cgccgcgcac	cagccccgca	gtggacttgg	aggaggagga	120										
ggaggagagc	tctgtggatg	gcaaagggga	ccggaagagc	acaggcctga	aactctccaa	180										
gaagaaagca	aggaggagac	acacggatga	ccaagcaag	gaatgcttca	ctctgaaatt	240										
tgacctgaat	gtggacattg	agacagagat	cgtcccagcc	atg	aag	aag	aag	tca	295							
				Met	Lys	Lys	Lys	Ser								
				1				5								
ctg	ggg	gag	gtg	ctg	ctg	cct	gta	ttt	gaa	agg	aag	ggc	att	gcg	ctg	343
Leu	Gly	Glu	Val	Leu	Leu	Pro	Val	Phe	Glu	Arg	Lys	Gly	Ile	Ala	Leu	
			10					15						20		
ggc	aaa	gtg	gac	atc	tac	ctg	gac	cag	tcc	aac	aca	ccc	ctg	tcc	ctc	391
Gly	Lys	Val	Asp	Ile	Tyr	Leu	Asp	Gln	Ser	Asn	Thr	Pro	Leu	Ser	Leu	
			25					30						35		
acc	ttc	gag	gcc	tac	agg	ttc	ggg	gga	cac	tac	ctt	cgt	gtc	aaa	gcc	439
Thr	Phe	Glu	Ala	Tyr	Arg	Phe	Gly	Gly	His	Tyr	Leu	Arg	Val	Lys	Ala	
		40					45					50				
cca	gcc	aag	cct	gga	gat	gag	ggc	aag	gtg	gag	cag	ggc	atg	aag	gac	487
Pro	Ala	Lys	Pro	Gly	Asp	Glu	Gly	Lys	Val	Glu	Gln	Gly	Met	Lys	Asp	
	55					60					65					
tcc	aag	tcc	ctg	agt	ttg	ccg	att	ctg	cgg	cca	gct	ggg	acc	ggg	ccc	535

Ser	Lys	Ser	Leu	Ser	Leu	Pro	Ile	Leu	Arg	Pro	Ala	Gly	Thr	Gly	Pro	
70					75					80					85	
ccc	gcc	ctg	gag	cgt	gtg	gac	gcc	cag	agc	cgc	cgg	gag	agc	ctg	gac	583
Pro	Ala	Leu	Glu	Arg	Val	Asp	Ala	Gln	Ser	Arg	Arg	Glu	Ser	Leu	Asp	
				90					95					100		
atc	ttg	gcc	cct	ggc	cgc	cgc	cgc	aag	aac	atg	tcg	gag	ttc	ctg	ggg	631
Ile	Leu	Ala	Pro	Gly	Arg	Arg	Arg	Lys	Asn	Met	Ser	Glu	Phe	Leu	Gly	
			105					110					115			
gag	gcg	agc	atc	ccc	ggg	cag	gag	ccc	ccc	acg	ccc	tcc	agc	tgc	tct	679
Glu	Ala	Ser	Ile	Pro	Gly	Gln	Glu	Pro	Pro	Thr	Pro	Ser	Ser	Cys	Ser	
		120					125					130				
ctg	ccc	agc	ggc	agc	agt	ggc	agc	acc	aac	act	ggc	gac	agc	tgg	aag	727
Leu	Pro	Ser	Gly	Ser	Ser	Gly	Ser	Thr	Asn	Thr	Gly	Asp	Ser	Trp	Lys	
	135					140					145					
aac	cgg	gcg	gcc	agt	cgc	ttc	agc	ggc	ttt	ttc	agc	tcc	ggc	ccc	agc	775
Asn	Arg	Ala	Ala	Ser	Arg	Phe	Ser	Gly	Phe	Phe	Ser	Ser	Gly	Pro	Ser	
150					155				160					165		
acc	agc	gcc	ttt	ggc	cgg	gag	gta	gac	aag	atg	gag	cag	ctg	gag	ggc	823
Thr	Ser	Ala	Phe	Gly	Arg	Glu	Val	Asp	Lys	Met	Glu	Gln	Leu	Glu	Gly	
				170					175					180		
aag	ctg	cac	acc	tac	agc	ctc	ttc	ggg	ctg	ccc	agg	ctg	ccc	cgg	ggg	871
Lys	Leu	His	Thr	Tyr	Ser	Leu	Phe	Gly	Leu	Pro	Arg	Leu	Pro	Arg	Gly	
			185					190					195			
ctg	cgc	ttc	gac	cat	gac	tcc	tgg	gag	gag	gag	tac	gat	gaa	gac	gag	919
Leu	Arg	Phe	Asp	His	Asp	Ser	Trp	Glu	Glu	Glu	Tyr	Asp	Glu	Asp	Glu	
		200					205					210				
gat	gag	gac	aat	gcc	tgc	ctg	agg	ctg	gag	gac	agc	tgg	cgg	gag	ctc	967
Asp	Glu	Asp	Asn	Ala	Cys	Leu	Arg	Leu	Glu	Asp	Ser	Trp	Arg	Glu	Leu	
	215					220					225					
att	gat	ggg	cat	gag	aag	ctg	acc	cgg	cgg	cag	tgc	cac	cag	cag	gag	1015
Ile	Asp	Gly	His	Glu	Lys	Leu	Thr	Arg	Arg	Gln	Cys	His	Gln	Gln	Glu	
230					235					240				245		
gcg	gtg	tgg	gag	ctg	ctg	cac	acg	gag	gcc	tcc	tac	atc	agg	aaa	ctg	1063
Ala	Val	Trp	Glu	Leu	Leu	His	Thr	Glu	Ala	Ser	Tyr	Ile	Arg	Lys	Leu	
				250					255					260		
cgg	gtg	atc	atc	aac	ctg	ttc	ttg	tgc	tgc	ctc	ctg	aac	ctg	caa	gag	1111
Arg	Val	Ile	Ile	Asn	Leu	Phe	Leu	Cys	Cys	Leu	Leu	Asn	Leu	Gln	Glu	
			265					270				275				
tca	ggg	ctg	ctg	tgt	gag	gtg	gag	gcg	gag	cgc	ctg	ttc	agc	aac	atc	1159
Ser	Gly	Leu	Leu	Cys	Glu	Val	Glu	Ala	Glu	Arg	Leu	Phe	Ser	Asn	Ile	
		280					285					290				
ccg	gag	atc	gcg	cag	ctg	cac	cgc	agg	ctg	tgg	gct	agc	gtg	atg	gcg	1207
Pro	Glu	Ile	Ala	Gln	Leu	His	Arg	Arg	Leu	Trp	Ala	Ser	Val	Met	Ala	

295	300	305	
ccg gtg ctg gag aag gcg cgg cgc acg cga gcg ctg cta cag ccc ggg			1255
Pro Val Leu Glu Lys Ala Arg Arg Thr Arg Ala Leu Leu Gln Pro Gly			
310	315	320	325
gac ttc ctc aaa ggc ttc aag atg ttc ggc tcg ctc ttc aag ccc tac			1303
Asp Phe Leu Lys Gly Phe Lys Met Phe Gly Ser Leu Phe Lys Pro Tyr			
	330	335	340
atc cgc tac tgc atg gag gag gag ggc tgc atg gag tac atg cgc ggc			1351
Ile Arg Tyr Cys Met Glu Glu Glu Gly Cys Met Glu Tyr Met Arg Gly			
	345	350	355
ctg ctg cgc gac aac gac ctc ttc cgg gcc tac atc acg tgg gcg gag			1399
Leu Leu Arg Asp Asn Asp Leu Phe Arg Ala Tyr Ile Thr Trp Ala Glu			
	360	365	370
aag cac cca cag tgc cag agg ctg aag ctg agc gac atg ctg gcc aaa			1447
Lys His Pro Gln Cys Gln Arg Leu Lys Leu Ser Asp Met Leu Ala Lys			
	375	380	385
ccc cac cag cgg ctc acc aag tac ccg ctg ctg ctc aag tcg gtg ctg			1495
Pro His Gln Arg Leu Thr Lys Tyr Pro Leu Leu Leu Lys Ser Val Leu			
390	395	400	405
agg aag acc gag gag ccg cgc gcc aag gag gcc gtc gtc gcc atg atc			1543
Arg Lys Thr Glu Glu Pro Arg Ala Lys Glu Ala Val Val Ala Met Ile			
	410	415	420
ggc tcc gtg gag cgc ttc atc cac cac gtg aac gcg tgc atg cgg cag			1591
Gly Ser Val Glu Arg Phe Ile His His Val Asn Ala Cys Met Arg Gln			
	425	430	435
cgg cag gag cgg cag cgg ctg gcg gcc gtg gtg agc cgc atc gac gcc			1639
Arg Gln Glu Arg Gln Arg Leu Ala Ala Val Val Ser Arg Ile Asp Ala			
	440	445	450
tac gag gtg gtg gaa agc agc agc gac gaa gtg gac aag ctc ctg aag			1687
Tyr Glu Val Val Glu Ser Ser Ser Asp Glu Val Asp Lys Leu Leu Lys			
	455	460	465
gaa ttt ctg cac ctg gac ttg aca gcg ccc atc cct ggc gcc tcc ccg			1735
Glu Phe Leu His Leu Asp Leu Thr Ala Pro Ile Pro Gly Ala Ser Pro			
470	475	480	485
gag gag acg cgg cag ctg ctg ctg gag ggg agc ctg agg atg aag gag			1783
Glu Glu Thr Arg Gln Leu Leu Leu Glu Gly Ser Leu Arg Met Lys Glu			
	490	495	500
ggg aag gac agc aag atg gat gtg tac tgc ttc ctc ttc acg gat ctg			1831
Gly Lys Asp Ser Lys Met Asp Val Tyr Cys Phe Leu Phe Thr Asp Leu			
	505	510	515
ctg ttg gtg acc aaa gca gtg aag aag gca gag agg acc agg gtc atc			1879
Leu Leu Val Thr Lys Ala Val Lys Lys Ala Glu Arg Thr Arg Val Ile			
	520	525	530

agg cca ccc ctg ctc gtg gac aag att gtg tgc cgg gag cta cgg gac	1927
Arg Pro Pro Leu Leu Val Asp Lys Ile Val Cys Arg Glu Leu Arg Asp	
535 540 545	
cct ggg tcc ttc ctc ctt atc tac ctg aat gag ttt cac agt gct gta	1975
Pro Gly Ser Phe Leu Leu Ile Tyr Leu Asn Glu Phe His Ser Ala Val	
550 555 560 565	
ggg gcc tac acg ttc cag gcc agt ggc cag gcc ttg tgc cgt ggc tgg	2023
Gly Ala Tyr Thr Phe Gln Ala Ser Gly Gln Ala Leu Cys Arg Gly Trp	
570 575 580	
gtg gac acc att tac aat gcc cag aac cag ctg caa cag ctg cgt gca	2071
Val Asp Thr Ile Tyr Asn Ala Gln Asn Gln Leu Gln Gln Leu Arg Ala	
585 590 595	
cag gag ccc cca ggc agt cag cag ccc ctg cag agc ctg gaa gag gag	2119
Gln Glu Pro Pro Gly Ser Gln Gln Pro Leu Gln Ser Leu Glu Glu Glu	
600 605 610	
gag gat gag cag gag gag gaa gag gag gag gag gag gag gag gag gaa	2167
Glu Asp Glu Gln Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu	
615 620 625	
ggc gag gac agt ggc act tca gct gcc agc tcc cct acc atc atg cgg	2215
Gly Glu Asp Ser Gly Thr Ser Ala Ala Ser Ser Pro Thr Ile Met Arg	
630 635 640 645	
aaa agc agc ggc agc ccc gac tct cag cac tgt gcc tca gat ggc tcc	2263
Lys Ser Ser Gly Ser Pro Asp Ser Gln His Cys Ala Ser Asp Gly Ser	
650 655 660	
acg gag acc ctg gcc atg gtt gtg gta gag cct ggg gac acg ctg tcc	2311
Thr Glu Thr Leu Ala Met Val Val Val Glu Pro Gly Asp Thr Leu Ser	
665 670 675	
tcc ccc gag ttc gac agc ggt cct ttc agc tcc cag tct gat gag acc	2359
Ser Pro Glu Phe Asp Ser Gly Pro Phe Ser Ser Gln Ser Asp Glu Thr	
680 685 690	
tct ctc agc acc act gcc tca tct gcc acg ccc acc agt gag ctg ctg	2407
Ser Leu Ser Thr Thr Ala Ser Ser Ala Thr Pro Thr Ser Glu Leu Leu	
695 700 705	
ccc ctg ggt ccg gtg gac ggc cgc tcc tgc tcc atg gac tct gcc tac	2455
Pro Leu Gly Pro Val Asp Gly Arg Ser Cys Ser Met Asp Ser Ala Tyr	
710 715 720 725	
ggc acc ctc tcc cca acc tcc tta caa gac ttt gtg gcc cca ggc cca	2503
Gly Thr Leu Ser Pro Thr Ser Leu Gln Asp Phe Val Ala Pro Gly Pro	
730 735 740	
atg gca gag cta gtg cct cgg gcc cca gag tcc cca cga gtt cct tcc	2551
Met Ala Glu Leu Val Pro Arg Ala Pro Glu Ser Pro Arg Val Pro Ser	
745 750 755	

cct cca ccc tcg ccc cgt ctc cgc cgc cgc acc cct gtc cag ctg ttg	2599	-	-	-
Pro Pro Pro Ser Pro Arg Leu Arg Arg Arg Thr Pro Val Gln Leu Leu				
760 765 770				
agc tgc ccg ccc cac ctg ctc aag tct aag tcc gag gcc agc ctc ctc	2647			
Ser Cys Pro Pro His Leu Leu Lys Ser Lys Ser Glu Ala Ser Leu Leu				
775 780 785				
cag ctg ctg gca ggg gct ggc acc cat ggg aca ccc tct gcc ccc agc	2695			
Gln Leu Leu Ala Gly Ala Gly Thr His Gly Thr Pro Ser Ala Pro Ser				
790 795 800 805				
cgc agc ctg tca gag ctc tgc ctg gct gtt cca gcc cca ggt att agg	2743			
Arg Ser Leu Ser Glu Leu Cys Leu Ala Val Pro Ala Pro Gly Ile Arg				
810 815 820				
act cag ggc tcc cct cag gaa gct ggg ccc agc tgg gat tgc cga ggg	2791			
Thr Gln Gly Ser Pro Gln Glu Ala Gly Pro Ser Trp Asp Cys Arg Gly				
825 830 835				
gcc cct agc cct ggc agc ggt cct ggg cta gtc ggc tgc ctg gcc ggg	2839			
Ala Pro Ser Pro Gly Ser Gly Pro Gly Leu Val Gly Cys Leu Ala Gly				
840 845 850				
gaa cct gca ggc tcc cac agg aag agg tgt gga gac ctg ccc tcg ggg	2887			
Glu Pro Ala Gly Ser His Arg Lys Arg Cys Gly Asp Leu Pro Ser Gly				
855 860 865				
gcc tct ccc agg gtc cag cct gag ccc cca cca ggg gtc tct gcc cag	2935			
Ala Ser Pro Arg Val Gln Pro Glu Pro Pro Pro Gly Val Ser Ala Gln				
870 875 880 885				
cac agg aag ctg acc ctg gcc cag ctc tac cga atc agg acc acc ctg	2983			
His Arg Lys Leu Thr Leu Ala Gln Leu Tyr Arg Ile Arg Thr Thr Leu				
890 895 900				
ctg ctt aac tcc acg ctc act gcc tcg gag gtc tgagcagagg gagggcccca	3036			
Leu Leu Asn Ser Thr Leu Thr Ala Ser Glu Val				
905 910				
agagtgccat tgaccaagag acagcagaca gcctgcctcc tggggcgtgc cggcacctgc	3096			
ttcagctact gcctcctgta tgcattgagcc ggatgctggg caggatccct gcctacgccc	3156			
gggcccgaatt tgcgctttgc cggactggat ggagtggagg aggcccaggc cacagtacca	3216			
ccccacctgc ccaggcagcc cctcgtcacc tactccccga agttaccagc tcagctcgag	3276			
tcttcagggc tgggctccta ggcctgccat cctacttcta cctcactgg cctccagtgg	3336			
gattcactcc tgccctgccc ccaccttccc agtcccacag gccacccctg gcttgggctg	3396			
ggttctgtga agttacgtat ttattgagct tttggttctt ttataaagac ttgtctagac	3456			

<210> 156

<211> 912

<212> PRT

<213> Homo sapiens

<400> 156

Met Lys Lys Lys Ser Leu Gly Glu Val Leu Leu Pro Val Phe Glu Arg
1 5 10 15

Lys Gly Ile Ala Leu Gly Lys Val Asp Ile Tyr Leu Asp Gln Ser Asn
20 25 30

Thr Pro Leu Ser Leu Thr Phe Glu Ala Tyr Arg Phe Gly Gly His Tyr
35 40 45

Leu Arg Val Lys Ala Pro Ala Lys Pro Gly Asp Glu Gly Lys Val Glu
50 55 60

Gln Gly Met Lys Asp Ser Lys Ser Leu Ser Leu Pro Ile Leu Arg Pro
65 70 75 80

Ala Gly Thr Gly Pro Pro Ala Leu Glu Arg Val Asp Ala Gln Ser Arg
85 90 95

Arg Glu Ser Leu Asp Ile Leu Ala Pro Gly Arg Arg Arg Lys Asn Met
100 105 110

Ser Glu Phe Leu Gly Glu Ala Ser Ile Pro Gly Gln Glu Pro Pro Thr
115 120 125

Pro Ser Ser Cys Ser Leu Pro Ser Gly Ser Ser Gly Ser Thr Asn Thr
130 135 140

Gly Asp Ser Trp Lys Asn Arg Ala Ala Ser Arg Phe Ser Gly Phe Phe
145 150 155 160

Ser Ser Gly Pro Ser Thr Ser Ala Phe Gly Arg Glu Val Asp Lys Met
165 170 175

Glu Gln Leu Glu Gly Lys Leu His Thr Tyr Ser Leu Phe Gly Leu Pro
180 185 190

Arg Leu Pro Arg Gly Leu Arg Phe Asp His Asp Ser Trp Glu Glu Glu
195 200 205

Tyr Asp Glu Asp Glu Asp Glu Asp Asn Ala Cys Leu Arg Leu Glu Asp
210 215 220

Ser Trp Arg Glu Leu Ile Asp Gly His Glu Lys Leu Thr Arg Arg Gln
225 230 235 240

Cys His Gln Gln Glu Ala Val Trp Glu Leu Leu His Thr Glu Ala Ser
245 250 255

Tyr Ile Arg Lys Leu Arg Val Ile Ile Asn Leu Phe Leu Cys Cys Leu
260 265 270

Leu Asn Leu Gln Glu Ser Gly Leu Leu Cys Glu Val Glu Ala Glu Arg
275 280 285

Leu	Phe	Ser	Asn	Ile	Pro	Glu	Ile	Ala	Gln	Leu	His	Arg	Arg	Leu	Trp
290						295					300				
Ala	Ser	Val	Met	Ala	Pro	Val	Leu	Glu	Lys	Ala	Arg	Arg	Thr	Arg	Ala
305					310					315					320
Leu	Leu	Gln	Pro	Gly	Asp	Phe	Leu	Lys	Gly	Phe	Lys	Met	Phe	Gly	Ser
				325					330					335	
Leu	Phe	Lys	Pro	Tyr	Ile	Arg	Tyr	Cys	Met	Glu	Glu	Glu	Gly	Cys	Met
			340					345					350		
Glu	Tyr	Met	Arg	Gly	Leu	Leu	Arg	Asp	Asn	Asp	Leu	Phe	Arg	Ala	Tyr
		355					360					365			
Ile	Thr	Trp	Ala	Glu	Lys	His	Pro	Gln	Cys	Gln	Arg	Leu	Lys	Leu	Ser
	370					375					380				
Asp	Met	Leu	Ala	Lys	Pro	His	Gln	Arg	Leu	Thr	Lys	Tyr	Pro	Leu	Leu
385					390					395					400
Leu	Lys	Ser	Val	Leu	Arg	Lys	Thr	Glu	Glu	Pro	Arg	Ala	Lys	Glu	Ala
				405					410					415	
Val	Val	Ala	Met	Ile	Gly	Ser	Val	Glu	Arg	Phe	Ile	His	His	Val	Asn
			420					425					430		
Ala	Cys	Met	Arg	Gln	Arg	Gln	Glu	Arg	Gln	Arg	Leu	Ala	Ala	Val	Val
		435					440					445			
Ser	Arg	Ile	Asp	Ala	Tyr	Glu	Val	Val	Glu	Ser	Ser	Ser	Asp	Glu	Val
		450				455					460				
Asp	Lys	Leu	Leu	Lys	Glu	Phe	Leu	His	Leu	Asp	Leu	Thr	Ala	Pro	Ile
465					470					475					480
Pro	Gly	Ala	Ser	Pro	Glu	Glu	Thr	Arg	Gln	Leu	Leu	Leu	Glu	Gly	Ser
				485					490					495	
Leu	Arg	Met	Lys	Glu	Gly	Lys	Asp	Ser	Lys	Met	Asp	Val	Tyr	Cys	Phe
			500					505					510		
Leu	Phe	Thr	Asp	Leu	Leu	Leu	Val	Thr	Lys	Ala	Val	Lys	Lys	Ala	Glu
		515					520					525			
Arg	Thr	Arg	Val	Ile	Arg	Pro	Pro	Leu	Leu	Val	Asp	Lys	Ile	Val	Cys
	530					535					540				
Arg	Glu	Leu	Arg	Asp	Pro	Gly	Ser	Phe	Leu	Leu	Ile	Tyr	Leu	Asn	Glu
545					550					555					560
Phe	His	Ser	Ala	Val	Gly	Ala	Tyr	Thr	Phe	Gln	Ala	Ser	Gly	Gln	Ala
				565					570					575	
Leu	Cys	Arg	Gly	Trp	Val	Asp	Thr	Ile	Tyr	Asn	Ala	Gln	Asn	Gln	Leu
			580					585					590		

	140	145	150	
gga gat gag ggc aag gtg gag cag ggc atg aag gac tcc aag tcc ctg				652
Gly Asp Glu Gly Lys Val Glu Gln Gly Met Lys Asp Ser Lys Ser Leu				
	155	160	165	
agt ttg ccg att ctg cgg cca gct ggg acc ggg ccc ccc gcc ctg gag				700
Ser Leu Pro Ile Leu Arg Pro Ala Gly Thr Gly Pro Pro Ala Leu Glu				
	170	175	180	
cgt gtg gac gcc cag agc cgc cgg gag agc ctg gac atc ttg gcc cct				748
Arg Val Asp Ala Gln Ser Arg Arg Glu Ser Leu Asp Ile Leu Ala Pro				
	185	190	195	
ggc cgc cgc cgc aag aac atg tgc gag ttc ctg ggg gag gcg agc atc				796
Gly Arg Arg Arg Lys Asn Met Ser Glu Phe Leu Gly Glu Ala Ser Ile				
	200	205	210	215
ccc ggg cag gag ccc ccc acg ccc tcc agc tgc tct ctg ccc agc ggc				844
Pro Gly Gln Glu Pro Pro Thr Pro Ser Ser Cys Ser Leu Pro Ser Gly				
	220	225	230	
agc agt ggc agc acc aac act ggc gac agc tgg aag aac cgg gcg gcc				892
Ser Ser Gly Ser Thr Asn Thr Gly Asp Ser Trp Lys Asn Arg Ala Ala				
	235	240	245	
agt cgc ttc agc ggc ttt ttc agc tcc ggc ccc agc acc agc gcc ttt				940
Ser Arg Phe Ser Gly Phe Phe Ser Ser Gly Pro Ser Thr Ser Ala Phe				
	250	255	260	
ggc cgg gag gta gac aag atg gag cag ctg gag ggc aag ctg cac acc				988
Gly Arg Glu Val Asp Lys Met Glu Gln Leu Glu Gly Lys Leu His Thr				
	265	270	275	
tac agc ctc ttc ggg ctg ccc agg ctg ccc cgg ggg ctg cgc ttc gac				1036
Tyr Ser Leu Phe Gly Leu Pro Arg Leu Pro Arg Gly Leu Arg Phe Asp				
	280	285	290	295
cat gac tcc tgg gag gag gag tac gat gaa gac gag gat gag gac aat				1084
His Asp Ser Trp Glu Glu Glu Tyr Asp Glu Asp Glu Asp Glu Asp Asn				
	300	305	310	
gcc tgc ctg agg ctg gag gac agc tgg cgg gag ctc att gat ggg cat				1132
Ala Cys Leu Arg Leu Glu Asp Ser Trp Arg Glu Leu Ile Asp Gly His				
	315	320	325	
gag aag ctg acc cgg cgg cag tgc cac cag cag gag gcg gtg tgg gag				1180
Glu Lys Leu Thr Arg Arg Gln Cys His Gln Gln Glu Ala Val Trp Glu				
	330	335	340	
ctg ctg cac acg gag gcc tcc tac atc agg aaa ctg cgg gtg atc atc				1228
Leu Leu His Thr Glu Ala Ser Tyr Ile Arg Lys Leu Arg Val Ile Ile				
	345	350	355	
aac ctg ttc ctg tgc tgc ctc ctg aac ctg caa gag tca ggg ctg ctg				1276
Asn Leu Phe Leu Cys Cys Leu Leu Asn Leu Gln Glu Ser Gly Leu Leu				
	360	365	370	375

tgt gag gtg gag gcg gag cgc ctg ttc agc aac atc ccg gag atc gcg	1324
Cys Glu Val Glu Ala Glu Arg Leu Phe Ser Asn Ile Pro Glu Ile Ala	
380 385 390	
cag ctg cac cgc agg ctg tgg gct agc gtg atg gcg ccg gtg ctg gag	1372
Gln Leu His Arg Arg Leu Trp Ala Ser Val Met Ala Pro Val Leu Glu	
395 400 405	
aag gcg cgg cgc acg cga gcg ctg cta cag ccc ggg gac ttc ctc aaa	1420
Lys Ala Arg Arg Thr Arg Ala Leu Leu Gln Pro Gly Asp Phe Leu Lys	
410 415 420	
ggc ttc aag atg ttc ggc tcg ctc ttc aag ccc tac atc cgc tac tgc	1468
Gly Phe Lys Met Phe Gly Ser Leu Phe Lys Pro Tyr Ile Arg Tyr Cys	
425 430 435	
atg gag gag gag ggc tgc atg gag tac atg cgc ggc ctg ctg cgc gac	1516
Met Glu Glu Glu Gly Cys Met Glu Tyr Met Arg Gly Leu Leu Arg Asp	
440 445 450 455	
aac gac ctc ttc cgg gcc tac atc acg tgg gcg gag aag cac cca cag	1564
Asn Asp Leu Phe Arg Ala Tyr Ile Thr Trp Ala Glu Lys His Pro Gln	
460 465 470	
tgc cag agg ctg aag ctg agc gac atg ctg gcc aaa ccc cac cag cgg	1612
Cys Gln Arg Leu Lys Leu Ser Asp Met Leu Ala Lys Pro His Gln Arg	
475 480 485	
ctc acc aag tac ccg ctg ctg ctc aag tcg gtg ctg agg aag acc gag	1660
Leu Thr Lys Tyr Pro Leu Leu Leu Lys Ser Val Leu Arg Lys Thr Glu	
490 495 500	
gag ccg cgc gcc aag gag gcc gtc gtc gcc atg atc ggc tcc gtg gag	1708
Glu Pro Arg Ala Lys Glu Ala Val Val Ala Met Ile Gly Ser Val Glu	
505 510 515	
cgc ttc atc cac cac gtg aac gcg tgc atg cgg cag cgg cag gag cgg	1756
Arg Phe Ile His His Val Asn Ala Cys Met Arg Gln Arg Gln Glu Arg	
520 525 530 535	
cag cgg ctg gcg gcc gtg gtg agc cgc atc gac gcc tac gag gtg gtg	1804
Gln Arg Leu Ala Ala Val Val Ser Arg Ile Asp Ala Tyr Glu Val Val	
540 545 550	
gaa agc agc agc gac gaa gtg gac aag ctc ctg aag gaa ttt ctg cac	1852
Glu Ser Ser Ser Asp Glu Val Asp Lys Leu Lys Glu Phe Leu His	
555 560 565	
ctg gac ttg aca gcg ccc atc cct ggc gcc tcc ccg gag gag acg cgg	1900
Leu Asp Leu Thr Ala Pro Ile Pro Gly Ala Ser Pro Glu Glu Thr Arg	
570 575 580	
cag ctg ctg ctg gag ggg agc ctg agg atg aag gag ggg aag gac agc	1948
Gln Leu Leu Leu Glu Gly Ser Leu Arg Met Lys Glu Gly Lys Asp Ser	
585 590 595	

aag Lys 600	atg Met	gat Asp	gtg Val	tac Tyr	tgc Cys 605	ttc Phe	ctc Leu	ttc Phe	acg Thr	gat Asp 610	ctg Leu	ctg Leu	ttg Leu	gtg Val	acc Thr 615	1996
aaa Lys	gca Ala	gtg Val	aag Lys	aag Lys 620	gca Ala	gag Glu	agg Arg	acc Thr	agg Arg 625	gtc Val	atc Ile	agg Arg	cca Pro	ccc Pro 630	ctg Leu	2044
ctc Leu	gtg Val	gac Asp	aag Lys 635	att Ile	gtg Val	tgc Cys	cgg Arg	gag Glu 640	cta Leu	cgg Arg	gac Asp	cct Pro	ggg Gly 645	tcc Ser	ttc Phe	2092
ctc Leu	ctt Leu	atc Ile 650	tac Tyr	ctg Leu	aat Asn	gag Glu	ttt Phe 655	cac His	agt Ser	gct Ala	gta Val	ggg Gly 660	gcc Ala	tac Tyr	acg Thr	2140
ttc Phe 665	cag Gln	gcc Ala	agt Ser	ggc Gly	cag Gln	gcc Ala 670	ttg Leu	tgc Cys	cgt Arg	ggc Gly	tgg Trp 675	gtg Val	gac Asp	acc Thr	att Ile	2188
tac Tyr 680	aat Asn	gcc Ala	cag Gln	aac Asn	cag Gln 685	ctg Leu	caa Gln	cag Gln	ctg Leu	cgt Arg 690	gca Ala	cag Gln	gag Glu	ccc Pro	cca Pro 695	2236
ggc Gly	agt Ser	cag Gln	cag Gln 700	ccc Pro	ctg Leu	cag Gln	agc Ser	ctg Leu	gaa Glu 705	gag Glu	gag Glu	gag Glu	gat Asp	gag Glu 710	cag Gln	2284
gag Glu 715	gag Glu	gaa Glu	gag Glu	gag Glu	gag Glu	gag Glu	gag Glu	gag Glu 720	gag Glu	gag Glu	gaa Glu	ggc Gly	gag Glu 725	gac Asp	agt Ser	2332
ggc Gly	act Thr	tca Ser	gct Ala	gcc Ala	agc Ser	tcc Ser 730	cct Pro	acc Thr	atc Ile	atg Met	cgg Arg	aaa Lys 740	agc Ser	agc Ser	ggc Gly	2380
agc Ser 745	ccc Pro	gac Asp	tct Ser	cag Gln	cac His	tgt Cys 750	gcc Ala	tca Ser	gat Asp	ggc Gly	tcc Ser 755	acg Thr	gag Glu	acc Thr	ctg Leu	2428
gcc Ala 760	atg Met	gtt Val	gtg Val	gta Val	gag Glu 765	cct Pro	ggg Gly	gac Asp	acg Thr	ctg Leu 770	tcc Ser	tcc Ser	ccc Pro	gag Glu	ttc Phe 775	2476
gac Asp	agc Ser	ggt Gly	cct Pro	ttc Phe 780	agc Ser	tcc Ser	cag Gln	tct Ser	gat Asp 785	gag Glu	acc Thr	tct Ser	ctc Leu	agc Ser 790	acc Thr	2524
act Thr	gcc Ala	tca Ser	tct Ser 795	gcc Ala	acg Thr	ccc Pro	acc Thr	agt Ser 800	gag Glu	ctg Leu	ctg Leu	ccc Pro	ctg Leu 805	ggt Gly	ccg Pro	2572
gtg Val	gac Asp	ggc Gly 810	cgc Arg	tcc Ser	tgc Cys	tcc Ser	atg Met 815	gac Asp	tct Ser	gcc Ala	tac Tyr	ggc Gly 820	acc Thr	ctc Leu	tcc Ser	2620
cca Val	acc Met	tcc Leu	tta Val	caa Val	gac Val	ttt Val	gtg Val	gcc Val	cca Val	ggc Val	cca Val	atg Val	gca Val	gag Val	cta Val	2668

Pro	Thr	Ser	Leu	Gln	Asp	Phe	Val	Ala	Pro	Gly	Pro	Met	Ala	Glu	Leu		
825						830					835						
gtg	cct	cgg	gcc	cca	gag	tcc	cca	cga	gtt	cct	tcc	cct	cca	ccc	tcg	2716	
Val	Pro	Arg	Ala	Pro	Glu	Ser	Pro	Arg	Val	Pro	Ser	Pro	Pro	Pro	Ser		
840					845					850					855		
ccc	cgt	ctc	cgc	cgc	cgc	acc	cct	gtc	cag	ctg	ttg	agc	tgc	ccg	ccc	2764	
Pro	Arg	Leu	Arg	Arg	Arg	Thr	Pro	Val	Gln	Leu	Leu	Ser	Cys	Pro	Pro		
				860					865					870			
cac	ctg	ctc	aag	tct	aag	tcc	gag	gcc	agc	ctc	ctc	cag	ctg	ctg	gca	2812	
His	Leu	Leu	Lys	Ser	Lys	Ser	Glu	Ala	Ser	Leu	Leu	Gln	Leu	Leu	Ala		
			875					880					885				
ggg	gct	ggc	acc	cat	ggg	aca	ccc	tct	gcc	ccc	agc	cgc	agc	ctg	tca	2860	
Gly	Ala	Gly	Thr	His	Gly	Thr	Pro	Ser	Ala	Pro	Ser	Arg	Ser	Leu	Ser		
		890					895					900					
gag	ctc	tgc	ctg	gct	gtt	cca	gcc	cca	ggg	att	agg	act	cag	ggc	tcc	2908	
Glu	Leu	Cys	Leu	Ala	Val	Pro	Ala	Pro	Gly	Ile	Arg	Thr	Gln	Gly	Ser		
		905				910					915						
cct	cag	gaa	gct	ggg	ccc	agc	tgg	gat	tgc	cga	ggg	gcc	cct	agc	cct	2956	
Pro	Gln	Glu	Ala	Gly	Pro	Ser	Trp	Asp	Cys	Arg	Gly	Ala	Pro	Ser	Pro		
920					925					930					935		
ggc	agc	ggg	cct	ggg	cta	gtc	ggc	tgc	ctg	gcc	ggg	gaa	cct	gca	ggc	3004	
Gly	Ser	Gly	Pro	Gly	Leu	Val	Gly	Cys	Leu	Ala	Gly	Glu	Pro	Ala	Gly		
				940					945					950			
tcc	cac	agg	aag	agg	tgt	gga	gac	ctg	ccc	tcg	ggg	gcc	tct	ccc	agg	3052	
Ser	His	Arg	Lys	Arg	Cys	Gly	Asp	Leu	Pro	Ser	Gly	Ala	Ser	Pro	Arg		
			955					960					965				
gtc	cag	cct	gag	ccc	cca	cca	ggg	gtc	tct	gcc	cag	cac	agg	aag	ctg	3100	
Val	Gln	Pro	Glu	Pro	Pro	Pro	Gly	Val	Ser	Ala	Gln	His	Arg	Lys	Leu		
		970					975					980					
acc	ctg	gcc	cag	ctc	tac	cga	atc	agg	acc	acc	ctg	ctg	ctt	aac	tcc	3148	
Thr	Leu	Ala	Gln	Leu	Tyr	Arg	Ile	Arg	Thr	Thr	Leu	Leu	Leu	Asn	Ser		
		985				990					995						
acg	ctc	act	gcc	tcg	gag	gtc	tgagcagagg	gaggccccca	agagtgccat							3199	
Thr	Leu	Thr	Ala	Ser	Glu	Val											
1000					1005												
tgaccaagag	acagcagaca	gctgcctcc	tggggcgtgc	cggcacctgc	ttcagctact											3259	
gcctcctgta	tgcatgagcc	ggatgctggg	caggatccct	gcctacgcc	gggcccatt											3319	
tgcgctttgc	cggactggat	ggagtggagg	aggcccaggc	cacagtacca	ccccacctgc											3379	
ccaggcagcc	cctcgtcacc	tactccccga	agttaccagc	tcagctcgag	tcttcagggc											3439	
tgggctccta	ggctgcccat	cctacttcta	ccctcactgg	cctccagtgg	gattcactcc											3499	

-- tgccctgcce-ccacettccc- agtcccacag gccacccctg gcttgggctg ggttctgtga 3559

agttacgtat ttattgagct tttggttctt ttataaagac ttgtctagac 3609

<210> 158
 <211> 1006
 <212> PRT
 <213> Homo sapiens

<400> 158
 Met His Tyr Asp Gly His Val Arg Phe Asp Leu Pro Pro Gln Gly Ser
 1 5 10 15
 Val Leu Ala Arg Asn Val Ser Thr Arg Ser Cys Pro Pro Arg Thr Ser
 20 25 30
 Pro Ala Val Asp Leu Glu Glu Glu Glu Glu Ser Ser Val Asp Gly
 35 40 45
 Lys Gly Asp Arg Lys Ser Thr Gly Leu Lys Leu Ser Lys Lys Lys Ala
 50 55 60
 Arg Arg Arg His Thr Asp Asp Pro Ser Lys Glu Cys Phe Thr Leu Lys
 65 70 75 80
 Phe Asp Leu Asn Val Asp Ile Glu Thr Glu Ile Val Pro Ala Met Lys
 85 90 95
 Lys Lys Ser Leu Gly Glu Val Leu Leu Pro Val Phe Glu Arg Lys Gly
 100 105 110
 Ile Ala Leu Gly Lys Val Asp Ile Tyr Leu Asp Gln Ser Asn Thr Pro
 115 120 125
 Leu Ser Leu Thr Phe Glu Ala Tyr Arg Phe Gly Gly His Tyr Leu Arg
 130 135 140
 Val Lys Ala Pro Ala Lys Pro Gly Asp Glu Gly Lys Val Glu Gln Gly
 145 150 155 160
 Met Lys Asp Ser Lys Ser Leu Ser Leu Pro Ile Leu Arg Pro Ala Gly
 165 170 175
 Thr Gly Pro Pro Ala Leu Glu Arg Val Asp Ala Gln Ser Arg Arg Glu
 180 185 190
 Ser Leu Asp Ile Leu Ala Pro Gly Arg Arg Arg Lys Asn Met Ser Glu
 195 200 205
 Phe Leu Gly Glu Ala Ser Ile Pro Gly Gln Glu Pro Pro Thr Pro Ser
 210 215 220
 Ser Cys Ser Leu Pro Ser Gly Ser Ser Gly Ser Thr Asn Thr Gly Asp
 225 230 235 240
 Ser Trp Lys Asn Arg Ala Ala Ser Arg Phe Ser Gly Phe Phe Ser Ser

				245					250					255			
Gly	Pro	Ser	Thr	Ser	Ala	Phe	Gly	Arg	Glu	Val	Asp	Lys	Met	Glu	Gln		
			260					265					270				
Leu	Glu	Gly	Lys	Leu	His	Thr	Tyr	Ser	Leu	Phe	Gly	Leu	Pro	Arg	Leu		
		275					280					285					
Pro	Arg	Gly	Leu	Arg	Phe	Asp	His	Asp	Ser	Trp	Glu	Glu	Glu	Tyr	Asp		
	290					295					300						
Glu	Asp	Glu	Asp	Glu	Asp	Asn	Ala	Cys	Leu	Arg	Leu	Glu	Asp	Ser	Trp		
305					310					315					320		
Arg	Glu	Leu	Ile	Asp	Gly	His	Glu	Lys	Leu	Thr	Arg	Arg	Gln	Cys	His		
				325					330					335			
Gln	Gln	Glu	Ala	Val	Trp	Glu	Leu	Leu	His	Thr	Glu	Ala	Ser	Tyr	Ile		
			340					345					350				
Arg	Lys	Leu	Arg	Val	Ile	Ile	Asn	Leu	Phe	Leu	Cys	Cys	Leu	Leu	Asn		
		355					360					365					
Leu	Gln	Glu	Ser	Gly	Leu	Leu	Cys	Glu	Val	Glu	Ala	Glu	Arg	Leu	Phe		
	370					375					380						
Ser	Asn	Ile	Pro	Glu	Ile	Ala	Gln	Leu	His	Arg	Arg	Leu	Trp	Ala	Ser		
385					390					395					400		
Val	Met	Ala	Pro	Val	Leu	Glu	Lys	Ala	Arg	Arg	Thr	Arg	Ala	Leu	Leu		
				405					410					415			
Gln	Pro	Gly	Asp	Phe	Leu	Lys	Gly	Phe	Lys	Met	Phe	Gly	Ser	Leu	Phe		
			420					425					430				
Lys	Pro	Tyr	Ile	Arg	Tyr	Cys	Met	Glu	Glu	Glu	Gly	Cys	Met	Glu	Tyr		
		435					440					445					
Met	Arg	Gly	Leu	Leu	Arg	Asp	Asn	Asp	Leu	Phe	Arg	Ala	Tyr	Ile	Thr		
	450					455					460						
Trp	Ala	Glu	Lys	His	Pro	Gln	Cys	Gln	Arg	Leu	Lys	Leu	Ser	Asp	Met		
465					470					475				480			
Leu	Ala	Lys	Pro	His	Gln	Arg	Leu	Thr	Lys	Tyr	Pro	Leu	Leu	Leu	Lys		
				485					490					495			
Ser	Val	Leu	Arg	Lys	Thr	Glu	Glu	Pro	Arg	Ala	Lys	Glu	Ala	Val	Val		
			500					505					510				
Ala	Met	Ile	Gly	Ser	Val	Glu	Arg	Phe	Ile	His	His	Val	Asn	Ala	Cys		
		515					520					525					
Met	Arg	Gln	Arg	Gln	Glu	Arg	Gln	Arg	Leu	Ala	Ala	Val	Val	Ser	Arg		
	530					535				540							
Ile	Asp	Ala	Tyr	Glu	Val	Val	Glu	Ser	Ser	Ser	Asp	Glu	Val	Asp	Lys		

545					550					555					560
Leu	Leu	Lys	Glu	Phe 565	Leu	His	Leu	Asp	Leu 570	Thr	Ala	Pro	Ile	Pro 575	Gly
Ala	Ser	Pro	Glu 580	Glu	Thr	Arg	Gln	Leu 585	Leu	Leu	Glu	Gly	Ser 590	Leu	Arg
Met	Lys	Glu 595	Gly	Lys	Asp	Ser	Lys 600	Met	Asp	Val	Tyr	Cys 605	Phe	Leu	Phe
Thr	Asp 610	Leu	Leu	Leu	Val	Thr 615	Lys	Ala	Val	Lys	Lys 620	Ala	Glu	Arg	Thr
Arg 625	Val	Ile	Arg	Pro	Pro 630	Leu	Leu	Val	Asp	Lys 635	Ile	Val	Cys	Arg	Glu 640
Leu	Arg	Asp	Pro	Gly 645	Ser	Phe	Leu	Leu	Ile 650	Tyr	Leu	Asn	Glu	Phe 655	His
Ser	Ala	Val	Gly 660	Ala	Tyr	Thr	Phe	Gln 665	Ala	Ser	Gly	Gln	Ala 670	Leu	Cys
Arg	Gly	Trp 675	Val	Asp	Thr	Ile	Tyr 680	Asn	Ala	Gln	Asn	Gln 685	Leu	Gln	Gln
Leu 690	Arg	Ala	Gln	Glu	Pro	Pro 695	Gly	Ser	Gln	Gln	Pro 700	Leu	Gln	Ser	Leu
Glu 705	Glu	Glu	Glu	Asp	Glu 710	Gln	Glu	Glu	Glu	Glu 715	Glu	Glu	Glu	Glu	Glu 720
Glu	Glu	Glu	Gly	Glu 725	Asp	Ser	Gly	Thr	Ser 730	Ala	Ala	Ser	Ser	Pro 735	Thr
Ile	Met	Arg	Lys 740	Ser	Ser	Gly	Ser	Pro 745	Asp	Ser	Gln	His	Cys 750	Ala	Ser
Asp	Gly	Ser 755	Thr	Glu	Thr	Leu	Ala 760	Met	Val	Val	Val	Glu 765	Pro	Gly	Asp
Thr 770	Leu	Ser	Ser	Pro	Glu	Phe 775	Asp	Ser	Gly	Pro	Phe 780	Ser	Ser	Gln	Ser
Asp 785	Glu	Thr	Ser	Leu	Ser 790	Thr	Thr	Ala	Ser	Ser 795	Ala	Thr	Pro	Thr	Ser 800
Glu	Leu	Leu	Pro	Leu 805	Gly	Pro	Val	Asp	Gly 810	Arg	Ser	Cys	Ser	Met 815	Asp
Ser	Ala	Tyr	Gly 820	Thr	Leu	Ser	Pro	Thr 825	Ser	Leu	Gln	Asp	Phe 830	Val	Ala
Pro	Gly	Pro 835	Met	Ala	Glu	Leu	Val 840	Pro	Arg	Ala	Pro	Glu 845	Ser	Pro	Arg
Val	Pro	Ser	Pro	Pro	Pro	Ser	Pro	Arg	Leu	Arg	Arg	Arg	Thr	Pro	Val

850 855 860

Gln Leu Leu Ser Cys Pro Pro His Leu Leu Lys Ser Lys Ser Glu Ala
865 870 875 880

Ser Leu Leu Gln Leu Leu Ala Gly Ala Gly Thr His Gly Thr Pro Ser
885 890 895

Ala Pro Ser Arg Ser Leu Ser Glu Leu Cys Leu Ala Val Pro Ala Pro
900 905 910

Gly Ile Arg Thr Gln Gly Ser Pro Gln Glu Ala Gly Pro Ser Trp Asp
915 920 925

Cys Arg Gly Ala Pro Ser Pro Gly Ser Gly Pro Gly Leu Val Gly Cys
930 935 940

Leu Ala Gly Glu Pro Ala Gly Ser His Arg Lys Arg Cys Gly Asp Leu
945 950 955 960

Pro Ser Gly Ala Ser Pro Arg Val Gln Pro Glu Pro Pro Pro Gly Val
965 970 975

Ser Ala Gln His Arg Lys Leu Thr Leu Ala Gln Leu Tyr Arg Ile Arg
980 985 990

Thr Thr Leu Leu Leu Asn Ser Thr Leu Thr Ala Ser Glu Val
995 1000 1005

<210> 159
<211> 3168
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (93)..(3089)

<400> 159
agtgcccggt ggcccaggag ggcttgggag ccgaagccg tccccgagtc gctcctaggt 60

cactggcgcg atgcgggccc tcctctcggc tg atg ggt tgg aag ccc agc gag 113
Met Gly Trp Lys Pro Ser Glu
1 5

gct aga ggc cag tcc caa agt ctc cag gca tca ggg ctg cag ccc agg 161
Ala Arg Gly Gln Ser Gln Ser Leu Gln Ala Ser Gly Leu Gln Pro Arg
10 15 20

agc ctc aag gcg gcc cgg cgg gcg act gga cgg ccg gac agg tcc cga 209
Ser Leu Lys Ala Ala Arg Arg Ala Thr Gly Arg Pro Asp Arg Ser Arg
25 30 35

gca gcc ccg ccc aac atg gac cca gac ccc cag gcg ggc gtg cag gtg 257
Ala Ala Pro Pro Asn Met Asp Pro Asp Pro Gln Ala Gly Val Gln Val
40 45 50 55

ggc atg cgg gtg gtg cgc ggc gtg gac tgg aag tgg ggc cag cag gac	305
Gly Met Arg Val Val Arg Gly Val Asp Trp Lys Trp Gly Gln Gln Asp	
60 65 70	
ggc ggc gag ggc ggc gtg ggc acg gtg gtg gag ctt ggc cgc cac ggc	353
Gly Gly Glu Gly Gly Val Gly Thr Val Val Glu Leu Gly Arg His Gly	
75 80 85	
agc ccc tcg aca ccc gac cgc aca gtg gtc gtg cag tgg gac cag ggc	401
Ser Pro Ser Thr Pro Asp Arg Thr Val Val Val Gln Trp Asp Gln Gly	
90 95 100	
acg cgc acc aac tac cgc gcc ggc tac cag ggc gcg cac gac ctg ctg	449
Thr Arg Thr Asn Tyr Arg Ala Gly Tyr Gln Gly Ala His Asp Leu Leu	
105 110 115	
ctg tac gac aac gcc cag atc ggc gtc cgg cac ccc aac atc atc tgt	497
Leu Tyr Asp Asn Ala Gln Ile Gly Val Arg His Pro Asn Ile Ile Cys	
120 125 130 135	
gac tgc tgc aag aag cac ggg ctg cgg ggg atg cgc tgg aag tgc cgt	545
Asp Cys Cys Lys Lys His Gly Leu Arg Gly Met Arg Trp Lys Cys Arg	
140 145 150	
gtg tgc ctg gac tac gac ctc tgc acg cag tgc tac atg cac aac aag	593
Val Cys Leu Asp Tyr Asp Leu Cys Thr Gln Cys Tyr Met His Asn Lys	
155 160 165	
cat gag ctc gcc cac gcc ttc gac cgc tac gag acc gct cac tcg cgc	641
His Glu Leu Ala His Ala Phe Asp Arg Tyr Glu Thr Ala His Ser Arg	
170 175 180	
cct gtc aca ctg agt ccc cgc cag ggc ctc ccg agg atc cca cta agg	689
Pro Val Thr Leu Ser Pro Arg Gln Gly Leu Pro Arg Ile Pro Leu Arg	
185 190 195	
ggc atc ttc cag gga gcg aag gtg gtg cga ggc ccc ttc tgg gag tgg	737
Gly Ile Phe Gln Gly Ala Lys Val Val Arg Gly Pro Phe Trp Glu Trp	
200 205 210 215	
ggc tca cag gat gga ggg gaa ggg aaa ccg ggc cgt gtg gtg gac atc	785
Gly Ser Gln Asp Gly Gly Glu Gly Lys Pro Gly Arg Val Val Asp Ile	
220 225 230	
cgt ggc tgg gat gtg gag aca ggc cgg agt gtg gcc agc gtg acg tgg	833
Arg Gly Trp Asp Val Glu Thr Gly Arg Ser Val Ala Ser Val Thr Trp	
235 240 245	
gct gat ggt acc acc aat gtg tac cgt gtg ggc cac aag ggc aag gtg	881
Ala Asp Gly Thr Thr Asn Val Tyr Arg Val Gly His Lys Gly Lys Val	
250 255 260	
gac ctc aag tgt gtg ggc gag gca gcg ggc ggc ttc tac tac aag gac	929
Asp Leu Lys Cys Val Gly Glu Ala Ala Gly Gly Phe Tyr Tyr Lys Asp	
265 270 275	

cac	ctc	cca	agg	ctc	ggc	aag	ccg	gcg	gag	ctg	cag	cgc	agg	gtg	agt	977
His	Leu	Pro	Arg	Leu	Gly	Lys	Pro	Ala	Glu	Leu	Gln	Arg	Arg	Val	Ser	
280					285					290					295	
gct	gac	agc	cag	ccc	ttc	cag	cac	ggg	gac	aag	gtc	aag	tgt	ctg	ctg	1025
Ala	Asp	Ser	Gln	Pro	Phe	Gln	His	Gly	Asp	Lys	Val	Lys	Cys	Leu	Leu	
				300					305					310		
gac	act	gat	gtc	ctg	cgg	gag	atg	cag	gaa	ggc	cac	ggc	ggc	tgg	aac	1073
Asp	Thr	Asp	Val	Leu	Arg	Glu	Met	Gln	Glu	Gly	His	Gly	Gly	Trp	Asn	
			315					320						325		
ccc	agg	atg	gcg	gag	ttt	atc	gga	cag	acg	ggc	acc	gtg	cat	cgt	atc	1121
Pro	Arg	Met	Ala	Glu	Phe	Ile	Gly	Gln	Thr	Gly	Thr	Val	His	Arg	Ile	
		330					335						340			
acg	gac	cgc	ggg	gac	gtg	cgc	gtg	cag	ttc	aac	cac	gag	acg	cgc	tgg	1169
Thr	Asp	Arg	Gly	Asp	Val	Arg	Val	Gln	Phe	Asn	His	Glu	Thr	Arg	Trp	
	345					350					355					
acc	ttc	cac	ccc	ggg	gcg	ctc	acc	aag	cac	cac	tcc	ttc	tgg	gtg	ggc	1217
Thr	Phe	His	Pro	Gly	Ala	Leu	Thr	Lys	His	His	Ser	Phe	Trp	Val	Gly	
360					365					370					375	
gac	gtg	gtc	cgg	gtc	atc	ggc	gac	ctt	gac	aca	gtg	aag	cgg	ctg	cag	1265
Asp	Val	Val	Arg	Val	Ile	Gly	Asp	Leu	Asp	Thr	Val	Lys	Arg	Leu	Gln	
				380					385					390		
gct	ggg	cat	ggc	gag	tgg	acg	gac	gac	atg	gcc	cct	gcc	ctg	ggc	cgc	1313
Ala	Gly	His	Gly	Glu	Trp	Thr	Asp	Asp	Met	Ala	Pro	Ala	Leu	Gly	Arg	
			395					400					405			
gtc	ggg	aag	gtg	gtg	aaa	gtg	ttt	gga	gac	ggg	aac	ctg	cgt	gta	gca	1361
Val	Gly	Lys	Val	Val	Lys	Val	Phe	Gly	Asp	Gly	Asn	Leu	Arg	Val	Ala	
		410					415					420				
gtc	gct	ggt	cag	cgg	tgg	acc	ttc	agc	ccc	tcc	tgc	ctg	gtg	gcc	tac	1409
Val	Ala	Gly	Gln	Arg	Trp	Thr	Phe	Ser	Pro	Ser	Cys	Leu	Val	Ala	Tyr	
		425				430					435					
cgg	ccc	gag	gag	gat	gcc	aac	ctg	gac	gtg	gcc	gag	cgc	gcc	cgg	gag	1457
Arg	Pro	Glu	Glu	Asp	Ala	Asn	Leu	Asp	Val	Ala	Glu	Arg	Ala	Arg	Glu	
440					445					450					455	
aac	aaa	agc	tca	ctg	agc	gtg	gcc	ctg	gac	aag	ctt	cgg	gcc	cag	aag	1505
Asn	Lys	Ser	Ser	Leu	Ser	Val	Ala	Leu	Asp	Lys	Leu	Arg	Ala	Gln	Lys	
				460					465					470		
agt	gac	cca	gag	cac	ccg	gga	agg	ctg	gtg	gtg	gag	gtg	gcg	ctg	ggt	1553
Ser	Asp	Pro	Glu	His	Pro	Gly	Arg	Leu	Val	Val	Glu	Val	Ala	Leu	Gly	
			475					480					485			
aac	gca	gcc	cgg	gct	ctg	gac	ctg	ctg	cgg	agg	cgc	cca	gag	caa	gtg	1601
Asn	Ala	Ala	Arg	Ala	Leu	Asp	Leu	Leu	Arg	Arg	Arg	Pro	Glu	Gln	Val	
		490				495						500				
gac	acc	aag	aac	caa	ggc	agg	acc	gct	ctg	caa	gtg	gct	gcc	tac	ctg	1649

Asp Thr Lys Asn Gln Gly Arg Thr Ala Leu Gln Val Ala Ala Tyr Leu	
505 510 515	
ggc cag gtg gag ttg ata cgg ctg ctg cta caa gcc agg gcg ggc gtg	1697
Gly Gln Val Glu Leu Ile Arg Leu Leu Leu Gln Ala Arg Ala Gly Val	
520 525 530 535	
gac ctg ccg gac gac gag ggc aac acg gca ctg cac tac gcg gcc ctg	1745
Asp Leu Pro Asp Asp Glu Gly Asn Thr Ala Leu His Tyr Ala Ala Leu	
540 545 550	
ggg aac cag ccc gag gcc acc agg gtg ctc ctg agt gct ggg tgc cgg	1793
Gly Asn Gln Pro Glu Ala Thr Arg Val Leu Leu Ser Ala Gly Cys Arg	
555 560 565	
gcg gac gcc atc aac agc acc cag agc aca gca ctg cac gtg gcc gtg	1841
Ala Asp Ala Ile Asn Ser Thr Gln Ser Thr Ala Leu His Val Ala Val	
570 575 580	
cag agg ggc ttc ctg gag gtg gtg cgg gcc ctg tgt gag cgc ggc tgt	1889
Gln Arg Gly Phe Leu Glu Val Val Arg Ala Leu Cys Glu Arg Gly Cys	
585 590 595	
gac gtc aac ctg ccc gac gcc cac tcg gac acg ccc ctg cac tcc gcc	1937
Asp Val Asn Leu Pro Asp Ala His Ser Asp Thr Pro Leu His Ser Ala	
600 605 610 615	
atc tcg gcg ggc act gga gcc agc ggc att gtc gag gtc ctc acg gag	1985
Ile Ser Ala Gly Thr Gly Ala Ser Gly Ile Val Glu Val Leu Thr Glu	
620 625 630	
gtg cca aac atc gat gtt acc gcc acc aac agc cag ggt ttc acc ctg	2033
Val Pro Asn Ile Asp Val Thr Ala Thr Asn Ser Gln Gly Phe Thr Leu	
635 640 645	
ctg cac cat gcc tcc ctc aag ggt cac gcg cta gct gtg aga aag att	2081
Leu His His Ala Ser Leu Lys Gly His Ala Leu Ala Val Arg Lys Ile	
650 655 660	
ctg gct cgg gcg cgg cag ctg gtg gac gcc aag aag gag gac ggc ttc	2129
Leu Ala Arg Ala Arg Gln Leu Val Asp Ala Lys Lys Glu Asp Gly Phe	
665 670 675	
acg gcg ctg cat ctg gct gcc ctc aac aac cac cgc gag gtg gcc cag	2177
Thr Ala Leu His Leu Ala Ala Leu Asn Asn His Arg Glu Val Ala Gln	
680 685 690 695	
atc ctc atc cgg gag ggc cgc tgt gac gtg aac gtg cgc aac cgg aag	2225
Ile Leu Ile Arg Glu Gly Arg Cys Asp Val Asn Val Arg Asn Arg Lys	
700 705 710	
ctg cag tcc ccg ctg cat ctc gcc gtg caa cag gcc cac gtg ggg ctg	2273
Leu Gln Ser Pro Leu His Leu Ala Val Gln Gln Ala His Val Gly Leu	
715 720 725	
gtg ccg cta ctg gtg gac gct ggg tgc agt gtc aac gcc gag gac gag	2321
Val Pro Leu Leu Val Asp Ala Gly Cys Ser Val Asn Ala Glu Asp Glu	

730					735					740						
gag	ggg	gac	aca	gcc	ctg	cac	gtg	gcg	ctg	cag	cgt	cat	cag	ctg	ctg	2369
Glu	Gly	Asp	Thr	Ala	Leu	His	Val	Ala	Leu	Gln	Arg	His	Gln	Leu	Leu	
	745						750				755					
ccc	ctg	gtg	gct	gat	ggg	gcc	ggg	ggg	gac	cca	ggg	ccc	ttg	cag	ctg	2417
Pro	Leu	Val	Ala	Asp	Gly	Ala	Gly	Gly	Asp	Pro	Gly	Pro	Leu	Gln	Leu	
	760					765				770					775	
ctg	tcc	agg	cta	cag	gcc	tcg	ggc	ctc	ccc	ggc	agc	gcg	gag	ctg	acg	2465
Leu	Ser	Arg	Leu	Gln	Ala	Ser	Gly	Leu	Pro	Gly	Ser	Ala	Glu	Leu	Thr	
				780					785					790		
gtg	ggc	gcg	gcg	gtc	gcc	tgc	ttc	ctg	gcg	ctg	gag	ggc	gcc	gac	gtg	2513
Val	Gly	Ala	Ala	Val	Ala	Cys	Phe	Leu	Ala	Leu	Glu	Gly	Ala	Asp	Val	
			795					800					805			
agc	tac	acc	aac	cac	cgc	ggt	cgg	agc	ccg	ctg	gac	ctg	gcc	gcc	gag	2561
Ser	Tyr	Thr	Asn	His	Arg	Gly	Arg	Ser	Pro	Leu	Asp	Leu	Ala	Ala	Glu	
		810					815					820				
ggt	cgc	gtg	ctc	aag	gcc	ctt	cag	ggc	tgc	gcc	cag	cgc	ttc	cgg	gag	2609
Gly	Arg	Val	Leu	Lys	Ala	Leu	Gln	Gly	Cys	Ala	Gln	Arg	Phe	Arg	Glu	
	825					830					835					
cgg	cag	gcg	ggc	ggg	ggc	gcg	gcc	ccg	ggc	ccc	agg	caa	acg	ctc	ggg	2657
Arg	Gln	Ala	Gly	Gly	Gly	Ala	Ala	Pro	Gly	Pro	Arg	Gln	Thr	Leu	Gly	
	840				845					850					855	
acc	ccc	aac	acc	gtg	acg	aac	ctg	cac	gtg	ggc	gcc	gcg	ccg	ggg	ccc	2705
Thr	Pro	Asn	Thr	Val	Thr	Asn	Leu	His	Val	Gly	Ala	Ala	Pro	Gly	Pro	
				860					865					870		
gag	gcc	gct	gag	tgc	ctg	gtg	tgc	tcc	gag	ctg	gcg	ctg	ctg	gtg	ctg	2753
Glu	Ala	Ala	Glu	Cys	Leu	Val	Cys	Ser	Glu	Leu	Ala	Leu	Leu	Val	Leu	
			875					880					885			
ttc	tgc	ccg	tgc	cag	cac	cgc	acc	gtg	tgt	gag	gag	tgc	gcg	cgc	agg	2801
Phe	Ser	Pro	Cys	Gln	His	Arg	Thr	Val	Cys	Glu	Glu	Cys	Ala	Arg	Arg	
		890					895					900				
atg	aag	aag	tgc	atc	agg	tgc	cag	gtg	gtc	gtc	agc	aag	aaa	ctg	cgc	2849
Met	Lys	Lys	Cys	Ile	Arg	Cys	Gln	Val	Val	Val	Ser	Lys	Lys	Leu	Arg	
	905					910					915					
cca	gac	ggc	tct	gag	gtg	gcg	agc	gcc	gcc	ccc	gcc	ccc	ggc	ccg	ccg	2897
Pro	Asp	Gly	Ser	Glu	Val	Ala	Ser	Ala	Ala	Pro	Ala	Pro	Gly	Pro	Pro	
	920				925					930					935	
cgc	cag	ctg	gtg	gag	gag	ctg	cag	agc	cgc	tac	cgg	cag	atg	gag	gaa	2945
Arg	Gln	Leu	Val	Glu	Glu	Leu	Gln	Ser	Arg	Tyr	Arg	Gln	Met	Glu	Glu	
			940					945					950			
cgc	atc	acc	tgc	ccc	atc	tgc	atc	gac	agg	cac	atc	cgc	ctc	gtg	ttc	2993
Arg	Ile	Thr	Cys	Pro	Ile	Cys	Ile	Asp	Arg	His	Ile	Arg	Leu	Val	Phe	
			955					960					965			

cag tgc ggc cac ggc gca tgc gcc ccc tgc ggc tcc gcg ctc agc gcc 3041
 Gln Cys Gly His Gly Ala Cys Ala Pro Cys Gly Ser Ala Leu Ser Ala
 970 975 980

 tgc ccc atc tgc cgc cag ccc atc cgc gac cgc atc cag atc ttc gtg 3089
 Cys Pro Ile Cys Arg Gln Pro Ile Arg Asp Arg Ile Gln Ile Phe Val
 985 990 995

 tgagccgcgc cgtccgccgc gcccgagctg ccttcgcgtg ccccgccct gtgttttata 3149
 aaaagaaaga ttctcggat 3168

<210> 160
 <211> 999
 <212> PRT
 <213> Homo sapiens

<400> 160
 Met Gly Trp Lys Pro Ser Glu Ala Arg Gly Gln Ser Gln Ser Leu Gln
 1 5 10 15

 Ala Ser Gly Leu Gln Pro Arg Ser Leu Lys Ala Ala Arg Arg Ala Thr
 20 25 30

 Gly Arg Pro Asp Arg Ser Arg Ala Ala Pro Pro Asn Met Asp Pro Asp
 35 40 45

 Pro Gln Ala Gly Val Gln Val Gly Met Arg Val Val Arg Gly Val Asp
 50 55 60

 Trp Lys Trp Gly Gln Gln Asp Gly Gly Glu Gly Gly Val Gly Thr Val
 65 70 75 80

 Val Glu Leu Gly Arg His Gly Ser Pro Ser Thr Pro Asp Arg Thr Val
 85 90 95

 Val Val Gln Trp Asp Gln Gly Thr Arg Thr Asn Tyr Arg Ala Gly Tyr
 100 105 110

 Gln Gly Ala His Asp Leu Leu Leu Tyr Asp Asn Ala Gln Ile Gly Val
 115 120 125

 Arg His Pro Asn Ile Ile Cys Asp Cys Cys Lys Lys His Gly Leu Arg
 130 135 140

 Gly Met Arg Trp Lys Cys Arg Val Cys Leu Asp Tyr Asp Leu Cys Thr
 145 150 155 160

 Gln Cys Tyr Met His Asn Lys His Glu Leu Ala His Ala Phe Asp Arg
 165 170 175

 Tyr Glu Thr Ala His Ser Arg Pro Val Thr Leu Ser Pro Arg Gln Gly
 180 185 190

 Leu Pro Arg Ile Pro Leu Arg Gly Ile Phe Gln Gly Ala Lys Val Val

195					200					205						
Arg	Gly	Pro	Phe	Trp	Glu	Trp	Gly	Ser	Gln	Asp	Gly	Gly	Glu	Gly	Lys	
210					215					220						
Pro	Gly	Arg	Val	Val	Asp	Ile	Arg	Gly	Trp	Asp	Val	Glu	Thr	Gly	Arg	
225					230					235					240	
Ser	Val	Ala	Ser	Val	Thr	Trp	Ala	Asp	Gly	Thr	Thr	Asn	Val	Tyr	Arg	
245					250					255						
Val	Gly	His	Lys	Gly	Lys	Val	Asp	Leu	Lys	Cys	Val	Gly	Glu	Ala	Ala	
260					265					270						
Gly	Gly	Phe	Tyr	Tyr	Lys	Asp	His	Leu	Pro	Arg	Leu	Gly	Lys	Pro	Ala	
275					280					285						
Glu	Leu	Gln	Arg	Arg	Val	Ser	Ala	Asp	Ser	Gln	Pro	Phe	Gln	His	Gly	
290					295					300						
Asp	Lys	Val	Lys	Cys	Leu	Leu	Asp	Thr	Asp	Val	Leu	Arg	Glu	Met	Gln	
305					310					315					320	
Glu	Gly	His	Gly	Gly	Trp	Asn	Pro	Arg	Met	Ala	Glu	Phe	Ile	Gly	Gln	
325					330					335						
Thr	Gly	Thr	Val	His	Arg	Ile	Thr	Asp	Arg	Gly	Asp	Val	Arg	Val	Gln	
340					345					350						
Phe	Asn	His	Glu	Thr	Arg	Trp	Thr	Phe	His	Pro	Gly	Ala	Leu	Thr	Lys	
355					360					365						
His	His	Ser	Phe	Trp	Val	Gly	Asp	Val	Val	Arg	Val	Ile	Gly	Asp	Leu	
370					375					380						
Asp	Thr	Val	Lys	Arg	Leu	Gln	Ala	Gly	His	Gly	Glu	Trp	Thr	Asp	Asp	
385					390					395					400	
Met	Ala	Pro	Ala	Leu	Gly	Arg	Val	Gly	Lys	Val	Val	Lys	Val	Phe	Gly	
405					410					415						
Asp	Gly	Asn	Leu	Arg	Val	Ala	Val	Ala	Gly	Gln	Arg	Trp	Thr	Phe	Ser	
420					425					430						
Pro	Ser	Cys	Leu	Val	Ala	Tyr	Arg	Pro	Glu	Glu	Asp	Ala	Asn	Leu	Asp	
435					440					445						
Val	Ala	Glu	Arg	Ala	Arg	Glu	Asn	Lys	Ser	Ser	Leu	Ser	Val	Ala	Leu	
450					455					460						
Asp	Lys	Leu	Arg	Ala	Gln	Lys	Ser	Asp	Pro	Glu	His	Pro	Gly	Arg	Leu	
465					470					475					480	
Val	Val	Glu	Val	Ala	Leu	Gly	Asn	Ala	Ala	Arg	Ala	Leu	Asp	Leu	Leu	
485					490					495						
Arg	Arg	Arg	Pro	Glu	Gln	Val	Asp	Thr	Lys	Asn	Gln	Gly	Arg	Thr	Ala	

500 505 510
 Leu Gln Val Ala Ala Tyr Leu Gly Gln Val Glu Leu Ile Arg Leu Leu
 515 520 525
 Leu Gln Ala Arg Ala Gly Val Asp Leu Pro Asp Asp Glu Gly Asn Thr
 530 535 540
 Ala Leu His Tyr Ala Ala Leu Gly Asn Gln Pro Glu Ala Thr Arg Val
 545 550 555 560
 Leu Leu Ser Ala Gly Cys Arg Ala Asp Ala Ile Asn Ser Thr Gln Ser
 565 570 575
 Thr Ala Leu His Val Ala Val Gln Arg Gly Phe Leu Glu Val Val Arg
 580 585 590
 Ala Leu Cys Glu Arg Gly Cys Asp Val Asn Leu Pro Asp Ala His Ser
 595 600 605
 Asp Thr Pro Leu His Ser Ala Ile Ser Ala Gly Thr Gly Ala Ser Gly
 610 615 620
 Ile Val Glu Val Leu Thr Glu Val Pro Asn Ile Asp Val Thr Ala Thr
 625 630 635 640
 Asn Ser Gln Gly Phe Thr Leu Leu His His Ala Ser Leu Lys Gly His
 645 650 655
 Ala Leu Ala Val Arg Lys Ile Leu Ala Arg Ala Arg Gln Leu Val Asp
 660 665 670
 Ala Lys Lys Glu Asp Gly Phe Thr Ala Leu His Leu Ala Ala Leu Asn
 675 680 685
 Asn His Arg Glu Val Ala Gln Ile Leu Ile Arg Glu Gly Arg Cys Asp
 690 695 700
 Val Asn Val Arg Asn Arg Lys Leu Gln Ser Pro Leu His Leu Ala Val
 705 710 715 720
 Gln Gln Ala His Val Gly Leu Val Pro Leu Leu Val Asp Ala Gly Cys
 725 730 735
 Ser Val Asn Ala Glu Asp Glu Glu Gly Asp Thr Ala Leu His Val Ala
 740 745 750
 Leu Gln Arg His Gln Leu Leu Pro Leu Val Ala Asp Gly Ala Gly Gly
 755 760 765
 Asp Pro Gly Pro Leu Gln Leu Leu Ser Arg Leu Gln Ala Ser Gly Leu
 770 775 780
 Pro Gly Ser Ala Glu Leu Thr Val Gly Ala Ala Val Ala Cys Phe Leu
 785 790 795 800
 Ala Leu Glu Gly Ala Asp Val Ser Tyr Thr Asn His Arg Gly Arg Ser

-805 - - - - - 810 - - - - - 815 -
 Pro Leu Asp Leu Ala Ala Glu Gly Arg Val Leu Lys Ala Leu Gln Gly
 820 825 830
 Cys Ala Gln Arg Phe Arg Glu Arg Gln Ala Gly Gly Gly Ala Ala Pro
 835 840 845
 Gly Pro Arg Gln Thr Leu Gly Thr Pro Asn Thr Val Thr Asn Leu His
 850 855 860
 Val Gly Ala Ala Pro Gly Pro Glu Ala Ala Glu Cys Leu Val Cys Ser
 865 870 875 880
 Glu Leu Ala Leu Leu Val Leu Phe Ser Pro Cys Gln His Arg Thr Val
 885 890 895
 Cys Glu Glu Cys Ala Arg Arg Met Lys Lys Cys Ile Arg Cys Gln Val
 900 905 910
 Val Val Ser Lys Lys Leu Arg Pro Asp Gly Ser Glu Val Ala Ser Ala
 915 920 925
 Ala Pro Ala Pro Gly Pro Pro Arg Gln Leu Val Glu Glu Leu Gln Ser
 930 935 940
 Arg Tyr Arg Gln Met Glu Glu Arg Ile Thr Cys Pro Ile Cys Ile Asp
 945 950 955 960
 Arg His Ile Arg Leu Val Phe Gln Cys Gly His Gly Ala Cys Ala Pro
 965 970 975
 Cys Gly Ser Ala Leu Ser Ala Cys Pro Ile Cys Arg Gln Pro Ile Arg
 980 985 990
 Asp Arg Ile Gln Ile Phe Val
 995

<210> 161
 <211> 3168
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (93)..(3089)

<400> 161
 agtgcgccgt ggcccaggag ggcttgggag cccgaagccg tccccgagtc gctcctaggt 60
 cactggcgcg atgcggggccg tcctctcggc tg atg ggt tgg aag ccc agc gag 113
 Met Gly Trp Lys Pro Ser Glu
 1 5
 gct aga ggc cag tcc caa agt ctc cag gca tca ggg ctg cag ccc agg 161
 Ala Arg Gly Gln Ser Gln Ser Leu Gln Ala Ser Gly Leu Gln Pro Arg

10										15										20										
agc	ctc	aag	gcg	gcc	cgg	cgg	gcg	act	gga	cgg	ccg	gac	agg	tcc	cga	209														
Ser	Leu	Lys	Ala	Ala	Arg	Arg	Ala	Thr	Gly	Arg	Pro	Asp	Arg	Ser	Arg															
25				30				35																						
gca	gcc	ccg	ccc	aac	atg	gac	cca	gac	ccc	cag	gcg	ggc	gtg	cag	gtg	257														
Ala	Ala	Pro	Pro	Asn	Met	Asp	Pro	Asp	Pro	Gln	Ala	Gly	Val	Gln	Val															
40				45				50						55																
ggc	atg	cgg	gtg	gtg	cgc	ggc	gtg	gac	tgg	aag	tgg	ggc	cag	cag	gac	305														
Gly	Met	Arg	Val	Val	Arg	Gly	Val	Asp	Trp	Lys	Trp	Gly	Gln	Gln	Asp															
				60				65						70																
ggc	ggc	gag	ggc	ggc	gtg	ggc	acg	gtg	gtg	gag	ctt	ggc	cgc	cac	ggc	353														
Gly	Gly	Glu	Gly	Gly	Val	Gly	Thr	Val	Val	Glu	Leu	Gly	Arg	His	Gly															
		75						80						85																
agc	ccc	tcg	aca	ccc	gac	cgc	aca	gtg	gtc	gtg	cag	tgg	gac	cag	ggc	401														
Ser	Pro	Ser	Thr	Pro	Asp	Arg	Thr	Val	Val	Val	Gln	Trp	Asp	Gln	Gly															
90						95						100																		
acg	cgc	acc	aac	tac	cgc	gcc	ggc	tac	cag	ggc	gcg	cac	gac	ctg	ctg	449														
Thr	Arg	Thr	Asn	Tyr	Arg	Ala	Gly	Tyr	Gln	Gly	Ala	His	Asp	Leu	Leu															
105						110						115																		
ctg	tac	gac	aac	gcc	cag	atc	ggc	gtc	cgg	cac	ccc	aac	atc	atc	tgt	497														
Leu	Tyr	Asp	Asn	Ala	Gln	Ile	Gly	Val	Arg	His	Pro	Asn	Ile	Ile	Cys															
120				125						130						135														
gac	tgc	tgc	aag	aag	cac	ggg	ctg	cgg	ggg	atg	cgc	tgg	aag	tgc	cgt	545														
Asp	Cys	Cys	Lys	Lys	His	Gly	Leu	Arg	Gly	Met	Arg	Trp	Lys	Cys	Arg															
				140				145						150																
gtg	tgc	ctg	gac	tac	gac	ctc	tgc	acg	cag	tgc	tac	atg	cac	aac	aag	593														
Val	Cys	Leu	Asp	Tyr	Asp	Leu	Cys	Thr	Gln	Cys	Tyr	Met	His	Asn	Lys															
		155						160						165																
cat	gag	ctc	gcc	cac	gcc	ttc	gac	cgc	tac	gag	acc	gct	cac	tgc	cgc	641														
His	Glu	Leu	Ala	His	Ala	Phe	Asp	Arg	Tyr	Glu	Thr	Ala	His	Ser	Arg															
170						175						180																		
cct	gtc	aca	ctg	agt	ccc	cgc	cag	ggc	ctc	ccg	agg	atc	cca	cta	agg	689														
Pro	Val	Thr	Leu	Ser	Pro	Arg	Gln	Gly	Leu	Pro	Arg	Ile	Pro	Leu	Arg															
185						190						195																		
ggc	atc	ttc	cag	gga	gcg	aag	gtg	gtg	cga	ggc	ccc	ttc	tgg	gag	tgg	737														
Gly	Ile	Phe	Gln	Gly	Ala	Lys	Val	Val	Arg	Gly	Pro	Phe	Trp	Glu	Trp															
200				205						210				215																
ggc	tca	cag	gat	gga	ggg	gaa	ggg	aaa	ccg	ggc	cgt	gtg	gtg	gac	atc	785														
Gly	Ser	Gln	Asp	Gly	Gly	Glu	Gly	Lys	Pro	Gly	Arg	Val	Val	Asp	Ile															
		220						225						230																
cgt	ggc	tgg	gat	gtg	gag	aca	ggc	cgg	agt	gtg	gcc	agc	gtg	acg	tgg	833														
Arg	Gly	Trp	Asp	Val	Glu	Thr	Gly	Arg	Ser	Val	Ala	Ser	Val	Thr	Trp															
		235				240						245																		

gct gat ggt acc acc aat gtg tac cgt gtg ggc cac aag ggc aag gtg	881
Ala Asp Gly Thr Thr Asn Val Tyr Arg Val Gly His Lys Gly Lys Val	
250 255 260	
gac ctc aag tgt gtg ggc gag gca gcg ggc ggc ttc tac tac aag gac	929
Asp Leu Lys Cys Val Gly Glu Ala Ala Gly Gly Phe Tyr Tyr Lys Asp	
265 270 275	
cac ctc cca agg ctc ggc aag ccg gcg gag ctg cag cgc agg gtg agt	977
His Leu Pro Arg Leu Gly Lys Pro Ala Glu Leu Gln Arg Arg Val Ser	
280 285 290 295	
gct gac agc cag ccc ttc cag cac ggg gac aag gtc aag tgt ctg ctg	1025
Ala Asp Ser Gln Pro Phe Gln His Gly Asp Lys Val Lys Cys Leu Leu	
300 305 310	
gac act gat gtc ctg cgg gag atg cag gaa ggc cac ggc ggc tgg aac	1073
Asp Thr Asp Val Leu Arg Glu Met Gln Glu Gly His Gly Gly Trp Asn	
315 320 325	
ccc agg atg gcg gag ttt atc gga cag acg ggc acc gtg cat cgt atc	1121
Pro Arg Met Ala Glu Phe Ile Gly Gln Thr Gly Thr Val His Arg Ile	
330 335 340	
acg gac cgc ggg gac gtg cgc gtg cag ttc aac cac gag acg cgc tgg	1169
Thr Asp Arg Gly Asp Val Arg Val Gln Phe Asn His Glu Thr Arg Trp	
345 350 355	
acc ttc cac ccc ggg gcg ctc acc aag cac cac tcc ttc tgg gtg ggc	1217
Thr Phe His Pro Gly Ala Leu Thr Lys His His Ser Phe Trp Val Gly	
360 365 370 375	
gac gtg gtc cgg gtc atc ggc gac ctt gac aca gtg aag cgg ctg cag	1265
Asp Val Val Arg Val Ile Gly Asp Leu Asp Thr Val Lys Arg Leu Gln	
380 385 390	
gct ggg cat ggc gag tgg acg gac gac atg gcc cct gcc ctg ggc cgc	1313
Ala Gly His Gly Glu Trp Thr Asp Asp Met Ala Pro Ala Leu Gly Arg	
395 400 405	
gtc ggg aag gtg gtg aaa gtg ttt gga gac ggg aac ctg cgt gta gca	1361
Val Gly Lys Val Val Lys Val Phe Gly Asp Gly Asn Leu Arg Val Ala	
410 415 420	
gtc gct ggt cag cgg tgg acc ttc agc ccc tcc tgc ctg gtg gcc tac	1409
Val Ala Gly Gln Arg Trp Thr Phe Ser Pro Ser Cys Leu Val Ala Tyr	
425 430 435	
cgg ccc gag gag gat gcc aac ctg gac gtg gcc gag cgc gcc cgg gag	1457
Arg Pro Glu Glu Asp Ala Asn Leu Asp Val Ala Glu Arg Ala Arg Glu	
440 445 450 455	
aac aaa agc tca ctg agc gtg gcc ctg gac aag ctt cgg gcc cag aag	1505
Asn Lys Ser Ser Leu Ser Val Ala Leu Asp Lys Leu Arg Ala Gln Lys	
460 465 470	

agt gac cca gag cac ccg gga agg ctg gtg gtg gag gtg gcg-ctg ggt	-1553-
Ser Asp Pro Glu His Pro Gly Arg Leu Val Val Glu Val Ala Leu Gly	
475 480 485	
aac gca gcc cgg gct ctg gac ctg ctg cgg agg cgc cca gag caa gtg	1601
Asn Ala Ala Arg Ala Leu Asp Leu Leu Arg Arg Arg Pro Glu Gln Val	
490 495 500	
gac acc aag aac caa ggc agg acc gct ctg caa gtg gct gcc tac ctg	1649
Asp Thr Lys Asn Gln Gly Arg Thr Ala Leu Gln Val Ala Ala Tyr Leu	
505 510 515	
ggc cag gtg gag ttg ata cgg ctg ctg cta caa gcc agg gcg ggc gtg	1697
Gly Gln Val Glu Leu Ile Arg Leu Leu Leu Gln Ala Arg Ala Gly Val	
520 525 530 535	
gac ctg ccg gac gac gag ggc aac acg gca ctg cac tac gcg gcc ctg	1745
Asp Leu Pro Asp Asp Glu Gly Asn Thr Ala Leu His Tyr Ala Ala Leu	
540 545 550	
ggg aac cag ccc gag gcc acc agg gtg ctc ctg agt gct ggg tgc cgg	1793
Gly Asn Gln Pro Glu Ala Thr Arg Val Leu Leu Ser Ala Gly Cys Arg	
555 560 565	
gcg gac gcc atc aac agc acc cag agc aca gca ctg cac gtg gcc gtg	1841
Ala Asp Ala Ile Asn Ser Thr Gln Ser Thr Ala Leu His Val Ala Val	
570 575 580	
cag agg ggc ttc ctg gag gtg gtg cgg gcc ctg tgt gag cgc ggc tgt	1889
Gln Arg Gly Phe Leu Glu Val Val Arg Ala Leu Cys Glu Arg Gly Cys	
585 590 595	
gac gtc aac ctg ccc gac gcc cac tcg gac acg ccc ctg cac tcc gcc	1937
Asp Val Asn Leu Pro Asp Ala His Ser Asp Thr Pro Leu His Ser Ala	
600 605 610 615	
atc tcg gcg ggc act gga gcc agc ggc att gtc gag gtc ctc acg gag	1985
Ile Ser Ala Gly Thr Gly Ala Ser Gly Ile Val Glu Val Leu Thr Glu	
620 625 630	
gtg cca aac atc gat gtt acc gcc acc aac agc cag ggt ttc acc ctg	2033
Val Pro Asn Ile Asp Val Thr Ala Thr Asn Ser Gln Gly Phe Thr Leu	
635 640 645	
ctg cac cat gcc tcc ctc aag ggt cac gcg cta gct gtg aga aag att	2081
Leu His His Ala Ser Leu Lys Gly His Ala Leu Ala Val Arg Lys Ile	
650 655 660	
ctg gct cgg gcg cgg cag ctg gtg gac gcc aag aag gag gac ggc ttc	2129
Leu Ala Arg Ala Arg Gln Leu Val Asp Ala Lys Lys Glu Asp Gly Phe	
665 670 675	
acg gcg ctg cat ctg gct gcc ctc aac aac cac cgc gag gtg gcc cag	2177
Thr Ala Leu His Leu Ala Ala Leu Asn Asn His Arg Glu Val Ala Gln	
680 685 690 695	
atc ctc atc cgg gag ggc cgc tgt gac gtg aac gtg cgc aac cgg aag	2225

Ile	Leu	Ile	Arg	Glu	Gly	Arg	Cys	Asp	Val	Asn	Val	Arg	Asn	Arg	Lys	
				700					705					710		
ctg	cag	tcc	ccg	ctg	cat	ctc	gcc	gtg	caa	cag	gcc	cac	gtg	ggg	ctg	2273
Leu	Gln	Ser	Pro	Leu	His	Leu	Ala	Val	Gln	Gln	Ala	His	Val	Gly	Leu	
			715					720					725			
gtg	ccg	cta	ctg	gtg	gac	gct	ggg	tgc	agt	gtc	aac	gcc	gag	gac	gag	2321
Val	Pro	Leu	Leu	Val	Asp	Ala	Gly	Cys	Ser	Val	Asn	Ala	Glu	Asp	Glu	
		730					735					740				
gag	ggg	gac	aca	gcc	ctg	cac	gtg	gcg	ctg	cag	cgt	cat	cag	ctg	ctg	2369
Glu	Gly	Asp	Thr	Ala	Leu	His	Val	Ala	Leu	Gln	Arg	His	Gln	Leu	Leu	
	745					750					755					
ccc	ctg	gtg	gct	gat	ggg	gcc	ggg	ggg	gac	cca	ggg	ccc	ttg	cag	ctg	2417
Pro	Leu	Val	Ala	Asp	Gly	Ala	Gly	Gly	Asp	Pro	Gly	Pro	Leu	Gln	Leu	
760					765				770						775	
ctg	tcc	agg	cta	cag	gcc	tgc	ggc	ctc	ccc	ggc	agc	gcg	gag	ctg	acg	2465
Leu	Ser	Arg	Leu	Gln	Ala	Ser	Gly	Leu	Pro	Gly	Ser	Ala	Glu	Leu	Thr	
				780					785					790		
gtg	ggc	gcg	gcg	gtc	gcc	tgc	ttc	ctg	gcg	ctg	gag	ggc	gcc	gac	gtg	2513
Val	Gly	Ala	Ala	Val	Ala	Cys	Phe	Leu	Ala	Leu	Glu	Gly	Ala	Asp	Val	
			795					800					805			
agc	tac	acc	aac	cac	cgc	ggt	cgg	agc	ccg	ctg	gac	ctg	gcc	gcc	gag	2561
Ser	Tyr	Thr	Asn	His	Arg	Gly	Arg	Ser	Pro	Leu	Asp	Leu	Ala	Ala	Glu	
		810					815					820				
ggt	cgc	gtg	ctc	aag	gcc	ctt	cag	ggc	tgc	gcc	cag	cgc	ttc	cgg	gag	2609
Gly	Arg	Val	Leu	Lys	Ala	Leu	Gln	Gly	Cys	Ala	Gln	Arg	Phe	Arg	Glu	
	825					830					835					
cgg	cag	gcg	ggc	ggg	ggc	gcg	gcc	ccg	ggc	ccc	agg	caa	acg	ctc	ggg	2657
Arg	Gln	Ala	Gly	Gly	Gly	Ala	Ala	Pro	Gly	Pro	Arg	Gln	Thr	Leu	Gly	
840					845					850					855	
acc	ccc	aac	acc	gtg	acg	aac	ctg	cac	gtg	ggc	gcc	gcg	ccg	ggg	ccc	2705
Thr	Pro	Asn	Thr	Val	Thr	Asn	Leu	His	Val	Gly	Ala	Ala	Pro	Gly	Pro	
				860					865					870		
gag	gcc	gct	gag	tgc	ctg	gtg	tgc	tcc	gag	ctg	gcg	ctg	ctg	gtg	ctg	2753
Glu	Ala	Ala	Glu	Cys	Leu	Val	Cys	Ser	Glu	Leu	Ala	Leu	Leu	Val	Leu	
			875					880						885		
ttc	tgc	ccg	tgc	cag	cac	cgc	acc	gtg	tgt	gag	gag	tgc	gcg	cgc	agg	2801
Phe	Ser	Pro	Cys	Gln	His	Arg	Thr	Val	Cys	Glu	Glu	Cys	Ala	Arg	Arg	
		890					895					900				
atg	aag	aag	tgc	atc	agg	tgc	cag	gtg	gtc	gtc	agc	aag	aaa	ctg	cgc	2849
Met	Lys	Lys	Cys	Ile	Arg	Cys	Gln	Val	Val	Val	Ser	Lys	Lys	Leu	Arg	
	905					910					915					
cca	gac	ggc	tct	gag	gtg	gcg	agc	gcc	gcc	ccc	gcc	ccc	ggc	ccg	ccg	2897
Pro	Asp	Gly	Ser	Glu	Val	Ala	Ser	Ala	Ala	Pro	Ala	Pro	Gly	Pro	Pro	

145					150					155					160
Gln	Cys	Tyr	Met	His	Asn	Lys	His	Glu	Leu	Ala	His	Ala	Phe	Asp	Arg
				165					170					175	
Tyr	Glu	Thr	Ala	His	Ser	Arg	Pro	Val	Thr	Leu	Ser	Pro	Arg	Gln	Gly
			180					185					190		
Leu	Pro	Arg	Ile	Pro	Leu	Arg	Gly	Ile	Phe	Gln	Gly	Ala	Lys	Val	Val
		195					200					205			
Arg	Gly	Pro	Phe	Trp	Glu	Trp	Gly	Ser	Gln	Asp	Gly	Gly	Glu	Gly	Lys
	210					215					220				
Pro	Gly	Arg	Val	Val	Asp	Ile	Arg	Gly	Trp	Asp	Val	Glu	Thr	Gly	Arg
225					230					235					240
Ser	Val	Ala	Ser	Val	Thr	Trp	Ala	Asp	Gly	Thr	Thr	Asn	Val	Tyr	Arg
				245					250					255	
Val	Gly	His	Lys	Gly	Lys	Val	Asp	Leu	Lys	Cys	Val	Gly	Glu	Ala	Ala
			260					265					270		
Gly	Gly	Phe	Tyr	Tyr	Lys	Asp	His	Leu	Pro	Arg	Leu	Gly	Lys	Pro	Ala
		275					280					285			
Glu	Leu	Gln	Arg	Arg	Val	Ser	Ala	Asp	Ser	Gln	Pro	Phe	Gln	His	Gly
	290					295					300				
Asp	Lys	Val	Lys	Cys	Leu	Leu	Asp	Thr	Asp	Val	Leu	Arg	Glu	Met	Gln
305					310					315					320
Glu	Gly	His	Gly	Gly	Trp	Asn	Pro	Arg	Met	Ala	Glu	Phe	Ile	Gly	Gln
				325					330					335	
Thr	Gly	Thr	Val	His	Arg	Ile	Thr	Asp	Arg	Gly	Asp	Val	Arg	Val	Gln
			340					345					350		
Phe	Asn	His	Glu	Thr	Arg	Trp	Thr	Phe	His	Pro	Gly	Ala	Leu	Thr	Lys
		355					360					365			
His	His	Ser	Phe	Trp	Val	Gly	Asp	Val	Val	Arg	Val	Ile	Gly	Asp	Leu
	370					375					380				
Asp	Thr	Val	Lys	Arg	Leu	Gln	Ala	Gly	His	Gly	Glu	Trp	Thr	Asp	Asp
385					390					395					400
Met	Ala	Pro	Ala	Leu	Gly	Arg	Val	Gly	Lys	Val	Val	Lys	Val	Phe	Gly
				405					410					415	
Asp	Gly	Asn	Leu	Arg	Val	Ala	Val	Ala	Gly	Gln	Arg	Trp	Thr	Phe	Ser
			420					425					430		
Pro	Ser	Cys	Leu	Val	Ala	Tyr	Arg	Pro	Glu	Glu	Asp	Ala	Asn	Leu	Asp
		435					440					445			
Val	Ala	Glu	Arg	Ala	Arg	Glu	Asn	Lys	Ser	Ser	Leu	Ser	Val	Ala	Leu

450	455	460															
Asp Lys Leu Arg Ala Gln Lys Ser Asp Pro Glu His Pro Gly Arg Leu																	
465		470						475								480	
Val Val Glu Val Ala Leu Gly Asn Ala Ala Arg Ala Leu Asp Leu Leu																	
		485						490								495	
Arg Arg Arg Pro Glu Gln Val Asp Thr Lys Asn Gln Gly Arg Thr Ala																	
		500						505							510		
Leu Gln Val Ala Ala Tyr Leu Gly Gln Val Glu Leu Ile Arg Leu Leu																	
		515						520							525		
Leu Gln Ala Arg Ala Gly Val Asp Leu Pro Asp Asp Glu Gly Asn Thr																	
		530						535							540		
Ala Leu His Tyr Ala Ala Leu Gly Asn Gln Pro Glu Ala Thr Arg Val																	
		545						550							555		560
Leu Leu Ser Ala Gly Cys Arg Ala Asp Ala Ile Asn Ser Thr Gln Ser																	
		565						570									575
Thr Ala Leu His Val Ala Val Gln Arg Gly Phe Leu Glu Val Val Arg																	
		580						585							590		
Ala Leu Cys Glu Arg Gly Cys Asp Val Asn Leu Pro Asp Ala His Ser																	
		595						600							605		
Asp Thr Pro Leu His Ser Ala Ile Ser Ala Gly Thr Gly Ala Ser Gly																	
		610						615							620		
Ile Val Glu Val Leu Thr Glu Val Pro Asn Ile Asp Val Thr Ala Thr																	
		625						630							635		640
Asn Ser Gln Gly Phe Thr Leu Leu His His Ala Ser Leu Lys Gly His																	
		645						650									655
Ala Leu Ala Val Arg Lys Ile Leu Ala Arg Ala Arg Gln Leu Val Asp																	
		660						665							670		
Ala Lys Lys Glu Asp Gly Phe Thr Ala Leu His Leu Ala Ala Leu Asn																	
		675						680							685		
Asn His Arg Glu Val Ala Gln Ile Leu Ile Arg Glu Gly Arg Cys Asp																	
		690						695							700		
Val Asn Val Arg Asn Arg Lys Leu Gln Ser Pro Leu His Leu Ala Val																	
		705						710							715		720
Gln Gln Ala His Val Gly Leu Val Pro Leu Leu Val Asp Ala Gly Cys																	
		725						730									735
Ser Val Asn Ala Glu Asp Glu Glu Gly Asp Thr Ala Leu His Val Ala																	
		740						745							750		
Leu Gln Arg His Gln Leu Leu Pro Leu Val Ala Asp Gly Ala Gly Gly																	

755 760 765
 Asp Pro Gly Pro Leu Gln Leu Leu Ser Arg Leu Gln Ala Ser Gly Leu
 770 775 780
 Pro Gly Ser Ala Glu Leu Thr Val Gly Ala Ala Val Ala Cys Phe Leu
 785 790 795 800
 Ala Leu Glu Gly Ala Asp Val Ser Tyr Thr Asn His Arg Gly Arg Ser
 805 810 815
 Pro Leu Asp Leu Ala Ala Glu Gly Arg Val Leu Lys Ala Leu Gln Gly
 820 825 830
 Cys Ala Gln Arg Phe Arg Glu Arg Gln Ala Gly Gly Gly Ala Ala Pro
 835 840 845
 Gly Pro Arg Gln Thr Leu Gly Thr Pro Asn Thr Val Thr Asn Leu His
 850 855 860
 Val Gly Ala Ala Pro Gly Pro Glu Ala Ala Glu Cys Leu Val Cys Ser
 865 870 875 880
 Glu Leu Ala Leu Leu Val Leu Phe Ser Pro Cys Gln His Arg Thr Val
 885 890 895
 Cys Glu Glu Cys Ala Arg Arg Met Lys Lys Cys Ile Arg Cys Gln Val
 900 905 910
 Val Val Ser Lys Lys Leu Arg Pro Asp Gly Ser Glu Val Ala Ser Ala
 915 920 925
 Ala Pro Ala Pro Gly Pro Pro Arg Gln Leu Val Glu Glu Leu Gln Ser
 930 935 940
 Arg Tyr Arg Gln Met Glu Glu Arg Ile Thr Cys Pro Ile Cys Ile Asp
 945 950 955 960
 Ser His Ile Arg Leu Val Phe Gln Cys Gly His Gly Ala Cys Ala Pro
 965 970 975
 Cys Gly Ser Ala Leu Ser Ala Cys Pro Ile Cys Arg Gln Pro Ile Arg
 980 985 990
 Asp Arg Ile Gln Ile Phe Val
 995

<210> 163
 <211> 4031
 <212> DNA
 <213> Mus musculus

 <220>
 <221> CDS
 <222> (91)..(2649)

```

<400>_163_
gtttctggtcc cggtagatg ctggaagctg ctgcggcagc cgcaacgcgc ccggtcgccg 60

tcccgtcgcc aatccccgcc gtcccgggcc atg atc gcc tgg cgt ctg ccc ttg 114
Met Ile Ala Trp Arg Leu Pro Leu
1 5

tgc gtg ctc ttg gtg gcc tcc gtc gag agc cac ctg ggg gcc ctg ggg 162
Cys Val Leu Leu Val Ala Ser Val Glu Ser His Leu Gly Ala Leu Gly
10 15 20

ccc aag aac gtc tcg cag aaa gac gcg gag ttt gag cgc acc tac gcg 210
Pro Lys Asn Val Ser Gln Lys Asp Ala Glu Phe Glu Arg Thr Tyr Ala
25 30 35 40

gac gac gtc aac agc gag ctg gtc aac atc tac acc ttc aac cac acc 258
Asp Asp Val Asn Ser Glu Leu Val Asn Ile Tyr Thr Phe Asn His Thr
45 50 55

gtg acc cgc aac cgg acc gag ggt gtg cga gtg tct gtg aat gtc ctg 306
Val Thr Arg Asn Arg Thr Glu Gly Val Arg Val Ser Val Asn Val Leu
60 65 70

aac aag cag aaa ggg gcg cct ttg ctg ttc gtg gtc cgc cag aag gag 354
Asn Lys Gln Lys Gly Ala Pro Leu Leu Phe Val Val Arg Gln Lys Glu
75 80 85

gct gtt gtg tcc ttc cag gtg ccc cta atc ctt cga gga ctg tat cag 402
Ala Val Val Ser Phe Gln Val Pro Leu Ile Leu Arg Gly Leu Tyr Gln
90 95 100

cgg aag tac ctc tac caa aaa gtg gaa cga act ctg tgt cag ccc ccc 450
Arg Lys Tyr Leu Tyr Gln Lys Val Glu Arg Thr Leu Cys Gln Pro Pro
105 110 115 120

acc aag aat gag tct gag atc cag ttt ttc tat gtg gac gtg tct acc 498
Thr Lys Asn Glu Ser Glu Ile Gln Phe Phe Tyr Val Asp Val Ser Thr
125 130 135

ctg tca ccc gtc aat acc act tac cag ctc cga gtc aac cgt gtg gac 546
Leu Ser Pro Val Asn Thr Thr Tyr Gln Leu Arg Val Asn Arg Val Asp
140 145 150

aat ttt gtg ctc agg act gga gag ctg ttt acc ttt aat acc act gca 594
Asn Phe Val Leu Arg Thr Gly Glu Leu Phe Thr Phe Asn Thr Thr Ala
155 160 165

gcc cag ccc cag tac ttc aaa tac gag ttt cct gat ggt gtg gac tcg 642
Ala Gln Pro Gln Tyr Phe Lys Tyr Glu Phe Pro Asp Gly Val Asp Ser
170 175 180

gta att gtc aag gtg acc tcc aag aag gcc ttc ccc tgc tca gtc atc 690
Val Ile Val Lys Val Thr Ser Lys Lys Ala Phe Pro Cys Ser Val Ile
185 190 195 200

tcc atc cag gat gtc ctg tgc cct gtc tat gat ctg gac aac agt gta 738
Ser Ile Gln Asp Val Leu Cys Pro Val Tyr Asp Leu Asp Asn Ser Val

```


205										210					215					
gcc	ttc	att	ggc	atg	tac	cag	acg	atg	act	aag	aag	gca	gcc	atc	act	786				
Ala	Phe	Ile	Gly	Met	Tyr	Gln	Thr	Met	Thr	Lys	Lys	Ala	Ala	Ile	Thr					
			220					225					230							
gtg	cag	cgg	aaa	gac	ttc	ccc	agc	aac	agc	ttc	tat	gtg	gtg	gtg	gta	834				
Val	Gln	Arg	Lys	Asp	Phe	Pro	Ser	Asn	Ser	Phe	Tyr	Val	Val	Val	Val					
			235				240					245								
gtg	aag	act	gag	gac	cag	gcc	tgc	gga	ggg	tcc	ttg	ccc	ttc	tac	cct	882				
Val	Lys	Thr	Glu	Asp	Gln	Ala	Cys	Gly	Gly	Ser	Leu	Pro	Phe	Tyr	Pro					
	250					255					260									
ttt	gtg	gaa	gat	gag	cca	gtg	gat	caa	ggg	cac	cgt	cag	aaa	aca	ctg	930				
Phe	Val	Glu	Asp	Glu	Pro	Val	Asp	Gln	Gly	His	Arg	Gln	Lys	Thr	Leu					
265					270				275						280					
tca	gtg	ctg	gtc	tct	cag	gct	gtc	aca	tct	gag	gcc	tat	gtt	ggg	ggg	978				
Ser	Val	Leu	Val	Ser	Gln	Ala	Val	Thr	Ser	Glu	Ala	Tyr	Val	Gly	Gly					
				285				290						295						
atg	ctc	ttt	tgc	ctg	ggc	ata	ttc	ttg	tcc	ttc	tac	ctg	ctg	act	gtg	1026				
Met	Leu	Phe	Cys	Leu	Gly	Ile	Phe	Leu	Ser	Phe	Tyr	Leu	Leu	Thr	Val					
			300				305						310							
ctg	ctg	gcc	tgt	tgg	gag	aac	tgg	agg	caa	agg	aag	aag	acc	ttg	ctg	1074				
Leu	Leu	Ala	Cys	Trp	Glu	Asn	Trp	Arg	Gln	Arg	Lys	Lys	Thr	Leu	Leu					
		315					320					325								
gtg	gcc	ata	gac	cga	gcc	tgc	cca	gaa	agt	ggg	cac	gct	cgg	gtc	ttg	1122				
Val	Ala	Ile	Asp	Arg	Ala	Cys	Pro	Glu	Ser	Gly	His	Ala	Arg	Val	Leu					
	330					335					340									
gct	gat	tca	ttt	cct	ggc	agt	gcc	cct	tac	gag	ggg	tac	aac	tat	ggc	1170				
Ala	Asp	Ser	Phe	Pro	Gly	Ser	Ala	Pro	Tyr	Glu	Gly	Tyr	Asn	Tyr	Gly					
345					350					355					360					
tcc	ttt	gaa	aat	ggg	tcc	gga	tcc	act	gac	ggg	ttg	gtt	gaa	agc	gca	1218				
Ser	Phe	Glu	Asn	Gly	Ser	Gly	Ser	Thr	Asp	Gly	Leu	Val	Glu	Ser	Ala					
				365				370						375						
ggg	tca	ggg	gac	ctc	tcc	tac	agt	tac	cag	ggg	cac	gac	cag	ttc	aag	1266				
Gly	Ser	Gly	Asp	Leu	Ser	Tyr	Ser	Tyr	Gln	Gly	His	Asp	Gln	Phe	Lys					
			380					385					390							
cgg	cgc	ctt	ccc	tct	ggc	cag	atg	cgg	cag	ctg	tgc	att	gcc	atg	gac	1314				
Arg	Arg	Leu	Pro	Ser	Gly	Gln	Met	Arg	Gln	Leu	Cys	Ile	Ala	Met	Asp					
		395					400					405								
cgc	tcc	ttt	gac	gca	gtg	ggg	cct	cgg	cct	cga	ctg	gac	tcc	atg	agc	1362				
Arg	Ser	Phe	Asp	Ala	Val	Gly	Pro	Arg	Pro	Arg	Leu	Asp	Ser	Met	Ser					
	410					415					420									
tcc	gtg	gaa	gag	gat	gac	tac	gac	acg	ctg	act	gac	atc	gac	tca	gac	1410				
Ser	Val	Glu	Glu	Asp	Asp	Tyr	Asp	Thr	Leu	Thr	Asp	Ile	Asp	Ser	Asp					
425					430				435						440					

aaa aac gtc att cga acc aag caa tac ctc tgt gtg gct gat ctg gca	1458
Lys Asn Val Ile Arg Thr Lys Gln Tyr Leu Cys Val Ala Asp Leu Ala	
445 450 455	
cga aag gac aaa cgt gtt ttg cgg aaa aag tac cag att tac ttc tgg	1506
Arg Lys Asp Lys Arg Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe Trp	
460 465 470	
aac ata gcc acc att gcg gtc ttc tac gca ctt cct gtg gtg cag ctg	1554
Asn Ile Ala Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Val Gln Leu	
475 480 485	
gtg atc acc tac cag acg gtg gtg aat gtc aca ggg aac cag gac atc	1602
Val Ile Thr Tyr Gln Thr Val Val Asn Val Thr Gly Asn Gln Asp Ile	
490 495 500	
tgc tac tac aac ttc ctc tgt gcc cac ccg ctg ggc aac ctc agc gcc	1650
Cys Tyr Tyr Asn Phe Leu Cys Ala His Pro Leu Gly Asn Leu Ser Ala	
505 510 515 520	
ttc aac aac atc ctc agc aac ttg ggg tac atc ctg ctg ggg ctg ctc	1698
Phe Asn Asn Ile Leu Ser Asn Leu Gly Tyr Ile Leu Leu Gly Leu Leu	
525 530 535	
ttc ctg ctc atc atc ctg cag cga gag atc aat cat aac cgg gcc ctg	1746
Phe Leu Leu Ile Ile Leu Gln Arg Glu Ile Asn His Asn Arg Ala Leu	
540 545 550	
ctg cgg aat gac ctc tat gct ctg gag tgt ggg atc ccc aaa cac ttt	1794
Leu Arg Asn Asp Leu Tyr Ala Leu Glu Cys Gly Ile Pro Lys His Phe	
555 560 565	
ggg ctg ttt tac gcc atg ggc aca gca ctg atg atg gag ggg cta ctt	1842
Gly Leu Phe Tyr Ala Met Gly Thr Ala Leu Met Met Glu Gly Leu Leu	
570 575 580	
agt gcc tgt tac cac gtc tgc ccc aac tac acc aac ttc cag ttt gat	1890
Ser Ala Cys Tyr His Val Cys Pro Asn Tyr Thr Asn Phe Gln Phe Asp	
585 590 595 600	
acc tcc ttc atg tac atg att gct ggc ctc tgc atg ctg aag ctc tac	1938
Thr Ser Phe Met Tyr Met Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr	
605 610 615	
cag aag cgg cac cca gat atc aac gcc agt gcc tac agt gca tat gcc	1986
Gln Lys Arg His Pro Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala	
620 625 630	
tgc ttg gcc atc gtc atc ttc ttc tcc gtt ctg ggc gtg gtg ttt ggc	2034
Cys Leu Ala Ile Val Ile Phe Phe Ser Val Leu Gly Val Val Phe Gly	
635 640 645	
aaa ggg aac acg gcc ttc tgg att gtc ttc tcc gtc att cac atc atc	2082
Lys Gly Asn Thr Ala Phe Trp Ile Val Phe Ser Val Ile His Ile Ile	
650 655 660	

tcc acc ctg ctc ctc agc act cag ctc tat tac atg ggc cgc tgg aag	2130
Ser Thr Leu Leu Leu Ser Thr Gln Leu Tyr Tyr Met Gly Arg Trp Lys	
665 670 675 680	
ctg gac ttc ggg atc ttc cgc cgc atc ctc cat gtg ctc tac aca gac	2178
Leu Asp Phe Gly Ile Phe Arg Arg Ile Leu His Val Leu Tyr Thr Asp	
685 690 695	
tgc atc cgg cag tgc agc ggg ccc ctt tac acg gac cgc atg gtg ctt	2226
Cys Ile Arg Gln Cys Ser Gly Pro Leu Tyr Thr Asp Arg Met Val Leu	
700 705 710	
ctg gtc atg ggc aac att atc aac tgg tgc ctg gct gca tac gga ctc	2274
Leu Val Met Gly Asn Ile Ile Asn Trp Ser Leu Ala Ala Tyr Gly Leu	
715 720 725	
atc atg cgc ccc aat gac ttt gct tcc tac ttg ctg gca att ggc atc	2322
Ile Met Arg Pro Asn Asp Phe Ala Ser Tyr Leu Leu Ala Ile Gly Ile	
730 735 740	
tgc aac ctg ctg ctt tat ttc gcc ttc tac atc atc atg aag ctc cgg	2370
Cys Asn Leu Leu Leu Tyr Phe Ala Phe Tyr Ile Ile Met Lys Leu Arg	
745 750 755 760	
agc ggc gag agg atc aag ctc atc cct ctg ctt tgc atc gtc tgc acc	2418
Ser Gly Glu Arg Ile Lys Leu Ile Pro Leu Leu Cys Ile Val Cys Thr	
765 770 775	
tcc gtg gtc tgg ggc ttc gcg ctc ttc ttc ttc ttc cag gga ctg agc	2466
Ser Val Val Trp Gly Phe Ala Leu Phe Phe Phe Phe Gln Gly Leu Ser	
780 785 790	
acg tgg cag aaa acc ccc gca gag tcc agg gag cac aac cgc gac tgc	2514
Thr Trp Gln Lys Thr Pro Ala Glu Ser Arg Glu His Asn Arg Asp Cys	
795 800 805	
atc ctc ctc gac ttc ttt gat gac cac gat atc tgg cac ttc ctg tcc	2562
Ile Leu Leu Asp Phe Phe Asp Asp His Asp Ile Trp His Phe Leu Ser	
810 815 820	
tcc att gcc atg ttt ggg tcc ttc ctg gtt ttg ctg acg ttg gat gac	2610
Ser Ile Ala Met Phe Gly Ser Phe Leu Val Leu Leu Thr Leu Asp Asp	
825 830 835 840	
gac ttg gac aca gta cag cgg gac aag atc tat gtc ttc tagcagcatc	2659
Asp Leu Asp Thr Val Gln Arg Asp Lys Ile Tyr Val Phe	
845 850	
tgtggtccag gcttcacctc acgggcctag cgctgcctc tgcatacact gccagttgcc	2719
acaagaacac cacgggtgtg agtcccagct ctgctgccca gcattggatg tcgtggcaag	2779
acagcgagat tccagcccag gcctgactca ggacagttcc tgggtggcact gaggccttgga	2839
gttgccctctg cggaggagga ggccctgctcc gcattcccca gacactggcc aaattgctgc	2899
tttctttctca gtgttgggtc ctcccagga ccctagtctg tccatctgtc ttgtttatcc	2959

actggctctc catttgtccc ttgggagagg aaggtgggaa ggcaatgtcc tgtcccattt 3019
 catgccttgc attctgcca tcccttccct cctctcagct taggacacac agccctttct 3079
 tcttcccatg ctctgtccag gaccacagtc tgggtgcctga ttctttgtcc atcaccagga 3139
 cctaagctct ccctgggtct gtagctggct gctatcactg ccactctga cctgccagga 3199
 cagatgcagg taggagactt tgggggctgg ccagctggtg ccaggctttc ggtgctaagg 3259
 cctggaaggg gcctaggtac gaccctcctc cctgacctgt gcttggagct ggctcttcag 3319
 cagtgagggc cagcccaagt tgagtcttct gatcggggac tgaattcaga ggccacctca 3379
 tcccaccagc cactagaatg atgccagcac tagggttggt gggaagtggc aactcactgt 3439
 ccccttccac accctcagtc ctgccaagcc ccagatgggg gcctctcagt gccattgaca 3499
 ctgccaaga atgtctagag gccacggaac ggtgccaagc acacagtccc ttttgcctct 3559
 ttcacgggag caggagtccc agtgcctgtc gtggaaaggg aggaacatgc caggtccctg 3619
 tgtgtccttg gccctgtctc accaaaggac tcagggctgg tttctgagtt tccgtccagt 3679
 atttagccaa gttctgtggt agtcacgtag gcctaagagc cttggcggtt acagagtcac 3739
 ccagctctgg cccctggcca ttctggctct tggcggtttac agagtcaccc agctccaggc 3799
 ccttggccac tttgggtactt gggttgcctt cacttcacca ggtccattcc agatgccaaag 3859
 agtgggcccc aggaatgtgt ttcttctctc ccacatggt tttatagctc ttgggctggg 3919
 agaagaggcg ggtctgggtc tttgtttctg agctttgttc tatgttcctc catgctacgg 3979
 ttgcaattgt tttctatgaa cgagtacatt caataaagac aaccagacct gg 4031

<210> 164
 <211> 853
 <212> PRT
 <213> Mus musculus

<400> 164
 Met Ile Ala Trp Arg Leu Pro Leu Cys Val Leu Leu Val Ala Ser Val
 1 5 10 15
 Glu Ser His Leu Gly Ala Leu Gly Pro Lys Asn Val Ser Gln Lys Asp
 20 25 30
 Ala Glu Phe Glu Arg Thr Tyr Ala Asp Asp Val Asn Ser Glu Leu Val
 35 40 45
 Asn Ile Tyr Thr Phe Asn His Thr Val Thr Arg Asn Arg Thr Glu Gly
 50 55 60
 Val Arg Val Ser Val Asn Val Leu Asn Lys Gln Lys Gly Ala Pro Leu

65	70	75	80
Leu Phe Val Val Arg Gln Lys Glu Ala Val Val Ser Phe Gln Val Pro	85	90	95
Leu Ile Leu Arg Gly Leu Tyr Gln Arg Lys Tyr Leu Tyr Gln Lys Val	100	105	110
Glu Arg Thr Leu Cys Gln Pro Pro Thr Lys Asn Glu Ser Glu Ile Gln	115	120	125
Phe Phe Tyr Val Asp Val Ser Thr Leu Ser Pro Val Asn Thr Thr Tyr	130	135	140
Gln Leu Arg Val Asn Arg Val Asp Asn Phe Val Leu Arg Thr Gly Glu	145	150	155
Leu Phe Thr Phe Asn Thr Thr Ala Ala Gln Pro Gln Tyr Phe Lys Tyr	165	170	175
Glu Phe Pro Asp Gly Val Asp Ser Val Ile Val Lys Val Thr Ser Lys	180	185	190
Lys Ala Phe Pro Cys Ser Val Ile Ser Ile Gln Asp Val Leu Cys Pro	195	200	205
Val Tyr Asp Leu Asp Asn Ser Val Ala Phe Ile Gly Met Tyr Gln Thr	210	215	220
Met Thr Lys Lys Ala Ala Ile Thr Val Gln Arg Lys Asp Phe Pro Ser	225	230	235
Asn Ser Phe Tyr Val Val Val Val Val Lys Thr Glu Asp Gln Ala Cys	245	250	255
Gly Gly Ser Leu Pro Phe Tyr Pro Phe Val Glu Asp Glu Pro Val Asp	260	265	270
Gln Gly His Arg Gln Lys Thr Leu Ser Val Leu Val Ser Gln Ala Val	275	280	285
Thr Ser Glu Ala Tyr Val Gly Gly Met Leu Phe Cys Leu Gly Ile Phe	290	295	300
Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu Ala Cys Trp Glu Asn Trp	305	310	315
Arg Gln Arg Lys Lys Thr Leu Leu Val Ala Ile Asp Arg Ala Cys Pro	325	330	335
Glu Ser Gly His Ala Arg Val Leu Ala Asp Ser Phe Pro Gly Ser Ala	340	345	350
Pro Tyr Glu Gly Tyr Asn Tyr Gly Ser Phe Glu Asn Gly Ser Gly Ser	355	360	365
Thr Asp Gly Leu Val Glu Ser Ala Gly Ser Gly Asp Leu Ser Tyr Ser			

370	375	380																	
Tyr	Gln	Gly	His	Asp	Gln	Phe	Lys	Arg	Arg	Leu	Pro	Ser	Gly	Gln	Met				
385					390					395					400				
Arg	Gln	Leu	Cys	Ile	Ala	Met	Asp	Arg	Ser	Phe	Asp	Ala	Val	Gly	Pro				
				405					410					415					
Arg	Pro	Arg	Leu	Asp	Ser	Met	Ser	Ser	Val	Glu	Glu	Asp	Asp	Tyr	Asp				
			420					425					430						
Thr	Leu	Thr	Asp	Ile	Asp	Ser	Asp	Lys	Asn	Val	Ile	Arg	Thr	Lys	Gln				
		435					440					445							
Tyr	Leu	Cys	Val	Ala	Asp	Leu	Ala	Arg	Lys	Asp	Lys	Arg	Val	Leu	Arg				
	450					455					460								
Lys	Lys	Tyr	Gln	Ile	Tyr	Phe	Trp	Asn	Ile	Ala	Thr	Ile	Ala	Val	Phe				
465					470					475					480				
Tyr	Ala	Leu	Pro	Val	Val	Gln	Leu	Val	Ile	Thr	Tyr	Gln	Thr	Val	Val				
				485				490						495					
Asn	Val	Thr	Gly	Asn	Gln	Asp	Ile	Cys	Tyr	Tyr	Asn	Phe	Leu	Cys	Ala				
			500					505					510						
His	Pro	Leu	Gly	Asn	Leu	Ser	Ala	Phe	Asn	Asn	Ile	Leu	Ser	Asn	Leu				
		515					520					525							
Gly	Tyr	Ile	Leu	Leu	Gly	Leu	Leu	Phe	Leu	Leu	Ile	Ile	Leu	Gln	Arg				
	530					535					540								
Glu	Ile	Asn	His	Asn	Arg	Ala	Leu	Leu	Arg	Asn	Asp	Leu	Tyr	Ala	Leu				
545					550					555					560				
Glu	Cys	Gly	Ile	Pro	Lys	His	Phe	Gly	Leu	Phe	Tyr	Ala	Met	Gly	Thr				
				565					570					575					
Ala	Leu	Met	Met	Glu	Gly	Leu	Leu	Ser	Ala	Cys	Tyr	His	Val	Cys	Pro				
			580					585					590						
Asn	Tyr	Thr	Asn	Phe	Gln	Phe	Asp	Thr	Ser	Phe	Met	Tyr	Met	Ile	Ala				
		595					600					605							
Gly	Leu	Cys	Met	Leu	Lys	Leu	Tyr	Gln	Lys	Arg	His	Pro	Asp	Ile	Asn				
	610					615					620								
Ala	Ser	Ala	Tyr	Ser	Ala	Tyr	Ala	Cys	Leu	Ala	Ile	Val	Ile	Phe	Phe				
625					630					635					640				
Ser	Val	Leu	Gly	Val	Val	Phe	Gly	Lys	Gly	Asn	Thr	Ala	Phe	Trp	Ile				
				645					650					655					
Val	Phe	Ser	Val	Ile	His	Ile	Ile	Ser	Thr	Leu	Leu	Leu	Ser	Thr	Gln				
			660					665					670						
Leu	Tyr	Tyr	Met	Gly	Arg	Trp	Lys	Leu	Asp	Phe	Gly	Ile	Phe	Arg	Arg				

675 680 685
 Ile Leu His Val Leu Tyr Thr Asp Cys Ile Arg Gln Cys Ser Gly Pro
 690 695 700
 Leu Tyr Thr Asp Arg Met Val Leu Leu Val Met Gly Asn Ile Ile Asn
 705 710 715 720
 Trp Ser Leu Ala Ala Tyr Gly Leu Ile Met Arg Pro Asn Asp Phe Ala
 725 730 735
 Ser Tyr Leu Leu Ala Ile Gly Ile Cys Asn Leu Leu Leu Tyr Phe Ala
 740 745 750
 Phe Tyr Ile Ile Met Lys Leu Arg Ser Gly Glu Arg Ile Lys Leu Ile
 755 760 765
 Pro Leu Leu Cys Ile Val Cys Thr Ser Val Val Trp Gly Phe Ala Leu
 770 775 780
 Phe Phe Phe Phe Gln Gly Leu Ser Thr Trp Gln Lys Thr Pro Ala Glu
 785 790 795 800
 Ser Arg Glu His Asn Arg Asp Cys Ile Leu Leu Asp Phe Phe Asp Asp
 805 810 815
 His Asp Ile Trp His Phe Leu Ser Ser Ile Ala Met Phe Gly Ser Phe
 820 825 830
 Leu Val Leu Leu Thr Leu Asp Asp Asp Leu Asp Thr Val Gln Arg Asp
 835 840 845
 Lys Ile Tyr Val Phe
 850

<210> 165
 <211> 3138
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (84)..(2648)

<400> 165
 gccgcaaccc gtcccgagg tgctctgtct cctgtcgccg ccgccgccgc caccaccgct 60
 gccactgccg cctgtccggg gcc atg ttc gct ctg ggc ttg ccc ttc ttg gtg 113
 Met Phe Ala Leu Gly Leu Pro Phe Leu Val
 1 5 10
 ctc ttg gtg gcc tcg gtc gag agc cat ctg ggg gtt ctg ggg ccc aag 161
 Leu Leu Val Ala Ser Val Glu Ser His Leu Gly Val Leu Gly Pro Lys
 15 20 25
 aac gtc tcg cag aaa gac gcc gag ttt gag cgc acc tac gtg gac gag 209

Asn	Val	Ser	Gln	Lys	Asp	Ala	Glu	Phe	Glu	Arg	Thr	Tyr	Val	Asp	Glu				
			30					35					40						
gtc	aac	agc	gag	ctg	gtc	aac	atc	tac	acc	ttc	aac	cat	act	gtg	acc	257			
Val	Asn	Ser	Glu	Leu	Val	Asn	Ile	Tyr	Thr	Phe	Asn	His	Thr	Val	Thr				
		45					50				55								
cgc	aac	agg	aca	gag	ggc	gtg	cgt	gtg	tct	gtg	aac	gtc	ctg	aac	aag	305			
Arg	Asn	Arg	Thr	Glu	Gly	Val	Arg	Val	Ser	Val	Asn	Val	Leu	Asn	Lys				
	60					65				70									
cag	aag	ggg	gcg	ccg	ttg	ctg	ttt	gtg	gtc	cgc	cag	aag	gag	gct	gtg	353			
Gln	Lys	Gly	Ala	Pro	Leu	Leu	Phe	Val	Val	Arg	Gln	Lys	Glu	Ala	Val				
	75				80					85					90				
gtg	tcc	ttc	cag	gtg	ccc	cta	atc	ctg	cga	ggg	atg	ttt	cag	cgc	aag	401			
Val	Ser	Phe	Gln	Val	Pro	Leu	Ile	Leu	Arg	Gly	Met	Phe	Gln	Arg	Lys				
			95					100					105						
tac	ctc	tac	caa	aaa	gtg	gaa	cga	acc	ctg	tgt	cag	ccc	ccc	acc	aag	449			
Tyr	Leu	Tyr	Gln	Lys	Val	Glu	Arg	Thr	Leu	Cys	Gln	Pro	Pro	Thr	Lys				
			110					115				120							
aat	gag	tcg	gag	att	cag	ttc	ttc	tac	gtg	gat	gtg	tcc	acc	ctg	tca	497			
Asn	Glu	Ser	Glu	Ile	Gln	Phe	Phe	Tyr	Val	Asp	Val	Ser	Thr	Leu	Ser				
		125				130					135								
cca	gtc	aac	acc	aca	tac	cag	ctc	cgg	gtc	agc	cgc	atg	gac	gat	ttt	545			
Pro	Val	Asn	Thr	Thr	Tyr	Gln	Leu	Arg	Val	Ser	Arg	Met	Asp	Asp	Phe				
	140					145				150									
gtg	ctc	agg	act	ggg	gag	cag	ttc	agc	ttc	aat	acc	aca	gca	gca	cag	593			
Val	Leu	Arg	Thr	Gly	Glu	Gln	Phe	Ser	Phe	Asn	Thr	Thr	Ala	Ala	Gln				
	155				160				165						170				
ccc	cag	tac	ttc	aag	tat	gag	ttc	cct	gaa	ggc	gtg	gac	tcg	gta	att	641			
Pro	Gln	Tyr	Phe	Lys	Tyr	Glu	Phe	Pro	Glu	Gly	Val	Asp	Ser	Val	Ile				
			175					180					185						
gtc	aag	gtg	acc	tcc	aac	aag	gcc	ttc	ccc	tgc	tca	gtc	atc	tcc	att	689			
Val	Lys	Val	Thr	Ser	Asn	Lys	Ala	Phe	Pro	Cys	Ser	Val	Ile	Ser	Ile				
		190					195					200							
cag	gat	gtg	ctg	tgt	cct	gtc	tat	gac	ctg	gac	aac	aac	gta	gcc	ttc	737			
Gln	Asp	Val	Leu	Cys	Pro	Val	Tyr	Asp	Leu	Asp	Asn	Asn	Val	Ala	Phe				
		205				210					215								
atc	ggc	atg	tac	cag	acg	atg	acc	aag	aag	gcg	gcc	atc	acc	gta	cag	785			
Ile	Gly	Met	Tyr	Gln	Thr	Met	Thr	Lys	Lys	Ala	Ala	Ile	Thr	Val	Gln				
	220					225				230									
cgc	aaa	gac	ttc	ccc	agc	aac	agc	ttt	tat	gtg	gtg	gtg	gtg	gtg	aag	833			
Arg	Lys	Asp	Phe	Pro	Ser	Asn	Ser	Phe	Tyr	Val	Val	Val	Val	Val	Lys				
	235				240			245							250				
acc	gaa	gac	caa	gcc	tgc	ggg	ggc	tcc	ctg	cct	ttc	tac	ccc	ttc	gca	881			
Thr	Glu	Asp	Gln	Ala	Cys	Gly	Gly	Ser	Leu	Pro	Phe	Tyr	Pro	Phe	Ala				

255										260					265					
gaa	gat	gaa	ccg	gtc	gat	caa	ggg	cac	cgc	cag	aaa	acc	ctg	tca	gtg	929				
Glu	Asp	Glu	Pro	Val	Asp	Gln	Gly	His	Arg	Gln	Lys	Thr	Leu	Ser	Val					
			270				275				280									
ctg	gtg	tct	caa	gca	gtc	acg	tct	gag	gca	tac	gtc	agt	ggg	atg	ctc	977				
Leu	Val	Ser	Gln	Ala	Val	Thr	Ser	Glu	Ala	Tyr	Val	Ser	Gly	Met	Leu					
			285				290				295									
ttt	tgc	ctg	ggg	ata	ttt	ctc	tcc	ttt	tac	ctg	ctg	acc	gtc	ctc	ctg	1025				
Phe	Cys	Leu	Gly	Ile	Phe	Leu	Ser	Phe	Tyr	Leu	Leu	Thr	Val	Leu	Leu					
			300				305				310									
gcc	tgc	tgg	gag	aac	tgg	agg	cag	aag	aag	aag	acc	ctg	ctg	gtg	gcc	1073				
Ala	Cys	Trp	Glu	Asn	Trp	Arg	Gln	Lys	Lys	Lys	Thr	Leu	Leu	Val	Ala					
315				320				325				330								
att	gac	cga	gcc	tgc	cca	gaa	agc	ggg	cac	cct	cga	gtc	ctg	gct	gat	1121				
Ile	Asp	Arg	Ala	Cys	Pro	Glu	Ser	Gly	His	Pro	Arg	Val	Leu	Ala	Asp					
			335				340				345									
tct	ttt	cct	ggc	agt	tcc	cct	tat	gag	ggg	tac	aac	tat	ggc	tcc	ttt	1169				
Ser	Phe	Pro	Gly	Ser	Ser	Pro	Tyr	Glu	Gly	Tyr	Asn	Tyr	Gly	Ser	Phe					
			350				355				360									
gag	aat	gtt	tct	gga	tct	acc	gat	ggg	ctg	gtt	gac	agc	gct	ggc	act	1217				
Glu	Asn	Val	Ser	Gly	Ser	Thr	Asp	Gly	Leu	Val	Asp	Ser	Ala	Gly	Thr					
			365				370				375									
ggg	gac	ctc	tct	tac	ggg	tac	cag	ggg	cac	gac	cag	ttc	aag	cgg	cgc	1265				
Gly	Asp	Leu	Ser	Tyr	Gly	Tyr	Gln	Gly	His	Asp	Gln	Phe	Lys	Arg	Arg					
			380				385				390									
ctc	ccc	tct	ggc	cag	atg	cgg	cag	ctg	tgc	att	gcc	atg	ggc	cgc	tcc	1313				
Leu	Pro	Ser	Gly	Gln	Met	Arg	Gln	Leu	Cys	Ile	Ala	Met	Gly	Arg	Ser					
395				400				405				410								
ttt	gaa	cct	gta	ggg	act	cgg	ccc	cga	gtg	gac	tcc	atg	agc	tct	gtg	1361				
Phe	Glu	Pro	Val	Gly	Thr	Arg	Pro	Arg	Val	Asp	Ser	Met	Ser	Ser	Val					
			415				420				425									
gag	gag	gat	gac	tac	gac	aca	ttg	acc	gac	atc	gat	tcc	gac	aag	aat	1409				
Glu	Glu	Asp	Asp	Tyr	Asp	Thr	Leu	Thr	Asp	Ile	Asp	Ser	Asp	Lys	Asn					
			430				435				440									
gtc	att	cgc	acc	aag	caa	tac	ctc	tat	gtg	gct	gac	ctg	gca	cgg	aag	1457				
Val	Ile	Arg	Thr	Lys	Gln	Tyr	Leu	Tyr	Val	Ala	Asp	Leu	Ala	Arg	Lys					
			445				450				455									
gac	aag	cgt	gtt	ctg	cgg	aaa	aag	tac	cag	atc	tac	ttc	tgg	aac	att	1505				
Asp	Lys	Arg	Val	Leu	Arg	Lys	Lys	Tyr	Gln	Ile	Tyr	Phe	Trp	Asn	Ile					
			460				465				470									
gcc	acc	att	gct	gtc	ttc	tat	gcc	ctt	cct	gtg	gtg	cag	ctg	gtg	atc	1553				
Ala	Thr	Ile	Ala	Val	Phe	Tyr	Ala	Leu	Pro	Val	Val	Gln	Leu	Val	Ile					
475				480				485				490								

acc tac cag acg gtg gtg aat gtc aca ggg aat cag gac atc tgc tac	1601
Thr Tyr Gln Thr Val Val Asn Val Thr Gly Asn Gln Asp Ile Cys Tyr	
495 500 505	
tac aac ttc ctc tgc gcc cac cca ctg ggc aat ctc agc gcc ttc aac	1649
Tyr Asn Phe Leu Cys Ala His Pro Leu Gly Asn Leu Ser Ala Phe Asn	
510 515 520	
aac atc ctc agc aac ctg ggg tac atc ctg ctg ggg ctg ctt ttc ctg	1697
Asn Ile Leu Ser Asn Leu Gly Tyr Ile Leu Leu Gly Leu Leu Phe Leu	
525 530 535	
ctc atc atc ctg caa cgg gag atc aac cac aac cgg gcc ctg ctg cgc	1745
Leu Ile Ile Leu Gln Arg Glu Ile Asn His Asn Arg Ala Leu Leu Arg	
540 545 550	
aat gac ctc tgt gcc ctg gaa tgt ggg atc ccc aaa cac ttt ggg ctt	1793
Asn Asp Leu Cys Ala Leu Glu Cys Gly Ile Pro Lys His Phe Gly Leu	
555 560 565 570	
ttc tac gcc atg ggc aca gcc ctg atg atg gag ggg ctg ctc agt gct	1841
Phe Tyr Ala Met Gly Thr Ala Leu Met Met Glu Gly Leu Leu Ser Ala	
575 580 585	
tgc tat cat gtg tgc ccc aac tat acc aat ttc cag ttt gac aca tcg	1889
Cys Tyr His Val Cys Pro Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser	
590 595 600	
ttc atg tac atg atc gcc gga ctc tgc atg ctg aag ctc tac cag aag	1937
Phe Met Tyr Met Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys	
605 610 615	
cgg cac ccg gac atc aac gcc agc gcc tac agt gcc tac gcc tgc ctg	1985
Arg His Pro Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu	
620 625 630	
gcc att gtc atc ttc ttc tct gtg ctg ggc gtg gtc ttt ggc aaa ggg	2033
Ala Ile Val Ile Phe Phe Ser Val Leu Gly Val Val Phe Gly Lys Gly	
635 640 645 650	
aac acg gcg ttc tgg atc gtc ttc tcc atc att cac atc atc gcc acc	2081
Asn Thr Ala Phe Trp Ile Val Phe Ser Ile Ile His Ile Ile Ala Thr	
655 660 665	
ctg ctc ctc agc acg cag ctc tat tac atg ggc cgg tgg aaa ctg gac	2129
Leu Leu Leu Ser Thr Gln Leu Tyr Tyr Met Gly Arg Trp Lys Leu Asp	
670 675 680	
tcg ggg atc ttc cgc cgc atc ctc cac gtg ctc tac aca gac tgc atc	2177
Ser Gly Ile Phe Arg Arg Ile Leu His Val Leu Tyr Thr Asp Cys Ile	
685 690 695	
cgg cag tgc agc ggg ccg ctc tac gtg gac cgc atg gtg ctg ctg gtc	2225
Arg Gln Cys Ser Gly Pro Leu Tyr Val Asp Arg Met Val Leu Leu Val	
700 705 710	

atg ggc aac gtc atc aac tgg tgc ctg gct gcc tat ggg ctt atc atg 2273
 Met Gly Asn Val Ile Asn Trp Ser Leu Ala Ala Tyr Gly Leu Ile Met
 715 720 725 730

 cgc ccc aat gat ttc gct tcc tac ttg ttg gcc att ggc atc tgc aac 2321
 Arg Pro Asn Asp Phe Ala Ser Tyr Leu Leu Ala Ile Gly Ile Cys Asn
 735 740 745

 ctg ctc ctt tac ttc gcc ttc tac atc atc atg aag ctc cgg agt ggg 2369
 Leu Leu Leu Tyr Phe Ala Phe Tyr Ile Ile Met Lys Leu Arg Ser Gly
 750 755 760

 gag agg atc aag ctc atc ccc ctg ctc tgc atc gtt tgc acc tcc gtg 2417
 Glu Arg Ile Lys Leu Ile Pro Leu Leu Cys Ile Val Cys Thr Ser Val
 765 770 775

 gtc tgg ggc ttc gcg ctc ttc ttc ttc ttc cag gga ctc agc acc tgg 2465
 Val Trp Gly Phe Ala Leu Phe Phe Phe Phe Gln Gly Leu Ser Thr Trp
 780 785 790

 cag aaa acc cct gca gag tgc agg gag cac aac cgg gac tgc atc ctc 2513
 Gln Lys Thr Pro Ala Glu Ser Arg Glu His Asn Arg Asp Cys Ile Leu
 795 800 805 810

 ctc gac ttc ttt gac gac cac gac atc tgg cac ttc ctc tcc tcc atc 2561
 Leu Asp Phe Phe Asp Asp His Asp Ile Trp His Phe Leu Ser Ser Ile
 815 820 825

 gcc atg ttc ggg tcc ttc ctg gta agc ggg cct ccc ggc cga gcc ggg 2609
 Ala Met Phe Gly Ser Phe Leu Val Ser Gly Pro Pro Gly Arg Ala Gly
 830 835 840

 tgg gta cgt gaa ggt agc agc tgc ctc ctt ccc tgt ggc tgatctggcg 2658
 Trp Val Arg Glu Gly Ser Ser Cys Leu Leu Pro Cys Gly
 845 850 855

 tccacacccc aggtgttgct gacactggat gacgacctgg atacttagaa aggggcttca 2718
 ggaaggggatg tgctgtttcc ctctacgtgc ccagtcctag cctcgctcta ggaccaggg 2778
 ctggcttcta agtttccgtc cagtcttcag gcaagttctg tgttagtcac gcacacacat 2838
 acctatgaaa ccttggagtt tacaagaat tgccccagct ctgggcaccc tggccaccct 2898
 ggtccttgga tccccttcgt ccacactggt ccaccccaga tgctgaggat gggggagctc 2958
 aggcggggcc tctgcttttg ggatgggaat gtgtttttct cccaaacttg tttttatagc 3018
 tctgcttgaa gggctgggag atgaggtggg tctggatctt ttctcagagc gtctccatgc 3078
 tatggttgca tttccgtttt ctatgaatga atttgcattc aataaacaac cagactcagt 3138

<210> 166
 <211> 855
 <212> PRT
 <213> Homo sapiens

<400> 166

Met	Phe	Ala	Leu	Gly	Leu	Pro	Phe	Leu	Val	Leu	Leu	Val	Ala	Ser	Val
1				5					10					15	
Glu	Ser	His	Leu	Gly	Val	Leu	Gly	Pro	Lys	Asn	Val	Ser	Gln	Lys	Asp
			20					25					30		
Ala	Glu	Phe	Glu	Arg	Thr	Tyr	Val	Asp	Glu	Val	Asn	Ser	Glu	Leu	Val
		35					40					45			
Asn	Ile	Tyr	Thr	Phe	Asn	His	Thr	Val	Thr	Arg	Asn	Arg	Thr	Glu	Gly
	50					55					60				
Val	Arg	Val	Ser	Val	Asn	Val	Leu	Asn	Lys	Gln	Lys	Gly	Ala	Pro	Leu
65					70					75					80
Leu	Phe	Val	Val	Arg	Gln	Lys	Glu	Ala	Val	Val	Ser	Phe	Gln	Val	Pro
				85					90					95	
Leu	Ile	Leu	Arg	Gly	Met	Phe	Gln	Arg	Lys	Tyr	Leu	Tyr	Gln	Lys	Val
		100						105					110		
Glu	Arg	Thr	Leu	Cys	Gln	Pro	Pro	Thr	Lys	Asn	Glu	Ser	Glu	Ile	Gln
		115					120					125			
Phe	Phe	Tyr	Val	Asp	Val	Ser	Thr	Leu	Ser	Pro	Val	Asn	Thr	Thr	Tyr
	130					135					140				
Gln	Leu	Arg	Val	Ser	Arg	Met	Asp	Asp	Phe	Val	Leu	Arg	Thr	Gly	Glu
145					150					155					160
Gln	Phe	Ser	Phe	Asn	Thr	Thr	Ala	Ala	Gln	Pro	Gln	Tyr	Phe	Lys	Tyr
				165					170					175	
Glu	Phe	Pro	Glu	Gly	Val	Asp	Ser	Val	Ile	Val	Lys	Val	Thr	Ser	Asn
			180					185					190		
Lys	Ala	Phe	Pro	Cys	Ser	Val	Ile	Ser	Ile	Gln	Asp	Val	Leu	Cys	Pro
	195						200					205			
Val	Tyr	Asp	Leu	Asp	Asn	Asn	Val	Ala	Phe	Ile	Gly	Met	Tyr	Gln	Thr
	210					215					220				
Met	Thr	Lys	Lys	Ala	Ala	Ile	Thr	Val	Gln	Arg	Lys	Asp	Phe	Pro	Ser
225					230					235					240
Asn	Ser	Phe	Tyr	Val	Val	Val	Val	Val	Lys	Thr	Glu	Asp	Gln	Ala	Cys
				245					250					255	
Gly	Gly	Ser	Leu	Pro	Phe	Tyr	Pro	Phe	Ala	Glu	Asp	Glu	Pro	Val	Asp
			260					265					270		
Gln	Gly	His	Arg	Gln	Lys	Thr	Leu	Ser	Val	Leu	Val	Ser	Gln	Ala	Val
		275					280					285			
Thr	Ser	Glu	Ala	Tyr	Val	Ser	Gly	Met	Leu	Phe	Cys	Leu	Gly	Ile	Phe

290	295	300
Leu Ser Phe Tyr Leu 305	Leu Thr Val Leu 310	Leu Ala Cys Trp Glu Asn Trp 315 320
Arg Gln Lys Lys 325	Lys Thr Leu Leu Val 330	Ala Ile Asp Arg Ala Cys Pro 335
Glu Ser Gly His 340	Pro Arg Val Leu 345	Ala Asp Ser Phe Pro Gly Ser Ser 350
Pro Tyr Glu Gly Tyr 355	Asn Tyr Gly Ser 360	Phe Glu Asn Val Ser Gly Ser 365
Thr Asp Gly Leu Val 370	Asp Ser Ala Gly Thr 375	Gly Asp Leu Ser Tyr Gly 380
Tyr Gln Gly His 385	Asp Gln Phe Lys Arg 390	Arg Arg Leu Pro Ser Gly Gln Met 395 400
Arg Gln Leu Cys 405	Ile Ala Met Gly Arg 410	Ser Phe Glu Pro Val Gly Thr 415
Arg Pro Arg Val 420	Asp Ser Met Ser 425	Ser Val Glu Glu Asp Asp Tyr Asp 430
Thr Leu Thr 435	Asp Ile Asp Ser 440	Asp Lys Asn Val Ile Arg Thr Lys Gln 445
Tyr Leu Tyr Val 450	Ala Asp Leu Ala Arg 455	Lys Asp Lys Arg Val Leu Arg 460
Lys Lys Tyr Gln 465	Ile Tyr Phe Trp Asn 470	Ile Ala Thr Ile Ala Val Phe 475 480
Tyr Ala Leu Pro 485	Val Val Gln Leu Val 490	Ile Thr Tyr Gln Thr Val Val 495
Asn Val Thr 500	Gly Asn Gln Asp Ile 505	Cys Tyr Tyr Asn Phe Leu Cys Ala 510
His Pro Leu 515	Gly Asn Leu Ser 520	Ala Phe Asn Asn Ile Leu Ser Asn Leu 525
Gly Tyr Ile Leu 530	Leu Gly Leu Leu 535	Phe Leu Leu Ile Ile Leu Gln Arg 540
Glu Ile Asn His 545	Asn Arg Ala Leu 550	Leu Arg Asn Asp Leu Cys Ala Leu 555 560
Glu Cys Gly Ile 565	Pro Lys His Phe 570	Gly Leu Phe Tyr Ala Met Gly Thr 575
Ala Leu Met 580	Met Glu Gly Leu 585	Leu Ser Ala Cys Tyr His Val Cys Pro 590
Asn Tyr Thr Asn 595	Phe Gln Phe Asp 600	Thr Ser Phe Met Tyr Met Ile Ala 605

595	600	605
Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His Pro Asp Ile Asn		
610	615	620
Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile Val Ile Phe Phe		
625	630	635 640
Ser Val Leu Gly Val Val Phe Gly Lys Gly Asn Thr Ala Phe Trp Ile		
	645	650 655
Val Phe Ser Ile Ile His Ile Ile Ala Thr Leu Leu Leu Ser Thr Gln		
	660	665 670
Leu Tyr Tyr Met Gly Arg Trp Lys Leu Asp Ser Gly Ile Phe Arg Arg		
	675	680 685
Ile Leu His Val Leu Tyr Thr Asp Cys Ile Arg Gln Cys Ser Gly Pro		
	690	695 700
Leu Tyr Val Asp Arg Met Val Leu Leu Val Met Gly Asn Val Ile Asn		
705	710	715 720
Trp Ser Leu Ala Ala Tyr Gly Leu Ile Met Arg Pro Asn Asp Phe Ala		
	725	730 735
Ser Tyr Leu Leu Ala Ile Gly Ile Cys Asn Leu Leu Leu Tyr Phe Ala		
	740	745 750
Phe Tyr Ile Ile Met Lys Leu Arg Ser Gly Glu Arg Ile Lys Leu Ile		
	755	760 765
Pro Leu Leu Cys Ile Val Cys Thr Ser Val Val Trp Gly Phe Ala Leu		
	770	775 780
Phe Phe Phe Phe Gln Gly Leu Ser Thr Trp Gln Lys Thr Pro Ala Glu		
785	790	795 800
Ser Arg Glu His Asn Arg Asp Cys Ile Leu Leu Asp Phe Phe Asp Asp		
	805	810 815
His Asp Ile Trp His Phe Leu Ser Ser Ile Ala Met Phe Gly Ser Phe		
	820	825 830
Leu Val Ser Gly Pro Pro Gly Arg Ala Gly Trp Val Arg Glu Gly Ser		
	835	840 845
Ser Cys Leu Leu Pro Cys Gly		
850	855	

<210> 167
 <211> 2815
 <212> DNA
 <213> Homo sapiens

<220>

<221> -CDS
 <222> (56)..(571)

<400> 167

```
gcgaagcgcg cctgcgaccc ggcgtccggg cgcgctggag aggacgcgag gagcc atg 58
                                         Met
                                         1

agg cgc cag cct gcg aag gtg gcg gcg ctg ctg ctc ggg ctg ctc ttg 106
Arg Arg Gln Pro Ala Lys Val Ala Ala Leu Leu Leu Gly Leu Leu Leu
      5                      10                      15

gag tgc aca gaa gcc aaa aag cat tgc tgg tat ttc gaa gga ctc tat 154
Glu Cys Thr Glu Ala Lys Lys His Cys Trp Tyr Phe Glu Gly Leu Tyr
      20                      25                      30

cca acc tat tat ata tgc cgc tcc tac gag gac tgc tgt ggc tcc agg 202
Pro Thr Tyr Tyr Ile Cys Arg Ser Tyr Glu Asp Cys Cys Gly Ser Arg
      35                      40                      45

tgc tgt gtg cgg gcc ctc tcc ata cag agg ctg tgg tac ttc tgg ttc 250
Cys Cys Val Arg Ala Leu Ser Ile Gln Arg Leu Trp Tyr Phe Trp Phe
      50                      55                      60                      65

ctt ctg atg atg ggc gtg ctt ttc tgc tgc gga gcc ggc ttc ttc atc 298
Leu Leu Met Met Gly Val Leu Phe Cys Cys Gly Ala Gly Phe Phe Ile
      70                      75                      80

cgg agg cgc atg tac ccc ccg ccg ctg atc gag gag cca gcc ttc aat 346
Arg Arg Arg Met Tyr Pro Pro Pro Leu Ile Glu Glu Pro Ala Phe Asn
      85                      90                      95

gtg tcc tac acc agg cag ccc cca aat ccc ggc cca gga gcc cag cag 394
Val Ser Tyr Thr Arg Gln Pro Pro Asn Pro Gly Pro Gly Ala Gln Gln
      100                      105                      110

ccg ggg ccg ccc tat tac acc gac cca gga gga ccg ggg atg aac cct 442
Pro Gly Pro Pro Tyr Tyr Thr Asp Pro Gly Gly Pro Gly Met Asn Pro
      115                      120                      125

gtc ggg aat tcc atg gca atg gct ttc cag gtc cca ccc aac tca ccc 490
Val Gly Asn Ser Met Ala Met Ala Phe Gln Val Pro Pro Asn Ser Pro
      130                      135                      140                      145

cag ggg agt gtg gcc tgc ccg ccc cct cca gcc tac tgc aac acg cct 538
Gln Gly Ser Val Ala Cys Pro Pro Pro Pro Ala Tyr Cys Asn Thr Pro
      150                      155                      160

ccg ccc ccg tac gaa cag gta gtg aag gcc aag tagtggggtg cccacgtgca 591
Pro Pro Pro Tyr Glu Gln Val Val Lys Ala Lys
      165                      170

agaggagggga caggagaggg cctttccctg gcctttctgt cttcgttgat gttcacttcc 651

aggaacgggtc tcgtgggctg ctaagggcag ttctcttgat atcctcacag caagcacagc 711

tctcttttcag gctttccatg gagtacaata tatgaactca cactttgtct cctctgttgc 771
```

ttctgtttct gacgcagtct gtgctctcac atggtagtgt ggtgacagtc cccgagggct 831
 gacgtcctta cgggtggcgtg accagatcta cgggagagag actgagagga agaaggcagt 891
 gctggaggtg caggtggcat gtagaggggc caggccgagc atcccaggca agcatccttc 951
 tgcccgggta ttaataggaa gcccacatgcc gggcggctca gccgatgaag cagcagccga 1011
 ctgagctgag cccagcaggt catctgctcc agcctgtcct ctogtcagcc ttctcttcc 1071
 agaagctggt ggagagacat tcaggagaga gcaagcccct tgtcatgttt ctgtctctgt 1131
 tcatatccta aagatagact tctcctgcac cgccaggga gggtagcacg tgcagctctc 1191
 accgcaggat ggggcctaga atcaggcttg ccttgaggc ctgacagtga tctgacatcc 1251
 actaagcaaa tttatttaaa ttcattggaa atcacttcct gcccacaaact gagacattgc 1311
 attttgtgag ctcttggtct gatttgagaga aaggactggt acccattttt ttggtgtggt 1371
 tatggaagtg catgtagagc gtccctgccct ttgaaatcag actgggtgtg tgtcttccct 1431
 ggacatcact gcctctccag ggcattctca ggcccggggg tctccttccc tcaggcagct 1491
 ccagtgggtg gttctgaagg gtgctttcaa aacggggcac atctggctgg gaagtcacat 1551
 ggactcttcc agggagagag accagctgag gogtctctct ctgaggttgt gttgggtcta 1611
 agcgggtgtg tgctgggctc caaggaggag gagcttgctg gggaaagaca ggagaagtac 1671
 tgactcaact gcactgacca tgttgtcata attagaataa agaagaagtg gtcggaaatg 1731
 cacattcctg gataggaatc acagctcacc ccaggatctc acaggtagtc tcctgagtag 1791
 ttgacggcta gcggggagct agttccgccg catagttata gtgttgatgt gtgaacgctg 1851
 acctgtcctg tgtgctaaga gctatgcagc ttagctgagg cgctagatt actagatgtg 1911
 ctgtatcacg gggaatgagg tgggggtgct tattttttta tgaactaatc agagcctctt 1971
 gagaaattgt tactcattga actggagcat caagacatct catggaagtg gatacggagt 2031
 gatttggtgt ccatgctttt cactctgagg acatttaatc ggagaacctc ctggggaatt 2091
 ttgtgggaga cacttgggaa caaacagac accctgggaa tgcagttgca agcacagatg 2151
 ctgccaccag tgtctctgac caccctggtg tgactgctga ctgccagcgt ggtacctccc 2211
 atgctgcagg cctccatcta aatgagacaa caaagcacia tgttactgt ttacaaccaa 2271
 gacaactgcg tgggtccaaa cactcctctt cctccaggtc atttgttttg catttttaat 2331
 gtctttatct tttgtaatga aaaagcacac taagctgcc ctggaatcgg gtgcagctga 2391
 ataggcacc aaaagtccgt gactaaatct cgtttgtctt tttgatagca aattatgtta 2451

agagacagtg atggctaggg ctcaacaatt ttgtattccc atgtttgtgt gagacagagt 2511
 ttgttttccc ttgaacttgg ttagaattgt gctactgtga acgtgatcc tgcatatgga 2571
 agttccgctt cggtgacatt tcttgcccat tcttgtttcc attgtgtgga tggtaggggtt 2631
 tgcccacttc ctggagtga acagctcctg gtgtgtagaa ttcccggagc gtccgtgggtt 2691
 cagagtaaac ttgaagcaga tctgtgcatg cttttcctct gcaacaattg gctcgtttct 2751
 cttttttgtt ctcttttgat aggatcctgt ttcctatgtg tgcaaaataa aaataaattt 2811
 gggc 2815

<210> 168
 <211> 172
 <212> PRT
 <213> Homo sapiens

<400> 168
 Met Arg Arg Gln Pro Ala Lys Val Ala Ala Leu Leu Leu Gly Leu Leu
 1 5 10 15
 Leu Glu Cys Thr Glu Ala Lys Lys His Cys Trp Tyr Phe Glu Gly Leu
 20 25 30
 Tyr Pro Thr Tyr Tyr Ile Cys Arg Ser Tyr Glu Asp Cys Cys Gly Ser
 35 40 45
 Arg Cys Cys Val Arg Ala Leu Ser Ile Gln Arg Leu Trp Tyr Phe Trp
 50 55 60
 Phe Leu Leu Met Met Gly Val Leu Phe Cys Cys Gly Ala Gly Phe Phe
 65 70 75 80
 Ile Arg Arg Arg Met Tyr Pro Pro Pro Leu Ile Glu Glu Pro Ala Phe
 85 90 95
 Asn Val Ser Tyr Thr Arg Gln Pro Pro Asn Pro Gly Pro Gly Ala Gln
 100 105 110
 Gln Pro Gly Pro Pro Tyr Tyr Thr Asp Pro Gly Gly Pro Gly Met Asn
 115 120 125
 Pro Val Gly Asn Ser Met Ala Met Ala Phe Gln Val Pro Pro Asn Ser
 130 135 140
 Pro Gln Gly Ser Val Ala Cys Pro Pro Pro Pro Ala Tyr Cys Asn Thr
 145 150 155 160
 Pro Pro Pro Pro Tyr Glu Gln Val Val Lys Ala Lys
 165 170

<210> 169
 <211> 3337

```

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (136)..(1755)

<400> 169
tctcgctgcg ggaaggggtcc tgggcccccg gcggcggtcg ccaggtctca gggccggggg 60

tacccgagtc tcgtttcttc tcagttccatc cacccttcat ggggccagag ccctctctcc 120

agaatctgag cagca atg ccg ttt gct gaa gac aag acc tat aag tat atc 171
      Met Pro Phe Ala Glu Asp Lys Thr Tyr Lys Tyr Ile
              1              5              10

tgc cgc aat ttc agc aat ttt tgc aat gtg gat gtt gta gag att ctg 219
Cys Arg Asn Phe Ser Asn Phe Cys Asn Val Asp Val Val Glu Ile Leu
      15              20              25

cct tac ctg ccc tgc ctc aca gca aga gac cag gat cga ctg cgg gcc 267
Pro Tyr Leu Pro Cys Leu Thr Ala Arg Asp Gln Asp Arg Leu Arg Ala
      30              35              40

acc tgc aca ctc tca ggg aac cgg gac acc ctc tgg cat ctc ttc aat 315
Thr Cys Thr Leu Ser Gly Asn Arg Asp Thr Leu Trp His Leu Phe Asn
      45              50              55              60

acc ctt cag cgg cgg ccc ggc tgg gtg gag tac ttc att gcg gca ctg 363
Thr Leu Gln Arg Arg Pro Gly Trp Val Glu Tyr Phe Ile Ala Ala Leu
              65              70              75

agg ggc tgt gag cta gtt gat ctc gcg gac gaa gtg gcc tct gtc tac 411
Arg Gly Cys Glu Leu Val Asp Leu Ala Asp Glu Val Ala Ser Val Tyr
      80              85              90

cag agc tac cag cct cgg acc tcg gac cgt ccc cca gac cca ctg gag 459
Gln Ser Tyr Gln Pro Arg Thr Ser Asp Arg Pro Pro Asp Pro Leu Glu
      95              100              105

cca ccg tca ctt cct gct gag agg cca ggg ccc ccc aca cct gct gcg 507
Pro Pro Ser Leu Pro Ala Glu Arg Pro Gly Pro Pro Thr Pro Ala Ala
      110              115              120

gcc cac agc atc ccc tac aac agc tgc aga gag aag gag cca agt tac 555
Ala His Ser Ile Pro Tyr Asn Ser Cys Arg Glu Lys Glu Pro Ser Tyr
      125              130              135              140

ccc atg cct gtc cag gag acc cag gcg cca gag tcc cca gga gag aat 603
Pro Met Pro Val Gln Glu Thr Gln Ala Pro Glu Ser Pro Gly Glu Asn
              145              150              155

tca gag caa gcc ctg cag acg ctc agc ccc aga gcc atc cca agg aat 651
Ser Glu Gln Ala Leu Gln Thr Leu Ser Pro Arg Ala Ile Pro Arg Asn
      160              165              170

cca gat ggt ggc ccc ctg gag tcc tcc tct gac ctg gca gcc ctc agc 699

```

Pro	Asp	Gly	Gly	Pro	Leu	Glu	Ser	Ser	Ser	Asp	Leu	Ala	Ala	Leu	Ser	-	-
		175					180					185					
cct	ctg	acc	tcc	agc	ggg	cat	cag	gag	cag	gac	aca	gaa	ctg	ggc	agt	747	
Pro	Leu	Thr	Ser	Ser	Gly	His	Gln	Glu	Gln	Asp	Thr	Glu	Leu	Gly	Ser		
	190					195				200							
acc	cac	aca	gca	ggg	gag	acc	tcc	agc	ctc	aca	cca	tcc	cgt	ggg	cct	795	
Thr	His	Thr	Ala	Gly	Ala	Thr	Ser	Ser	Leu	Thr	Pro	Ser	Arg	Gly	Pro		
205					210					215					220		
gtg	tct	cca	tct	gtc	tcc	ttc	cag	ccc	ctg	gcc	cgt	tcc	acc	ccc	agg	843	
Val	Ser	Pro	Ser	Val	Ser	Phe	Gln	Pro	Leu	Ala	Arg	Ser	Thr	Pro	Arg		
				225					230					235			
gca	agc	cgc	ttg	cct	gga	ccc	aca	ggg	tca	gtt	gta	tct	act	ggc	acc	891	
Ala	Ser	Arg	Leu	Pro	Gly	Pro	Thr	Gly	Ser	Val	Val	Ser	Thr	Gly	Thr		
			240					245					250				
tcc	ttc	tcc	tcc	tca	tcc	cct	ggc	ttg	gcc	tct	gca	ggg	gct	gca	gag	939	
Ser	Phe	Ser	Ser	Ser	Ser	Pro	Gly	Leu	Ala	Ser	Ala	Gly	Ala	Ala	Glu		
		255					260					265					
ggg	aaa	cag	ggg	gca	gag	agt	gac	cag	gcc	gag	cct	atc	atc	tgc	tcc	987	
Gly	Lys	Gln	Gly	Ala	Glu	Ser	Asp	Gln	Ala	Glu	Pro	Ile	Ile	Cys	Ser		
	270					275					280						
agt	ggg	gca	gag	gca	cct	gcc	aac	tct	ctg	ccc	tcc	aaa	gtg	cct	acc	1035	
Ser	Gly	Ala	Glu	Ala	Pro	Ala	Asn	Ser	Leu	Pro	Ser	Lys	Val	Pro	Thr		
285					290					295					300		
acc	ttg	atg	cct	gtg	aac	aca	gtg	gcc	ctg	aaa	gtg	cct	gcc	aac	cca	1083	
Thr	Leu	Met	Pro	Val	Asn	Thr	Val	Ala	Leu	Lys	Val	Pro	Ala	Asn	Pro		
				305					310					315			
gca	tct	gtc	agc	aca	gtg	ccc	tcc	aag	ttg	cca	act	agc	tca	aag	ccc	1131	
Ala	Ser	Val	Ser	Thr	Val	Pro	Ser	Lys	Leu	Pro	Thr	Ser	Ser	Lys	Pro		
			320					325					330				
cct	ggg	gca	gtg	cct	tct	aat	gag	ctc	acc	aat	cca	gca	cca	tcc	aaa	1179	
Pro	Gly	Ala	Val	Pro	Ser	Asn	Ala	Leu	Thr	Asn	Pro	Ala	Pro	Ser	Lys		
		335					340					345					
ttg	ccc	atc	aac	tca	acc	cgt	gct	ggc	atg	gtg	cca	tcc	aaa	gtg	cct	1227	
Leu	Pro	Ile	Asn	Ser	Thr	Arg	Ala	Gly	Met	Val	Pro	Ser	Lys	Val	Pro		
	350					355					360						
act	agc	atg	gtg	ctc	acc	aag	gtg	tct	gcc	agc	aca	gtc	ccc	act	gac	1275	
Thr	Ser	Met	Val	Leu	Thr	Lys	Val	Ser	Ala	Ser	Thr	Val	Pro	Thr	Asp		
365					370				375						380		
ggg	agc	agc	aga	aat	gag	gag	acc	cca	gca	gct	cca	aca	ccc	gcc	ggc	1323	
Gly	Ser	Ser	Arg	Asn	Glu	Glu	Thr	Pro	Ala	Ala	Pro	Thr	Pro	Ala	Gly		
			385					390						395			
gcc	act	gga	ggc	agc	tca	gcc	tgg	cta	gac	agc	agc	tct	gag	aat	agg	1371	
Ala	Thr	Gly	Gly	Ser	Ser	Ala	Trp	Leu	Asp	Ser	Ser	Ser	Glu	Asn	Arg		

	400	405	410	
ggc ctt ggg tgc gag ctg agt aag cct ggc gtg ctg gca tcc cag gta				1419
Gly Leu Gly Ser Glu Leu Ser Lys Pro Gly Val Leu Ala Ser Gln Val				
	415	420	425	
gac agc ccg ttc tgc ggc tgc ttc gag gat ctt gcc atc agt gcc agc				1467
Asp Ser Pro Phe Ser Gly Cys Phe Glu Asp Leu Ala Ile Ser Ala Ser				
	430	435	440	
acc tcc ttg ggc atg ggg ccc tgc cat ggc cca gag gag aat gag tat				1515
Thr Ser Leu Gly Met Gly Pro Cys His Gly Pro Glu Glu Asn Glu Tyr				
	445	450	455	460
aag tcc gag ggc acc ttt ggg atc cac gtg gct gag aac ccc agc atc				1563
Lys Ser Glu Gly Thr Phe Gly Ile His Val Ala Glu Asn Pro Ser Ile				
	465	470	475	
cag ctc ctg gag ggc aac cct ggg cca cct gcg gac ccg gat ggc ggc				1611
Gln Leu Leu Glu Gly Asn Pro Gly Pro Pro Ala Asp Pro Asp Gly Gly				
	480	485	490	
ccc agg cca caa gcc gac cgg aag ttc cag gag agg gag gtg cca tgc				1659
Pro Arg Pro Gln Ala Asp Arg Lys Phe Gln Glu Arg Glu Val Pro Cys				
	495	500	505	
cac agg ccc tca cct ggg gct ctg tgg ctc cag gtg gct gtg aca ggg				1707
His Arg Pro Ser Pro Gly Ala Leu Trp Leu Gln Val Ala Val Thr Gly				
	510	515	520	
gtg ctg gta gtc aca ctc ctg gtg gtg ctg tac cgg cgg cgt ctg cac				1755
Val Leu Val Val Thr Leu Leu Val Val Leu Tyr Arg Arg Arg Leu His				
	525	530	535	540
tagtgaagcc ctgggctctt cccaccaccc atctgttccg ttcctgcagt atacctggcc				1815
cctctccgaa gcccctcttt ccctcccctc tgggtctccat tctcttcagc tccctacatg				1875
ggctggggag gagacacctg gtgggcagag ctccaggcaga ggtttggatt tcagctccct				1935
cacttccggg gctgtgtggc tttggcagat gtcagacttc tggctcttgct tctccacgtg				1995
gacagtgagt atctggctca ttcttcactg gggtcttctg agattgaacc tacagggtgtt				2055
tgccaagtgc ctggcccaga gcaagtggcc actgcttctc ccatctctct cctgcccac				2115
ctggtagagc tgagggcatg agaggcagag tgcacagtgg tcaaggggtg agctctgcgg				2175
cacaggcagc ctaggcctgc gtcccaacct gcctctcacc agctctgtga ccttgggcaa				2235
gggatttata tgtctgtccc ttagttttct cacctgtaaa aggaggataa gtatatatat				2295
atatttccca gtgttgtgaa gattaaagga gtttatcgat gtaggtctta ggatgagtcc				2355
tggcatttac caagggttgg atatatgtta ttatcactat taagtgttga ggggccaggc				2415
atgctgggca acagggaccc catctctaca aaaaagttaa aaaaattagc caggcgtggt				2475

ggtgcacctg tcgtcttagc tacttgggag gctgaggtgg gaggatcgct tgagcccgga 2535
 agcttgaagc tgcagtgagc taggatcgtg ccactgcact ccaacctggg tgagagagcg 2595
 agaccctgtc tcaagaaaaa gaaaaatgca gagaaacagg agtcttggct actcctttag 2655
 aggcagactc agaccctcct gcctcacagc tttatctttg tatttgcccc ttactttatc 2715
 ttgtgccttg agaaattgct ggggagagag gtatgtccac tgggcagctg tacaggatgg 2775
 aggatatagg gcgtttccac tcccagcagc caggttccct caccccaagc tcaccactg 2835
 ttggggagat tatctacaat aacaccagaa acacattggg gtggattggg ggtatcctta 2895
 tgggttcttt tcaggaacc attgctggac aaggcacagg agccacctcc atttctgagc 2955
 tctgcaaggg acaagaacta gagccatcag gggctgggct cactgtggcc ccacccaag 3015
 ccgtcagcct ccagggatct acacctgcc ttggctgcta cagcttttcc actccactgc 3075
 cctaggggag ttcagcaacc taatgatctc tatctctgaa catctcttca tcccatgctc 3135
 caagtccagc aacctgcacc ctggaaccag gagtggaccc taccgggct gtctgtatta 3195
 atccccatcc cccaccacca atcttaaaaa gccctctgtc cccctaccct aaaccccagt 3255
 taggtacca tgctgggcag gtcagttaac aatttatgca caggtagtag ttttattgta 3315
 ttaccgttcc agggtagctt tg 3337

<210> 170
 <211> 540
 <212> PRT
 <213> Homo sapiens

<400> 170
 Met Pro Phe Ala Glu Asp Lys Thr Tyr Lys Tyr Ile Cys Arg Asn Phe
 1 5 10 15
 Ser Asn Phe Cys Asn Val Asp Val Val Glu Ile Leu Pro Tyr Leu Pro
 20 25 30
 Cys Leu Thr Ala Arg Asp Gln Asp Arg Leu Arg Ala Thr Cys Thr Leu
 35 40 45
 Ser Gly Asn Arg Asp Thr Leu Trp His Leu Phe Asn Thr Leu Gln Arg
 50 55 60
 Arg Pro Gly Trp Val Glu Tyr Phe Ile Ala Ala Leu Arg Gly Cys Glu
 65 70 75 80
 Leu Val Asp Leu Ala Asp Glu Val Ala Ser Val Tyr Gln Ser Tyr Gln
 85 90 95
 Pro Arg Thr Ser Asp Arg Pro Pro Asp Pro Leu Glu Pro Pro Ser Leu

100	105	110
Pro Ala Glu Arg Pro Gly Pro Pro Thr Pro Ala Ala Ala His Ser Ile 115 120 125		
Pro Tyr Asn Ser Cys Arg Glu Lys Glu Pro Ser Tyr Pro Met Pro Val 130 135 140		
Gln Glu Thr Gln Ala Pro Glu Ser Pro Gly Glu Asn Ser Glu Gln Ala 145 150 155 160		
Leu Gln Thr Leu Ser Pro Arg Ala Ile Pro Arg Asn Pro Asp Gly Gly 165 170 175		
Pro Leu Glu Ser Ser Ser Asp Leu Ala Ala Leu Ser Pro Leu Thr Ser 180 185 190		
Ser Gly His Gln Glu Gln Asp Thr Glu Leu Gly Ser Thr His Thr Ala 195 200 205		
Gly Ala Thr Ser Ser Leu Thr Pro Ser Arg Gly Pro Val Ser Pro Ser 210 215 220		
Val Ser Phe Gln Pro Leu Ala Arg Ser Thr Pro Arg Ala Ser Arg Leu 225 230 235 240		
Pro Gly Pro Thr Gly Ser Val Val Ser Thr Gly Thr Ser Phe Ser Ser 245 250 255		
Ser Ser Pro Gly Leu Ala Ser Ala Gly Ala Ala Glu Gly Lys Gln Gly 260 265 270		
Ala Glu Ser Asp Gln Ala Glu Pro Ile Ile Cys Ser Ser Gly Ala Glu 275 280 285		
Ala Pro Ala Asn Ser Leu Pro Ser Lys Val Pro Thr Thr Leu Met Pro 290 295 300		
Val Asn Thr Val Ala Leu Lys Val Pro Ala Asn Pro Ala Ser Val Ser 305 310 315 320		
Thr Val Pro Ser Lys Leu Pro Thr Ser Ser Lys Pro Pro Gly Ala Val 325 330 335		
Pro Ser Asn Ala Leu Thr Asn Pro Ala Pro Ser Lys Leu Pro Ile Asn 340 345 350		
Ser Thr Arg Ala Gly Met Val Pro Ser Lys Val Pro Thr Ser Met Val 355 360 365		
Leu Thr Lys Val Ser Ala Ser Thr Val Pro Thr Asp Gly Ser Ser Arg 370 375 380		
Asn Glu Glu Thr Pro Ala Ala Pro Thr Pro Ala Gly Ala Thr Gly Gly 385 390 395 400		
Ser Ser Ala Trp Leu Asp Ser Ser Ser Glu Asn Arg Gly Leu Gly Ser		

405 410 415
 Glu Leu Ser Lys Pro Gly Val Leu Ala Ser Gln Val Asp Ser Pro Phe
 420 425 430
 Ser Gly Cys Phe Glu Asp Leu Ala Ile Ser Ala Ser Thr Ser Leu Gly
 435 440 445
 Met Gly Pro Cys His Gly Pro Glu Glu Asn Glu Tyr Lys Ser Glu Gly
 450 455 460
 Thr Phe Gly Ile His Val Ala Glu Asn Pro Ser Ile Gln Leu Leu Glu
 465 470 475 480
 Gly Asn Pro Gly Pro Pro Ala Asp Pro Asp Gly Gly Pro Arg Pro Gln
 485 490 495
 Ala Asp Arg Lys Phe Gln Glu Arg Glu Val Pro Cys His Arg Pro Ser
 500 505 510
 Pro Gly Ala Leu Trp Leu Gln Val Ala Val Thr Gly Val Leu Val Val
 515 520 525
 Thr Leu Leu Val Val Leu Tyr Arg Arg Arg Leu His
 530 535 540

<210> 171
 <211> 3579
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (242)..(3094)

<400> 171
 gtagtttcgg ctcggcagac ccggcgagcc cagtggccgc gctccggtgc ggcggcgccc 60
 gaggcccgag gcggaagtgg gacggccaag cagggaagcg agggctcggg atcgacggcc 120
 gcggggcgcc gacgaggagt gcaggactca ggaagggcga gtgcgcggcg acagagcccg 180
 gggaaggagg cagggaagg ccgggcttgg gggcaggtgg tccgggcatc cagccttgaa 240
 g atg cac aag agg aaa gga ccc ccg gga ccc ccg ggc aga ggc gcc gcg 289
 Met His Lys Arg Lys Gly Pro Pro Gly Pro Pro Gly Arg Gly Ala Ala
 1 5 10 15
 gcc gcc cgc cag ctg ggc ctg ctg gtt gac ctc tcc cca gat ggc ctg 337
 Ala Ala Arg Gln Leu Gly Leu Leu Val Asp Leu Ser Pro Asp Gly Leu
 20 25 30
 atg atc cct gag gac ggg gct aac gat gaa gaa ctg gag gct gag ttc 385
 Met Ile Pro Glu Asp Gly Ala Asn Asp Glu Glu Leu Glu Ala Glu Phe
 35 40 45

ttg gct ttg gtc ggg ggc cag ccc cca gcc ctg gag aag ctc aaa ggc	433
Leu Ala Leu Val Gly Gly Gln Pro Pro Ala Leu Glu Lys Leu Lys Gly	
50 55 60	
aaa ggt ccc ttg ccg atg gag gcc att gag aag atg gcc agc ctg tgc	481
Lys Gly Pro Leu Pro Met Glu Ala Ile Glu Lys Met Ala Ser Leu Cys	
65 70 75 80	
atg aga gac ccg gat gag gat gag gag gag ggg acg gat gag gac gac	529
Met Arg Asp Pro Asp Glu Asp Glu Glu Glu Gly Thr Asp Glu Asp Asp	
85 90 95	
ttg gag gct gat gat gac ctg ctg gcg gag cta aat gag gtc ctt gga	577
Leu Glu Ala Asp Asp Asp Leu Leu Ala Glu Leu Asn Glu Val Leu Gly	
100 105 110	
gag gag cag aag gct tca gag acc cca cct cct gtg gcc cag ccg aag	625
Glu Glu Gln Lys Ala Ser Glu Thr Pro Pro Pro Val Ala Gln Pro Lys	
115 120 125	
cct gag gcc cct cat ccg ggg ctg gag acc acc ttg cag gag agg ctg	673
Pro Glu Ala Pro His Pro Gly Leu Glu Thr Thr Leu Gln Glu Arg Leu	
130 135 140	
gcg ctc tat cag aca gca att gaa agc gcc aga caa gct gga gac agc	721
Ala Leu Tyr Gln Thr Ala Ile Glu Ser Ala Arg Gln Ala Gly Asp Ser	
145 150 155 160	
gcc aag atg cgg cgc tac gat cgg ggg ctt aaa aca ctg gaa aac ctg	769
Ala Lys Met Arg Arg Tyr Asp Arg Gly Leu Lys Thr Leu Glu Asn Leu	
165 170 175	
ctc gcc tcc atc cgt aag ggc aat gcc att gac gaa gcg gac atc ccg	817
Leu Ala Ser Ile Arg Lys Gly Asn Ala Ile Asp Glu Ala Asp Ile Pro	
180 185 190	
ccg cca gtg gcc ata gga aaa ggc ccg gcg tcc acg cct acc tac agc	865
Pro Pro Val Ala Ile Gly Lys Gly Pro Ala Ser Thr Pro Thr Tyr Ser	
195 200 205	
cct gca ccc acc cag ccg gcc cct aga atc gcg tca gcc cca gag ccc	913
Pro Ala Pro Thr Gln Pro Ala Pro Arg Ile Ala Ser Ala Pro Glu Pro	
210 215 220	
agg gtc acc ctg gag gga cct tct gcc acc gcc cca gcc tca tct cca	961
Arg Val Thr Leu Glu Gly Pro Ser Ala Thr Ala Pro Ala Ser Ser Pro	
225 230 235 240	
ggc ttg gct aag ccc cag atg ccc cca ggt ccc tgc agc cct ggc cct	1009
Gly Leu Ala Lys Pro Gln Met Pro Pro Gly Pro Cys Ser Pro Gly Pro	
245 250 255	
ctg gcc cag ttg cag agc cgc cag cgc gac tac aag ctg gct gcc ctc	1057
Leu Ala Gln Leu Gln Ser Arg Gln Arg Asp Tyr Lys Leu Ala Ala Leu	
260 265 270	
cac gcc aag cag cag gga gat acc act gct gcc gct aga cac ttc cgc	1105

His	Ala	Lys	Gln	Gln	Gly	Asp	Thr	Thr	Ala	Ala	Ala	Arg	His	Phe	Arg	
		275				280						285				
gtg	gct	aag	agc	ttt	gat	gct	gtc	ttg	gag	gcc	ctg	agc	cgg	ggt	gag	1153
Val	Ala	Lys	Ser	Phe	Asp	Ala	Val	Leu	Glu	Ala	Leu	Ser	Arg	Gly	Glu	
		290				295					300					
ccc	gtg	gac	ctc	tcc	tgc	ctg	ccc	cct	cca	ccc	gac	cag	ctg	ccc	cca	1201
Pro	Val	Asp	Leu	Ser	Cys	Leu	Pro	Pro	Pro	Pro	Asp	Gln	Leu	Pro	Pro	
305					310					315					320	
gac	cca	ccg	tca	cca	ccg	tcg	cag	cct	ccg	acc	ccc	gct	acg	gcg	ccc	1249
Asp	Pro	Pro	Ser	Pro	Pro	Ser	Gln	Pro	Pro	Thr	Pro	Ala	Thr	Ala	Pro	
				325					330					335		
tcc	aca	aca	gag	gtg	ccc	cca	ccc	ccg	agg	acc	ctg	ctg	gag	gcg	ctg	1297
Ser	Thr	Thr	Glu	Val	Pro	Pro	Pro	Pro	Arg	Thr	Leu	Leu	Glu	Ala	Leu	
			340					345					350			
gag	cag	cgg	atg	gag	cgg	tac	cag	gtg	gcc	gca	gcc	cag	gcc	aag	agc	1345
Glu	Gln	Arg	Met	Glu	Arg	Tyr	Gln	Val	Ala	Ala	Ala	Gln	Ala	Lys	Ser	
		355					360					365				
aag	ggg	gac	cag	cgg	aaa	gct	cga	atg	cac	gag	cgc	atc	gtc	aag	caa	1393
Lys	Gly	Asp	Gln	Arg	Lys	Ala	Arg	Met	His	Glu	Arg	Ile	Val	Lys	Gln	
		370				375					380					
tac	caa	gat	gcc	atc	cga	gcc	cac	aag	gct	ggc	cga	gcc	gtg	gat	gtc	1441
Tyr	Gln	Asp	Ala	Ile	Arg	Ala	His	Lys	Ala	Gly	Arg	Ala	Val	Asp	Val	
385					390					395					400	
gct	gaa	ttg	ccc	gtg	ccc	cca	ggc	ttc	ccc	cca	atc	cag	ggc	ctg	gag	1489
Ala	Glu	Leu	Pro	Val	Pro	Pro	Gly	Phe	Pro	Pro	Ile	Gln	Gly	Leu	Glu	
				405					410					415		
gcc	acc	aag	ccc	acc	cag	cag	agt	ctg	gtg	ggc	gtc	ctg	gag	act	gcc	1537
Ala	Thr	Lys	Pro	Thr	Gln	Gln	Ser	Leu	Val	Gly	Val	Leu	Glu	Thr	Ala	
			420					425					430			
atg	aag	ctg	gcc	aac	cag	gat	gaa	ggc	cca	gag	gat	gaa	gag	gat	gag	1585
Met	Lys	Leu	Ala	Asn	Gln	Asp	Glu	Gly	Pro	Glu	Asp	Glu	Glu	Asp	Glu	
		435					440					445				
gtg	cct	aag	aag	cag	aac	agc	cct	gtg	gcc	ccc	aca	gcc	cag	ccc	aaa	1633
Val	Pro	Lys	Lys	Gln	Asn	Ser	Pro	Val	Ala	Pro	Thr	Ala	Gln	Pro	Lys	
		450				455					460					
gcc	cca	ccc	tca	aga	act	ccc	cag	tcg	gga	tca	gcc	cca	aca	gcc	aaa	1681
Ala	Pro	Pro	Ser	Arg	Thr	Pro	Gln	Ser	Gly	Ser	Ala	Pro	Thr	Ala	Lys	
465					470					475					480	
gcg	ccc	ccc	aaa	gcc	aca	tcc	acc	aga	gcc	cag	cag	cag	ctg	gcc	ttc	1729
Ala	Pro	Pro	Lys	Ala	Thr	Ser	Thr	Arg	Ala	Gln	Gln	Gln	Leu	Ala	Phe	
				48												

500										505					510					
cag	aaa	aac	gac	gtg	gag	ggt	gcc	aag	atg	cac	ctg	cgc	caa	gcc	aag	1825				
Gln	Lys	Asn	Asp	Val	Glu	Gly	Ala	Lys	Met	His	Leu	Arg	Gln	Ala	Lys					
		515					520					525								
gga	ctg	gag	cct	atg	ctg	gag	gcc	tcg	cgc	aat	ggg	ctg	cct	gtg	gac	1873				
Gly	Leu	Glu	Pro	Met	Leu	Glu	Ala	Ser	Arg	Asn	Gly	Leu	Pro	Val	Asp					
	530					535					540									
atc	acc	aag	gtg	ccg	cct	gcc	cct	gtc	aac	aag	gac	gac	ttt	gcc	ctg	1921				
Ile	Thr	Lys	Val	Pro	Pro	Ala	Pro	Val	Asn	Lys	Asp	Asp	Phe	Ala	Leu					
545					550				555					560						
gtc	cag	cgg	cct	ggc	ccg	ggt	ctg	tct	cag	gag	gcc	gcc	cgg	cgc	tat	1969				
Val	Gln	Arg	Pro	Gly	Pro	Gly	Leu	Ser	Gln	Glu	Ala	Ala	Arg	Arg	Tyr					
			565					570						575						
ggt	gaa	ctc	acc	aag	ctc	ata	cgg	cag	cag	cac	gag	atg	tgc	ctg	aac	2017				
Gly	Glu	Leu	Thr	Lys	Leu	Ile	Arg	Gln	Gln	His	Glu	Met	Cys	Leu	Asn					
			580					585					590							
cac	tca	aac	caa	ttc	acc	cag	ctg	ggc	aac	atc	act	gaa	acc	acc	aag	2065				
His	Ser	Asn	Gln	Phe	Thr	Gln	Leu	Gly	Asn	Ile	Thr	Glu	Thr	Thr	Lys					
		595					600					605								
ttt	gaa	aag	ttg	gcg	gag	gac	tgt	aag	cgg	agc	atg	gac	att	ctg	aag	2113				
Phe	Glu	Lys	Leu	Ala	Glu	Asp	Cys	Lys	Arg	Ser	Met	Asp	Ile	Leu	Lys					
	610					615					620									
caa	gcc	ttc	gtc	cgg	ggt	ctc	ccc	acg	ccc	acc	gcc	cgc	ttt	gag	caa	2161				
Gln	Ala	Phe	Val	Arg	Gly	Leu	Pro	Thr	Pro	Thr	Ala	Arg	Phe	Glu	Gln					
625					630					635				640						
agg	acc	ttc	agc	gtc	atc	aag	atc	ttc	cct	gac	ctc	agc	agc	aac	gac	2209				
Arg	Thr	Phe	Ser	Val	Ile	Lys	Ile	Phe	Pro	Asp	Leu	Ser	Ser	Asn	Asp					
				645					650					655						
atg	ctc	ctc	ttc	atc	gtg	aag	ggc	atc	aac	ttg	ccc	aca	ccc	cca	gga	2257				
Met	Leu	Leu	Phe	Ile	Val	Lys	Gly	Ile	Asn	Leu	Pro	Thr	Pro	Pro	Gly					
			660					665					670							
ctg	tcc	cct	ggc	gat	ctg	gat	gtc	ttt	gtt	cgg	ttt	gac	ttc	ccc	tat	2305				
Leu	Ser	Pro	Gly	Asp	Leu	Asp	Val	Phe	Val	Arg	Phe	Asp	Phe	Pro	Tyr					
		675					680					685								
ccc	aac	gtg	gaa	gaa	gct	cag	aaa	gac	aag	acc	agt	gtg	atc	aag	aac	2353				
Pro	Asn	Val	Glu	Glu	Ala	Gln	Lys	Asp	Lys	Thr	Ser	Val	Ile	Lys	Asn					
	690					695					700									
aca	gac	tcc	cct	gag	ttc	aag	gag	cag	ttc	aaa	ctc	tgc	atc	aac	cgc	2401				
Thr	Asp	Ser	Pro	Glu	Phe	Lys	Glu	Gln	Phe	Lys	Leu	Cys	Ile	Asn	Arg					
705					710				715					720						
agc	cac	cgt	ggc	ttc	cga	agg	gcc	atc	cag	acc	aag	ggc	atc	aag	ttc	2449				
Ser	His	Arg	Gly	Phe	Arg	Arg	Ala	Ile	Gln	Thr	Lys	Gly	Ile	Lys	Phe					
			725					730					735							

gaa gtg gtt cac aag ggg ggg ctg ttc aag act gac cgg gtg ctg ggg Glu Val Val His Lys Gly Gly Leu Phe Lys Thr Asp Arg Val Leu Gly 740 745 750	2497
aca gcc cag ctg aag ctg gat gca ctg gag ata gca tgt gag gtc cgg Thr Ala Gln Leu Lys Leu Asp Ala Leu Glu Ile Ala Cys Glu Val Arg 755 760 765	2545
gag atc ctt gag gtc ctg gat ggt cgc cgg ccc aca ggg ggg cga ctg Glu Ile Leu Glu Val Leu Asp Gly Arg Arg Pro Thr Gly Gly Arg Leu 770 775 780	2593
gag gta atg gtc cgg att cgg gag cca ctg aca gcc cag cag ttg gag Glu Val Met Val Arg Ile Arg Glu Pro Leu Thr Ala Gln Gln Leu Glu 785 790 795 800	2641
acg acg aca gag agg tgg ctg gtc att gac cct gtg ccg gca gct gtg Thr Thr Thr Glu Arg Trp Leu Val Ile Asp Pro Val Pro Ala Ala Val 805 810 815	2689
ccc aca cag gtt gct ggg ccc aaa ggg aag gcc cct cct gtg cct gcc Pro Thr Gln Val Ala Gly Pro Lys Gly Lys Ala Pro Pro Val Pro Ala 820 825 830	2737
cct gca agg gag tca ggg aac aga tca gcc cgg ccc ctg cat agc ctc Pro Ala Arg Glu Ser Gly Asn Arg Ser Ala Arg Pro Leu His Ser Leu 835 840 845	2785
agt gtg ctg gcg ttt gac caa gag cgt ctg gag cgg aag atc ctg gcc Ser Val Leu Ala Phe Asp Gln Glu Arg Leu Glu Arg Lys Ile Leu Ala 850 855 860	2833
ctc agg cag gcg cgg cgg ccg gtg ccc cca gaa gtg gcc cag cag tac Leu Arg Gln Ala Arg Arg Pro Val Pro Pro Glu Val Ala Gln Gln Tyr 865 870 875 880	2881
cag gac atc atg caa cgc agc cag tgg cag agg gca cag ctg gag cag Gln Asp Ile Met Gln Arg Ser Gln Trp Gln Arg Ala Gln Leu Glu Gln 885 890 895	2929
ggg ggt gtg ggc atc cga cgg gaa tac aca gcc cag ctg gag cgg cag Gly Gly Val Gly Ile Arg Arg Glu Tyr Thr Ala Gln Leu Glu Arg Gln 900 905 910	2977
ctg cag ttc tac acg gag gct gcc cgg cgc ctg ggc aac gat ggc agc Leu Gln Phe Tyr Thr Glu Ala Ala Arg Arg Leu Gly Asn Asp Gly Ser 915 920 925	3025
agg gat gct gca aag gag gcg ctc tat agg cgg aat ctg gta ggg agt Arg Asp Ala Ala Lys Glu Ala Leu Tyr Arg Arg Asn Leu Val Gly Ser 930 935 940	3073
gag ctg cag cgg ctc cgc agg tgaggagccc atggggcgagg cagccccag Glu Leu Gln Arg Leu Arg Arg 945 950	3124

aaagcgggca gcaggccccg ataccgggaa gagccgacac agccacgaac cagacaagca 3184
 gacaatcagc ggacaatcgg ttctggactc acccctcadc cgggccccca gccccgccag 3244
 agcctccgtg gctgcgggtg ttgggaacca tgcctgccag ccagtatgtg cccctcacc 3304
 aggccctggct gggccctgga gagtcctggt tgcacagccc aggggtgtcc ggcctctggc 3364
 ccgccccgga gcagggaggg cggctggggc caagccccga gggccctgc aagcacttta 3424
 ctctctgttc ctccccagcc ttaaccccaa agccctcctg ccccccaaag aagccactga 3484
 ggctggccga gccacactgt ctccccaggg gcgtcgacct ggcccagctg ggtccccagg 3544
 ccagcacatg gaataaaata gccagggcc cactc 3579

<210> 172
 <211> 951
 <212> PRT
 <213> Homo sapiens

<400> 172
 Met His Lys Arg Lys Gly Pro Pro Gly Pro Pro Gly Arg Gly Ala Ala
 1 5 10 15
 Ala Ala Arg Gln Leu Gly Leu Leu Val Asp Leu Ser Pro Asp Gly Leu
 20 25 30
 Met Ile Pro Glu Asp Gly Ala Asn Asp Glu Glu Leu Glu Ala Glu Phe
 35 40 45
 Leu Ala Leu Val Gly Gly Gln Pro Pro Ala Leu Glu Lys Leu Lys Gly
 50 55 60
 Lys Gly Pro Leu Pro Met Glu Ala Ile Glu Lys Met Ala Ser Leu Cys
 65 70 75 80
 Met Arg Asp Pro Asp Glu Asp Glu Glu Glu Gly Thr Asp Glu Asp Asp
 85 90 95
 Leu Glu Ala Asp Asp Asp Leu Leu Ala Glu Leu Asn Glu Val Leu Gly
 100 105 110
 Glu Glu Gln Lys Ala Ser Glu Thr Pro Pro Pro Val Ala Gln Pro Lys
 115 120 125
 Pro Glu Ala Pro His Pro Gly Leu Glu Thr Thr Leu Gln Glu Arg Leu
 130 135 140
 Ala Leu Tyr Gln Thr Ala Ile Glu Ser Ala Arg Gln Ala Gly Asp Ser
 145 150 155 160
 Ala Lys Met Arg Arg Tyr Asp Arg Gly Leu Lys Thr Leu Glu Asn Leu
 165 170 175
 Leu Ala Ser Ile Arg Lys Gly Asn Ala Ile Asp Glu Ala Asp Ile Pro

180					185					190					
Pro	Pro	Val	Ala	Ile	Gly	Lys	Gly	Pro	Ala	Ser	Thr	Pro	Thr	Tyr	Ser
		195					200					205			
Pro	Ala	Pro	Thr	Gln	Pro	Ala	Pro	Arg	Ile	Ala	Ser	Ala	Pro	Glu	Pro
	210					215					220				
Arg	Val	Thr	Leu	Glu	Gly	Pro	Ser	Ala	Thr	Ala	Pro	Ala	Ser	Ser	Pro
225					230					235					240
Gly	Leu	Ala	Lys	Pro	Gln	Met	Pro	Pro	Gly	Pro	Cys	Ser	Pro	Gly	Pro
			245						250					255	
Leu	Ala	Gln	Leu	Gln	Ser	Arg	Gln	Arg	Asp	Tyr	Lys	Leu	Ala	Ala	Leu
		260						265					270		
His	Ala	Lys	Gln	Gln	Gly	Asp	Thr	Thr	Ala	Ala	Ala	Arg	His	Phe	Arg
		275					280					285			
Val	Ala	Lys	Ser	Phe	Asp	Ala	Val	Leu	Glu	Ala	Leu	Ser	Arg	Gly	Glu
	290					295					300				
Pro	Val	Asp	Leu	Ser	Cys	Leu	Pro	Pro	Pro	Pro	Asp	Gln	Leu	Pro	Pro
305					310					315					320
Asp	Pro	Pro	Ser	Pro	Pro	Ser	Gln	Pro	Pro	Thr	Pro	Ala	Thr	Ala	Pro
			325						330					335	
Ser	Thr	Thr	Glu	Val	Pro	Pro	Pro	Pro	Arg	Thr	Leu	Leu	Glu	Ala	Leu
			340					345					350		
Glu	Gln	Arg	Met	Glu	Arg	Tyr	Gln	Val	Ala	Ala	Ala	Gln	Ala	Lys	Ser
		355					360					365			
Lys	Gly	Asp	Gln	Arg	Lys	Ala	Arg	Met	His	Glu	Arg	Ile	Val	Lys	Gln
	370					375					380				
Tyr	Gln	Asp	Ala	Ile	Arg	Ala	His	Lys	Ala	Gly	Arg	Ala	Val	Asp	Val
385					390					395					400
Ala	Glu	Leu	Pro	Val	Pro	Pro	Gly	Phe	Pro	Pro	Ile	Gln	Gly	Leu	Glu
			405					410						415	
Ala	Thr	Lys	Pro	Thr	Gln	Gln	Ser	Leu	Val	Gly	Val	Leu	Glu	Thr	Ala
		420						425					430		
Met	Lys	Leu	Ala	Asn	Gln	Asp	Glu	Gly	Pro	Glu	Asp	Glu	Glu	Asp	Glu
		435					440					445			
Val	Pro	Lys	Lys	Gln	Asn	Ser	Pro	Val	Ala	Pro	Thr	Ala	Gln	Pro	Lys
	450					455						460			
Ala	Pro	Pro	Ser	Arg	Thr	Pro	Gln	Ser	Gly	Ser	Ala	Pro	Thr	Ala	Lys
465					470					475					480
Ala	Pro	Pro	Lys	Ala	Thr	Ser	Thr	Arg	Ala	Gln	Gln	Gln	Leu	Ala	Phe

				485						490					495	
Leu	Glu	Gly	Arg	Lys	Lys	Gln	Leu	Leu	Gln	Ala	Ala	Leu	Arg	Ala	Lys	
			500					505					510			
Gln	Lys	Asn	Asp	Val	Glu	Gly	Ala	Lys	Met	His	Leu	Arg	Gln	Ala	Lys	
		515					520					525				
Gly	Leu	Glu	Pro	Met	Leu	Glu	Ala	Ser	Arg	Asn	Gly	Leu	Pro	Val	Asp	
	530					535					540					
Ile	Thr	Lys	Val	Pro	Pro	Ala	Pro	Val	Asn	Lys	Asp	Asp	Phe	Ala	Leu	
545					550				555						560	
Val	Gln	Arg	Pro	Gly	Pro	Gly	Leu	Ser	Gln	Glu	Ala	Ala	Arg	Arg	Tyr	
				565					570					575		
Gly	Glu	Leu	Thr	Lys	Leu	Ile	Arg	Gln	Gln	His	Glu	Met	Cys	Leu	Asn	
			580					585					590			
His	Ser	Asn	Gln	Phe	Thr	Gln	Leu	Gly	Asn	Ile	Thr	Glu	Thr	Thr	Lys	
		595					600					605				
Phe	Glu	Lys	Leu	Ala	Glu	Asp	Cys	Lys	Arg	Ser	Met	Asp	Ile	Leu	Lys	
	610					615					620					
Gln	Ala	Phe	Val	Arg	Gly	Leu	Pro	Thr	Pro	Thr	Ala	Arg	Phe	Glu	Gln	
625					630					635					640	
Arg	Thr	Phe	Ser	Val	Ile	Lys	Ile	Phe	Pro	Asp	Leu	Ser	Ser	Asn	Asp	
				645					650					655		
Met	Leu	Leu	Phe	Ile	Val	Lys	Gly	Ile	Asn	Leu	Pro	Thr	Pro	Pro	Gly	
			660					665					670			
Leu	Ser	Pro	Gly	Asp	Leu	Asp	Val	Phe	Val	Arg	Phe	Asp	Phe	Pro	Tyr	
		675					680					685				
Pro	Asn	Val	Glu	Glu	Ala	Gln	Lys	Asp	Lys	Thr	Ser	Val	Ile	Lys	Asn	
	690					695					700					
Thr	Asp	Ser	Pro	Glu	Phe	Lys	Glu	Gln	Phe	Lys	Leu	Cys	Ile	Asn	Arg	
705					710					715					720	
Ser	His	Arg	Gly	Phe	Arg	Arg	Ala	Ile	Gln	Thr	Lys	Gly	Ile	Lys	Phe	
				725					730					735		
Glu	Val	Val	His	Lys	Gly	Gly	Leu	Phe	Lys	Thr	Asp	Arg	Val	Leu	Gly	
			740					745					750			
Thr	Ala	Gln	Leu	Lys	Leu	Asp	Ala	Leu	Glu	Ile	Ala	Cys	Glu	Val	Arg	
		755					760					765				
Glu	Ile	Leu	Glu	Val	Leu	Asp	Gly	Arg	Arg	Pro	Thr	Gly	Gly	Arg	Leu	
	770					775					780					
Glu	Val	Met	Val	Arg	Ile	Arg	Glu	Pro	Leu	Thr	Ala	Gln	Gln	Leu	Glu	

785		790		795		800
Thr Thr Thr Glu Arg Trp Leu Val Ile Asp Pro Val Pro Ala Ala Val						
	805			810		815
Pro Thr Gln Val Ala Gly Pro Lys Gly Lys Ala Pro Pro Val Pro Ala						
	820			825		830
Pro Ala Arg Glu Ser Gly Asn Arg Ser Ala Arg Pro Leu His Ser Leu						
	835			840		845
Ser Val Leu Ala Phe Asp Gln Glu Arg Leu Glu Arg Lys Ile Leu Ala						
	850			855		860
Leu Arg Gln Ala Arg Arg Pro Val Pro Pro Glu Val Ala Gln Gln Tyr						
	865			870		875
Gln Asp Ile Met Gln Arg Ser Gln Trp Gln Arg Ala Gln Leu Glu Gln						
	885			890		895
Gly Gly Val Gly Ile Arg Arg Glu Tyr Thr Ala Gln Leu Glu Arg Gln						
	900			905		910
Leu Gln Phe Tyr Thr Glu Ala Ala Arg Arg Leu Gly Asn Asp Gly Ser						
	915			920		925
Arg Asp Ala Ala Lys Glu Ala Leu Tyr Arg Arg Asn Leu Val Gly Ser						
	930			935		940
Glu Leu Gln Arg Leu Arg Arg						
	945			950		

<210> 173
 <211> 2796
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (574)..(1683)

<400> 173
 aagcatttcc tattgagacc cccaagagtt cccccggcgg cctcgggctc cagcaagact 60
 ttgggccttt tcttgtgtcc tgtttggttaa aggcattgagg gctccagcat taaagagggc 120
 tagtccttaa caaagggaaa gcgataaatg taaataagct cacattttca gaatgagcgg 180
 tttgcagtaa ggagctgcgg cagcccagag tctgctcttt ttgggctggg ctaacctttc 240
 cctgtttttt gttttttggt ttgttttggt tttgtttttt atggataaaa atatgcgctt 300
 ccgaagtgcg agttgccagt ttacacgttt attagctaac tatctacagg catgagcaca 360
 ttctctcatc tagcacactc tttcttgggc actcaattga ggaactctct gatcgtctgc 420

ctccagaaaa ttcattgatt atccaagtct cagataaatc tgggtgccaga gtttggtttg 480
aactaactaa tgaagaaagc attctctact ggtcctcagt ctcaagagtg gtgaaccct 540
gcacctagca ggctctctgg gaaaaaaaaa tcc atg ggt gac aga aga ttt att 594
Met Gly Asp Arg Arg Phe Ile
1 5
gac ttc caa ttc caa gat tta aat tca agt ctc aga ccc agg ttg gga 642
Asp Phe Gln Phe Gln Asp Leu Asn Ser Ser Leu Arg Pro Arg Leu Gly
10 15 20
aat gca act gcc aat aat act tgc att gtt gat gat tcc ttc aag tat 690
Asn Ala Thr Ala Asn Asn Thr Cys Ile Val Asp Asp Ser Phe Lys Tyr
25 30 35
aat ttg aat ggt gct gtc tat agt gtt gta ttc atc ctg ggt cta ata 738
Asn Leu Asn Gly Ala Val Tyr Ser Val Val Phe Ile Leu Gly Leu Ile
40 45 50 55
acc aac agt gcc tcc ctg ttt gtc ttc tgc ttc cgc atg aaa atg aga 786
Thr Asn Ser Ala Ser Leu Phe Val Phe Cys Phe Arg Met Lys Met Arg
60 65 70
agt gag acg gct act ttc atc acc aac ctg gcc ctc tct gat ttg ctt 834
Ser Glu Thr Ala Thr Phe Ile Thr Asn Leu Ala Leu Ser Asp Leu Leu
75 80 85
ttt gtt tgt acc cta cct ttc aaa ata ttt tac aac ttt aat cgc cac 882
Phe Val Cys Thr Leu Pro Phe Lys Ile Phe Tyr Asn Phe Asn Arg His
90 95 100
tgg cct ttt ggt gac acc ctc tgt aag atc tca ggg act gcg ttc ctc 930
Trp Pro Phe Gly Asp Thr Leu Cys Lys Ile Ser Gly Thr Ala Phe Leu
105 110 115
acc aac atc tat ggg agc atg ctc ttc ctc acc tgc atc agt gtg gat 978
Thr Asn Ile Tyr Gly Ser Met Leu Phe Leu Thr Cys Ile Ser Val Asp
120 125 130 135
cgt ttc cta gcc att gtc tat ccc ttc cga tgc cgt acc atc agg acc 1026
Arg Phe Leu Ala Ile Val Tyr Pro Phe Arg Ser Arg Thr Ile Arg Thr
140 145 150
agg agg aat tcc gcc att gtg tgc gct gga gtc tgg atc cta gtc ctc 1074
Arg Arg Asn Ser Ala Ile Val Cys Ala Gly Val Trp Ile Leu Val Leu
155 160 165
agt ggt ggt att tca gct tct ttg ttc tcc acc act aat gtc aac aat 1122
Ser Gly Gly Ile Ser Ala Ser Leu Phe Ser Thr Thr Asn Val Asn Asn
170 175 180
gcg acc acc act tgc ttt gaa ggc ttc tcc aaa cgt gtc tgg aag aca 1170
Ala Thr Thr Thr Cys Phe Glu Gly Phe Ser Lys Arg Val Trp Lys Thr
185 190 195
tac ctg tcc aag atc act ata ttc att gaa gtt gtt gga ttc atc att 1218

Tyr	Leu	Ser	Lys	Ile	Thr	Ile	Phe	Ile	Glu	Val	Val	Gly	Phe	Ile	Ile		
200					205					210					215		
cct	ctg	ata	ttg	aat	gtt	tct	tgt	tct	tct	gtg	gtg	ctt	aga	acc	ctc	1266	
Pro	Leu	Ile	Leu	Asn	Val	Ser	Cys	Ser	Ser	Val	Val	Leu	Arg	Thr	Leu		
				220					225					230			
cgc	aag	cct	gca	aca	ttg	tct	cag	att	ggg	acc	aat	aag	aaa	aaa	gtg	1314	
Arg	Lys	Pro	Ala	Thr	Leu	Ser	Gln	Ile	Gly	Thr	Asn	Lys	Lys	Lys	Val		
			235					240					245				
ttg	aag	atg	atc	aca	gtg	cat	atg	gca	gtg	ttt	gtg	gta	tgc	ttt	gta	1362	
Leu	Lys	Met	Ile	Thr	Val	His	Met	Ala	Val	Phe	Val	Val	Cys	Phe	Val		
		250					255					260					
cca	tac	aac	tcc	gtt	ctc	ttt	tta	tat	gcc	ttg	gta	cgc	tcc	caa	gcc	1410	
Pro	Tyr	Asn	Ser	Val	Leu	Phe	Leu	Tyr	Ala	Leu	Val	Arg	Ser	Gln	Ala		
	265					270					275						
att	act	aat	tgc	tta	ttg	gaa	agg	ttt	gca	aag	atc	atg	tac	cca	att	1458	
Ile	Thr	Asn	Cys	Leu	Leu	Glu	Arg	Phe	Ala	Lys	Ile	Met	Tyr	Pro	Ile		
280					285					290					295		
acc	ttg	tgc	ctt	gca	act	ctg	aat	tgt	tgc	ttt	gat	cct	ttt	atc	tat	1506	
Thr	Leu	Cys	Leu	Ala	Thr	Leu	Asn	Cys	Cys	Phe	Asp	Pro	Phe	Ile	Tyr		
				300					305					310			
tac	ttc	act	ctt	gaa	tcc	ttt	cag	aag	tcc	ttt	tat	atc	aat	aca	cat	1554	
Tyr	Phe	Thr	Leu	Glu	Ser	Phe	Gln	Lys	Ser	Phe	Tyr	Ile	Asn	Thr	His		
			315					320					325				
ata	agg	atg	gag	tcg	ctg	ttt	aag	act	gag	aca	cct	ctg	acc	ccc	aaa	1602	
Ile	Arg	Met	Glu	Ser	Leu	Phe	Lys	Thr	Glu	Thr	Pro	Leu	Thr	Pro	Lys		
		330					335					340					
cct	tcc	ctt	cca	gct	atc	caa	gag	gaa	gtt	agt	gat	caa	aca	aca	aat	1650	
Pro	Ser	Leu	Pro	Ala	Ile	Gln	Glu	Glu	Val	Ser	Asp	Gln	Thr	Thr	Asn		
	345					350					355						
aat	ggt	ggt	gaa	tta	atg	ctg	gaa	tcc	acc	ttc	taggtaccag	aattgtcttt				1703	
Asn	Gly	Gly	Glu	Leu	Met	Leu	Glu	Ser	Thr	Phe							
360					365					370							
cagggttcagc	tacagtgtct	cttatgattt	ttttcctatg	ctataaatag	gagaaacaaa											1763	
ttgaagctaa	tgatactgag	aatagagtaa	tgtaccaa	atgcagtcagat	acatttgttt											1823	
gaacactatt	gtacatat	tggtttgttc	agtaattata	ggtcaagtct	aattacaaca											1883	
acaaaaacag	atcagcctct	tctgttgagt	tgacttttca	ttacctaa	atgaccagtgg											1943	
cttgactttt	agtgatgtga	gggttat	tttaacttaa	aaaaaaggca	ttccagta											2003	
tttggttaatt	gggttgggcc	tataaatata	gaacaaat	agggattatt	taaaaacatc											2063	
tgtgttacta	ctgatatatg	ctagtatt	tttctttt	tgaattaata	ttgaatttat											2123	

ttttaaaaaa gaactatattt tacctaattct taataagaca tactgagaaa-gagaaatgtg 2183
 ttgaatttta aaatattggc aaattttacc tagattttta aaacctaaat gaagtgtttg 2243
 aatgaatatg ggtgggaaat ttggaattta gacaacattt acgcatttat aataaccaca 2303
 attagtgtca gcttttaaaa ctttcttttt aaaataattc tagaattttc atatgaaatt 2363
 gttaatcctg aaaggtgcta cttatgtgcc tggcaggtat aaaatggaaa actcataaaa 2423
 ttaacagtgt caatttaaaa aaaaaaaac tttaagcaac actatattat ttcttaagat 2483
 ttccatttat cctttatggg ggtggggatt ggcttgtaga aaatatttat tcttcatgtt 2543
 aaatgttggg gacacattac agccagagag ctacagtatt tgtgcccagg tcaggagtaa 2603
 attgaaaaag taagtgaata gaatagtagc agcaagatat cttagagctt atattagtag 2663
 tttttaaggt ggtgggttaga tagctgtaat tttgaaatcc atactctctt ctgtacattt 2723
 tggagcacat tgtagccaag gcgctgctga atttgtgctc aggtcgggag catattgaaa 2783
 aagatgtgta cat 2796

<210> 174
 <211> 370
 <212> PRT
 <213> Mus musculus

<400> 174
 Met Gly Asp Arg Arg Phe Ile Asp Phe Gln Phe Gln Asp Leu Asn Ser
 1 5 10 15
 Ser Leu Arg Pro Arg Leu Gly Asn Ala Thr Ala Asn Asn Thr Cys Ile
 20 25 30
 Val Asp Asp Ser Phe Lys Tyr Asn Leu Asn Gly Ala Val Tyr Ser Val
 35 40 45
 Val Phe Ile Leu Gly Leu Ile Thr Asn Ser Ala Ser Leu Phe Val Phe
 50 55 60
 Cys Phe Arg Met Lys Met Arg Ser Glu Thr Ala Thr Phe Ile Thr Asn
 65 70 75 80
 Leu Ala Leu Ser Asp Leu Leu Phe Val Cys Thr Leu Pro Phe Lys Ile
 85 90 95
 Phe Tyr Asn Phe Asn Arg His Trp Pro Phe Gly Asp Thr Leu Cys Lys
 100 105 110
 Ile Ser Gly Thr Ala Phe Leu Thr Asn Ile Tyr Gly Ser Met Leu Phe
 115 120 125
 Leu Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr Pro Phe
 130 135 140

Arg	Ser	Arg	Thr	Ile	Arg	Thr	Arg	Arg	Asn	Ser	Ala	Ile	Val	Cys	Ala	
145					150					155					160	
Gly	Val	Trp	Ile	Leu	Val	Leu	Ser	Gly	Gly	Ile	Ser	Ala	Ser	Leu	Phe	
				165					170					175		
Ser	Thr	Thr	Asn	Val	Asn	Asn	Ala	Thr	Thr	Thr	Cys	Phe	Glu	Gly	Phe	
			180					185					190			
Ser	Lys	Arg	Val	Trp	Lys	Thr	Tyr	Leu	Ser	Lys	Ile	Thr	Ile	Phe	Ile	
		195					200					205				
Glu	Val	Val	Gly	Phe	Ile	Ile	Pro	Leu	Ile	Leu	Asn	Val	Ser	Cys	Ser	
	210					215					220					
Ser	Val	Val	Leu	Arg	Thr	Leu	Arg	Lys	Pro	Ala	Thr	Leu	Ser	Gln	Ile	
225					230					235					240	
Gly	Thr	Asn	Lys	Lys	Lys	Val	Leu	Lys	Met	Ile	Thr	Val	His	Met	Ala	
			245						250					255		
Val	Phe	Val	Val	Cys	Phe	Val	Pro	Tyr	Asn	Ser	Val	Leu	Phe	Leu	Tyr	
			260					265					270			
Ala	Leu	Val	Arg	Ser	Gln	Ala	Ile	Thr	Asn	Cys	Leu	Leu	Glu	Arg	Phe	
		275					280						285			
Ala	Lys	Ile	Met	Tyr	Pro	Ile	Thr	Leu	Cys	Leu	Ala	Thr	Leu	Asn	Cys	
	290					295					300					
Cys	Phe	Asp	Pro	Phe	Ile	Tyr	Tyr	Phe	Thr	Leu	Glu	Ser	Phe	Gln	Lys	
305					310					315					320	
Ser	Phe	Tyr	Ile	Asn	Thr	His	Ile	Arg	Met	Glu	Ser	Leu	Phe	Lys	Thr	
				325					330					335		
Glu	Thr	Pro	Leu	Thr	Pro	Lys	Pro	Ser	Leu	Pro	Ala	Ile	Gln	Glu	Glu	
			340					345					350			
Val	Ser	Asp	Gln	Thr	Thr	Asn	Asn	Gly	Gly	Glu	Leu	Met	Leu	Glu	Ser	
		355					360					365				
Thr	Phe															
	370															

<210> 175
 <211> 2299
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (67)..(1176)

<400> 175

cctaccgggtc catagtgtca gagtgggtgaa cccctgcagc cagcaggcct cctgaaaaaa 60

aagtcc atg ggt gac aga aga ttc att gac ttc caa ttc caa gat tca 108
Met Gly Asp Arg Arg Phe Ile Asp Phe Gln Phe Gln Asp Ser
1 5 10

aat tca agc ctc aga ccc agg ttg ggc aat gct act gcc aat aat act 156
Asn Ser Ser Leu Arg Pro Arg Leu Gly Asn Ala Thr Ala Asn Asn Thr
15 20 25 30

tgc att gtt gat gat tcc ttc aag tat aat ctc aat ggt gct gtc tac 204
Cys Ile Val Asp Asp Ser Phe Lys Tyr Asn Leu Asn Gly Ala Val Tyr
35 40 45

agt gtt gta ttc atc ttg ggt ctg ata acc aac agt gtc tct ctg ttt 252
Ser Val Val Phe Ile Leu Gly Leu Ile Thr Asn Ser Val Ser Leu Phe
50 55 60

gtc ttc tgt ttc cgc atg aaa atg aga agt gag act gct att ttt atc 300
Val Phe Cys Phe Arg Met Lys Met Arg Ser Glu Thr Ala Ile Phe Ile
65 70 75

acc aat cta gct gtc tct gat ttg ctt ttt gtc tgt aca cta cct ttt 348
Thr Asn Leu Ala Val Ser Asp Leu Leu Phe Val Cys Thr Leu Pro Phe
80 85 90

aaa ata ttt tac aac ttc aac cgc cac tgg cct ttt ggt gac acc ctc 396
Lys Ile Phe Tyr Asn Phe Asn Arg His Trp Pro Phe Gly Asp Thr Leu
95 100 105 110

tgc aag atc tct gga act gca ttc ctt acc aac atc tat ggg agc atg 444
Cys Lys Ile Ser Gly Thr Ala Phe Leu Thr Asn Ile Tyr Gly Ser Met
115 120 125

ctc ttt ctc acc tgt att agt gtg gat cgt ttc ctg gcc att gtc tat 492
Leu Phe Leu Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr
130 135 140

cct ttt cga tct cgt act att agg act agg agg aat tct gcc att gtg 540
Pro Phe Arg Ser Arg Thr Ile Arg Thr Arg Arg Asn Ser Ala Ile Val
145 150 155

tgt gct ggt gtc tgg atc cta gtc ctc agt ggc ggt att tca gcc tct 588
Cys Ala Gly Val Trp Ile Leu Val Leu Ser Gly Gly Ile Ser Ala Ser
160 165 170

ttg ttt tcc acc act aat gtc aac aat gca acc acc acc tgc ttt gaa 636
Leu Phe Ser Thr Thr Asn Val Asn Asn Ala Thr Thr Thr Cys Phe Glu
175 180 185 190

ggc ttc tcc aaa cgt gtc tgg aag act tat tta tcc aag atc aca ata 684
Gly Phe Ser Lys Arg Val Trp Lys Thr Tyr Leu Ser Lys Ile Thr Ile
195 200 205

ttt att gaa gtt gtt ggg ttt atc att cct cta ata ttg aat gtc tct 732
Phe Ile Glu Val Val Gly Phe Ile Ile Pro Leu Ile Leu Asn Val Ser
210 215 220

tgc tct tct gtg gtg ctg aga act ctt cgc aag cct gct act ctg tct	780
Cys Ser Ser Val Val Leu Arg Thr Leu Arg Lys Pro Ala Thr Leu Ser	
225 230 235	
caa att ggg acc aat aag aaa aaa gta ctg aaa atg atc aca gta cat	828
Gln Ile Gly Thr Asn Lys Lys Lys Val Leu Lys Met Ile Thr Val His	
240 245 250	
atg gca gtc ttt gtg gta tgc ttt gta ccc tac aac tct gtc ctc ttc	876
Met Ala Val Phe Val Val Cys Phe Val Pro Tyr Asn Ser Val Leu Phe	
255 260 265 270	
ttg tat gcc ctg gtg cgc tcc caa gct att act aat tgc ttt ttg gaa	924
Leu Tyr Ala Leu Val Arg Ser Gln Ala Ile Thr Asn Cys Phe Leu Glu	
275 280 285	
aga ttt gca aag atc atg tac cca atc acc ttg tgc ctt gca act ctg	972
Arg Phe Ala Lys Ile Met Tyr Pro Ile Thr Leu Cys Leu Ala Thr Leu	
290 295 300	
aac tgt tgt ttt gac cct ttc atc tat tac ttc acc ctt gaa tcc ttt	1020
Asn Cys Cys Phe Asp Pro Phe Ile Tyr Tyr Phe Thr Leu Glu Ser Phe	
305 310 315	
cag aag tcc ttc tac atc aat gcc cac atc aga atg gag tcc ctg ttt	1068
Gln Lys Ser Phe Tyr Ile Asn Ala His Ile Arg Met Glu Ser Leu Phe	
320 325 330	
aag act gaa aca cct ttg acc aca aag cct tcc ctt cca gct att caa	1116
Lys Thr Glu Thr Pro Leu Thr Thr Lys Pro Ser Leu Pro Ala Ile Gln	
335 340 345 350	
gag gaa gtg agt gat caa aca aca aat aat ggt ggt gaa tta atg cta	1164
Glu Glu Val Ser Asp Gln Thr Thr Asn Asn Gly Gly Glu Leu Met Leu	
355 360 365	
gaa tcc acc ttt taggtatgag aaatgtgttc aggtccagat atggtttctc	1216
Glu Ser Thr Phe	
370	
ctataatttt tcctatgcta taaactaaag atttgaagct aatgatactg agaataatgc	1276
accaaatacca gtcagataca tttgtttgaa ggtatactgt agagttttta ttgctgtttt	1336
gttcagtaaat tatagggtcaa atctaattac aacaaccaag atggattgcc aaactcttct	1396
gcttggttgg aatttcattg tatcgcatca tccaggtggc tagtggcatt tgataatata	1456
gagatgactt tgaaactttc aaaaaggtat ttctattcca atgatatttg gtaattaggt	1516
tgggcctata aatatagaac aaattcaggg atttttaaaa aattgtgtta ctactgatat	1576
atgctagttt tattttattt ttttggactg tcattgagtt tatttttagca caagaatatt	1636
tttagcctaa cattattaat aagaaatgtg tcaaattttt aacattggta aaatatgtta	1696

~~tg~~gtgcattttt gaaaacagaa aacaaattgc gttggcatgt acgtgggtgg gaagaaaaag 1756
 aaaattaaca ggatttacac aattataatc accagcagtg tgagtttaaa aaacttcggt 1816
 gtttttacac caaattaaaa tttcatgtc aaacttcaaa gccagaaagc tgctaaatac 1876
 gtgtctggca ggtaaaagct ggaaaattac ttaaacaggg aaagtgtcaa taaaaaaact 1936
 tgagcaacac caacatattt tttcttaaaa tgtcacgtta tcttcatttt gggaaactag 1996
 gttctataaa atatttatcc tccctggtat actttggagc acagcacagc cagaaagggg 2056
 ctgcatttgt gcccaggtca ggagcaaatt gaaaaaaaaa ataaagtaat actaaaaaat 2116
 caaactataa acccaaaaaca tttattaaaa cctgaattaa tcctttttgg agggaggagt 2176
 agagatatat aacctgaaaa tacttattct ttcttatcga attttggagc ctaatatagc 2236
 caggagctgc tgaatttgtg cccctggatt ggaaccaaat aaaaaaaaaa aaaaaaaatt 2296
 cct 2299

<210> 176
 <211> 370
 <212> PRT
 <213> Homo sapiens

<400> 176
 Met Gly Asp Arg Arg Phe Ile Asp Phe Gln Phe Gln Asp Ser Asn Ser
 1 5 10 15
 Ser Leu Arg Pro Arg Leu Gly Asn Ala Thr Ala Asn Asn Thr Cys Ile
 20 25 30
 Val Asp Asp Ser Phe Lys Tyr Asn Leu Asn Gly Ala Val Tyr Ser Val
 35 40 45
 Val Phe Ile Leu Gly Leu Ile Thr Asn Ser Val Ser Leu Phe Val Phe
 50 55 60
 Cys Phe Arg Met Lys Met Arg Ser Glu Thr Ala Ile Phe Ile Thr Asn
 65 70 75 80
 Leu Ala Val Ser Asp Leu Leu Phe Val Cys Thr Leu Pro Phe Lys Ile
 85 90 95
 Phe Tyr Asn Phe Asn Arg His Trp Pro Phe Gly Asp Thr Leu Cys Lys
 100 105 110
 Ile Ser Gly Thr Ala Phe Leu Thr Asn Ile Tyr Gly Ser Met Leu Phe
 115 120 125
 Leu Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr Pro Phe
 130 135 140
 Arg Ser Arg Thr Ile Arg Thr Arg Arg Asn Ser Ala Ile Val Cys Ala

	1	5	
ttg ctg cgg ctc ctc gtg ctg ggg ctc tgg ctg gcg ttg ctg cgc tcc			101
Leu Leu Arg Leu Leu Val Leu Gly Leu Trp Leu Ala Leu Leu Arg Ser			
10	15	20	
gtg gcc ggg gag caa gcg cca ggc acc gcc ccc tgc tcc cgc ggc agc			149
Val Ala Gly Glu Gln Ala Pro Gly Thr Ala Pro Cys Ser Arg Gly Ser			
25	30	35	40
tcc tgg agc gcg gac ctg gac aag tgc atg gac tgc gcg tct tgc agg			197
Ser Trp Ser Ala Asp Leu Asp Lys Cys Met Asp Cys Ala Ser Cys Arg			
45	50	55	
gcg cga ccg cac agc gac ttc tgc ctg ggc tgc gct gca gca cct cct			245
Ala Arg Pro His Ser Asp Phe Cys Leu Gly Cys Ala Ala Ala Pro Pro			
60	65	70	
gcc ccc ttc cgg ctg ctt tgg ccc atc ctt ggg ggc gct ctg agc ctg			293
Ala Pro Phe Arg Leu Leu Trp Pro Ile Leu Gly Gly Ala Leu Ser Leu			
75	80	85	
acc ttc gtg ctg ggg ctg ctt tct ggc ttt ttg gtc tgg aga cga tgc			341
Thr Phe Val Leu Gly Leu Leu Ser Gly Phe Leu Val Trp Arg Arg Cys			
90	95	100	
cgc agg aga gag aag ttc acc acc ccc ata gag gag acc ggc gga gag			389
Arg Arg Arg Glu Lys Phe Thr Thr Pro Ile Glu Glu Thr Gly Gly Glu			
105	110	115	120
ggc tgc cca gct gtg gcg ctg atc cag tgacaatgtg cccctgccca			436
Gly Cys Pro Ala Val Ala Leu Ile Gln			
125			
gccgggggctc gcccaactcat cattcattca tccattctag agccagtctc tgcctcccag			496
acgcggcggg agccaagctc ctccaaccac aaggggggtg gggggcggtg aatcacctcc			556
gaggcctggg tccagggttc aggggaacct tccaagggtg ctggttgccc tgcctctggc			616
tccagaacag aaaggagacc tcacgctggc tcacacaaaa cagctgacac tgactaagga			676
actgcagcat ttgcacaggg gaggggggtg ccctccttcc tagaggccct gggggccagg			736
ctgacttggg gggcagactt gacactaggc cccactcact cagatgtcct gaaattccac			796
cacgggggtc accctggggg gttagggaacc tatttttaac actagggggc tggcccacta			856
ggagggctgg ccctaagata cagaccccc caactcccc aagcggggag gagatattta			916
ttttggggag agtttggagg ggaggagaa tttattaata aaagaatctt taacttt			973

<210> 178
 <211> 129
 <212> PRT
 <213> Homo sapiens

<400> 178
Met Ala Arg Gly Ser Leu Arg Arg Leu Leu Arg Leu Leu Val Leu Gly
1 5 10 15
Leu Trp Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly
20 25 30
Thr Ala Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys
35 40 45
Cys Met Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys
50 55 60
Leu Gly Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Pro
65 70 75 80
Ile Leu Gly Gly Ala Leu Ser Leu Thr Phe Val Leu Gly Leu Leu Ser
85 90 95
Gly Phe Leu Val Trp Arg Arg Cys Arg Arg Arg Glu Lys Phe Thr Thr
100 105 110
Pro Ile Glu Glu Thr Gly Gly Glu Gly Cys Pro Ala Val Ala Leu Ile
115 120 125

Gln

<210> 179
<211> 3631
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (191)..(3244)

<400> 179
tctaaatcag cggccgctga attctagggc gctgctggcg ctgcagctgc acttgctccg 60
ggcgctggcg caagatgatg ttgctccata ttttaaaacg gagccaggcc taccacagat 120
ccacctggaa ggggaaccgcc ttgttctcac ctgccttgcc gaagggagct ggcctttgga 180
gttcaagtgg atg cgc gat gac agt gag ctc acc acc tac agc agc gaa 229
Met Arg Asp Asp Ser Glu Leu Thr Thr Tyr Ser Ser Glu
1 5 10
tat aag tac att att cca tct ttg cag aag ctc gat gct ggg ttt tac 277
Tyr Lys Tyr Ile Ile Pro Ser Leu Gln Lys Leu Asp Ala Gly Phe Tyr
15 20 25
cgc tgc gtg gtg cga aac aga atg gga gca ctc ctg caa aga aaa tca 325
Arg Cys Val Val Arg Asn Arg Met Gly Ala Leu Leu Gln Arg Lys Ser
30 35 40 45

gaa gtt caa gtc gca tat atg gga agt ttc atg gat acg gac cag agg	373
Glu Val Gln Val Ala Tyr Met Gly Ser Phe Met Asp Thr Asp Gln Arg	
50 55 60	
aaa aca gtt tct caa gga cgt gca gcg att cta aac ctg ctg ccc atc	421
Lys Thr Val Ser Gln Gly Arg Ala Ala Ile Leu Asn Leu Leu Pro Ile	
65 70 75	
acc agc tac ccc aga cct caa gtg act tgg ttt aga gaa ggg cac aag	469
Thr Ser Tyr Pro Arg Pro Gln Val Thr Trp Phe Arg Glu Gly His Lys	
80 85 90	
att att cca agc aac aga ata gcc atc aca ttg gag aat cag ctg gtg	517
Ile Ile Pro Ser Asn Arg Ile Ala Ile Thr Leu Glu Asn Gln Leu Val	
95 100 105	
atc ctc gcc acc aca acc agt gat gcc ggg gca tac tac gtg cag gcc	565
Ile Leu Ala Thr Thr Thr Ser Asp Ala Gly Ala Tyr Tyr Val Gln Ala	
110 115 120 125	
gtg aat gag aaa aat gga gaa aac aag aca agc cca ttc att cat ttg	613
Val Asn Glu Lys Asn Gly Glu Asn Lys Thr Ser Pro Phe Ile His Leu	
130 135 140	
agc ata gca aga gat gtt ggc aca cct gaa acc atg gcc cca acc att	661
Ser Ile Ala Arg Asp Val Gly Thr Pro Glu Thr Met Ala Pro Thr Ile	
145 150 155	
gtg gtt ccc ccg ggc aac aga agt gtg gtg gct gga tcc agt gag acc	709
Val Val Pro Pro Gly Asn Arg Ser Val Val Ala Gly Ser Ser Glu Thr	
160 165 170	
acc ttg gaa tgt ata gcc agt gcc agg cct gtg gag gac ctg agt gtg	757
Thr Leu Glu Cys Ile Ala Ser Ala Arg Pro Val Glu Asp Leu Ser Val	
175 180 185	
acc tgg aag agg aat gga gtg aga atc acc agt ggc ctc cac agc ttt	805
Thr Trp Lys Arg Asn Gly Val Arg Ile Thr Ser Gly Leu His Ser Phe	
190 195 200 205	
gga aga cgc ctc acc atc agc aac ccg acg tcc gcg gac acc ggg cca	853
Gly Arg Arg Leu Thr Ile Ser Asn Pro Thr Ser Ala Asp Thr Gly Pro	
210 215 220	
tac gtc tgc gag gcg gcg ctg ccg ggg agc gct ttt gaa ccg gcc agg	901
Tyr Val Cys Glu Ala Ala Leu Pro Gly Ser Ala Phe Glu Pro Ala Arg	
225 230 235	
gcg acg gcc ttt ctt ttc atc ata gag cca cca tat ttt act gct gag	949
Ala Thr Ala Phe Leu Phe Ile Ile Glu Pro Pro Tyr Phe Thr Ala Glu	
240 245 250	
ccc gag agt cgg att tca gct gaa gta gaa gaa act gtg gac atc gga	997
Pro Glu Ser Arg Ile Ser Ala Glu Val Glu Glu Thr Val Asp Ile Gly	
255 260 265	

tgt	caa	gcc	atg	ggg	gtc	ccc	ett	ccc	acc	etc	cag	tgg	tac	aag	gat	1045
Cys	Gln	Ala	Met	Gly	Val	Pro	Leu	Pro	Thr	Leu	Gln	Trp	Tyr	Lys	Asp	
270					275					280					285	
gcc	atc	tcc	atc	agc	agg	ctc	cag	aat	cct	cga	tac	aaa	gtg	ctc	gcc	1093
Ala	Ile	Ser	Ile	Ser	Arg	Leu	Gln	Asn	Pro	Arg	Tyr	Lys	Val	Leu	Ala	
				290					295					300		
agc	gga	ggc	ctg	cgc	atc	cag	aag	ctg	cgt	cca	gag	gac	tcc	gga	atc	1141
Ser	Gly	Gly	Leu	Arg	Ile	Gln	Lys	Leu	Arg	Pro	Glu	Asp	Ser	Gly	Ile	
			305					310					315			
ttc	cag	tgc	ttc	gcc	agc	aat	gaa	gga	ggg	gag	atc	cag	acc	cac	acc	1189
Phe	Gln	Cys	Phe	Ala	Ser	Asn	Glu	Gly	Gly	Glu	Ile	Gln	Thr	His	Thr	
		320					325					330				
tac	ctg	gat	gta	acc	aat	atc	gct	cca	gtg	ttc	acc	cag	cgg	cca	gtg	1237
Tyr	Leu	Asp	Val	Thr	Asn	Ile	Ala	Pro	Val	Phe	Thr	Gln	Arg	Pro	Val	
	335					340					345					
gac	acc	aca	gtt	act	gac	ggg	atg	aca	gcc	att	cta	agg	tgt	gag	gtg	1285
Asp	Thr	Thr	Val	Thr	Asp	Gly	Met	Thr	Ala	Ile	Leu	Arg	Cys	Glu	Val	
350					355				360					365		
tcc	ggg	gct	ccc	aaa	ccc	gcc	atc	acc	tgg	aaa	aga	gaa	aac	cac	att	1333
Ser	Gly	Ala	Pro	Lys	Pro	Ala	Ile	Thr	Trp	Lys	Arg	Glu	Asn	His	Ile	
				370					375					380		
ctg	gcc	agt	ggc	tct	gtc	cgg	att	cct	agg	ttc	atg	ctt	ctt	gaa	tcg	1381
Leu	Ala	Ser	Gly	Ser	Val	Arg	Ile	Pro	Arg	Phe	Met	Leu	Leu	Glu	Ser	
			385					390					395			
ggg	ggt	cta	cag	atc	gcg	ccc	gtc	ttc	atc	cag	gat	gcc	ggc	aac	tac	1429
Gly	Gly	Leu	Gln	Ile	Ala	Pro	Val	Phe	Ile	Gln	Asp	Ala	Gly	Asn	Tyr	
	400						405					410				
acc	tgc	tat	gcg	gcc	aac	aca	gag	ggc	tcc	ctg	aat	gca	tcg	gcc	acg	1477
Thr	Cys	Tyr	Ala	Ala	Asn	Thr	Glu	Gly	Ser	Leu	Asn	Ala	Ser	Ala	Thr	
	415					420					425					
ctc	act	gtg	tgg	aat	cgg	acg	tcc	atc	gtc	cac	cct	cct	gag	gac	cac	1525
Leu	Thr	Val	Trp	Asn	Arg	Thr	Ser	Ile	Val	His	Pro	Pro	Glu	Asp	His	
430					435					440				445		
gtg	gtg	att	aag	ggg	acc	acg	gcc	acg	ctg	cac	tgt	ggt	gcc	aca	cat	1573
Val	Val	Ile	Lys	Gly	Thr	Thr	Ala	Thr	Leu	His	Cys	Gly	Ala	Thr	His	
			450					455					460			
gac	ccc	cgg	gtt	tca	ctc	cgc	tac	gtt	tgg	aag	aag	gac	aac	gtg	gcc	1621
Asp	Pro	Arg	Val	Ser	Leu	Arg	Tyr	Val	Trp	Lys	Lys	Asp	Asn	Val	Ala	
			465					470					475			
ctg	act	cca	tcg	agc	acg	tct	agg	atc	gtg	gtg	gag	aag	gac	ggg	tcc	1669
Leu	Thr	Pro	Ser	Ser	Thr	Ser	Arg	Ile	Val	Val	Glu	Lys	Asp	Gly	Ser	
		480					485					490				
ctt	ctc	atc	agc	cag	acg	tgg	tca	ggc	gac	atc	ggt	gac	tac	agc	tgc	1717

Leu	Leu	Ile	Ser	Gln	Thr	Trp	Ser	Gly	Asp	Ile	Gly	Asp	Tyr	Ser	Cys	
495						500					505					
gag	att	gtt	tct	gaa	gga	ggg	aat	gac	tcc	agg	atg	gcc	cgg	ctg	gaa	1765
Glu	Ile	Val	Ser	Glu	Gly	Gly	Asn	Asp	Ser	Arg	Met	Ala	Arg	Leu	Glu	
510					515					520					525	
gtg	att	gaa	ctg	cct	cat	tca	cct	cag	aac	ctc	ctg	gtc	agc	cct	aat	1813
Val	Ile	Glu	Leu	Pro	His	Ser	Pro	Gln	Asn	Leu	Leu	Val	Ser	Pro	Asn	
				530						535					540	
tct	tcc	cac	agc	cac	gcc	gtg	gtg	ctc	tct	tgg	gtc	cgg	ccc	ttt	gat	1861
Ser	Ser	His	Ser	His	Ala	Val	Val	Leu	Ser	Trp	Val	Arg	Pro	Phe	Asp	
			545					550						555		
gga	aac	agt	cct	att	ctt	tat	tac	atc	gtg	gag	ctg	tct	gaa	aac	aac	1909
Gly	Asn	Ser	Pro	Ile	Leu	Tyr	Tyr	Ile	Val	Glu	Leu	Ser	Glu	Asn	Asn	
		560					565					570				
tct	cca	tgg	aag	gtg	cat	ctg	tca	aac	gtt	ggc	cct	gag	atg	aca	ggc	1957
Ser	Pro	Trp	Lys	Val	His	Leu	Ser	Asn	Val	Gly	Pro	Glu	Met	Thr	Gly	
		575				580					585					
gtc	acc	gtg	agt	ggc	ctg	act	ccg	gct	cgt	acc	tat	caa	ttc	cgg	gtg	2005
Val	Thr	Val	Ser	Gly	Leu	Thr	Pro	Ala	Arg	Thr	Tyr	Gln	Phe	Arg	Val	
590					595					600					605	
tgc	gcg	gtg	aat	gaa	gtg	ggc	agg	ggc	cag	tac	agt	gcc	gag	aca	agc	2053
Cys	Ala	Val	Asn	Glu	Val	Gly	Arg	Gly	Gln	Tyr	Ser	Ala	Glu	Thr	Ser	
				610					615						620	
agg	ttg	atg	cta	cct	gaa	gaa	cca	ccc	agt	gct	ccc	ccg	aaa	aat	ata	2101
Arg	Leu	Met	Leu	Pro	Glu	Glu	Pro	Pro	Ser	Ala	Pro	Pro	Lys	Asn	Ile	
			625					630						635		
gtg	gcc	agt	ggg	cgg	act	aat	cag	tcc	att	atg	gtc	cag	tgg	cag	cca	2149
Val	Ala	Ser	Gly	Arg	Thr	Asn	Gln	Ser	Ile	Met	Val	Gln	Trp	Gln	Pro	
		640					645					650				
ccc	cca	gaa	aca	gag	cac	aac	ggg	gtg	ttg	cgt	gga	tac	atc	ctc	agg	2197
Pro	Pro	Glu	Thr	Glu	His	Asn	Gly	Val	Leu	Arg	Gly	Tyr	Ile	Leu	Arg	
		655				660					665					
tac	cgc	ctg	gct	ggc	ctt	ccc	gga	gag	tac	cag	cag	cgg	aac	atc	acc	2245
Tyr	Arg	Leu	Ala	Gly	Leu	Pro	Gly	Glu	Tyr	Gln	Gln	Arg	Asn	Ile	Thr	
670					675					680					685	
agc	ccg	gag	gtg	aac	tac	tgc	ctg	gtg	aca	gac	ctg	atc	atc	tgg	aca	2293
Ser	Pro	Glu	Val	Asn	Tyr	Cys	Leu	Val	Thr	Asp	Leu	Ile	Ile	Trp	Thr	
				690					695					700		
cag	tat	gag	ata	cag	gtg	gcg	gcg	tac	aac	ggg	gcc	ggg	ctg	ggc	gtc	2341
Gln	Tyr	Glu	Ile	Gln	Val	Ala	Ala	Tyr	Asn	Gly	Ala	Gly	Leu	Gly	Val	
			705					710					715			
ttc	agc	agg	gca	gtg	acc	gag	tac	acc	ttg	cag	gga	gtg	ccc	acc	gcg	2389
Phe	Ser	Arg	Ala	Val	Thr	Glu	Tyr	Thr	Leu	Gln	Gly	Val	Pro	Thr	Ala	

ccc ccg cag aac gtg cag acg gaa gcc gtg aac tcc acc acc att cag	2437
Pro Pro Gln Asn Val Gln Thr Glu Ala Val Asn Ser Thr Thr Ile Gln	
735 740 745	
ttc ctg tgg aac cct ccg cct cag cag ttt atc aat ggc atc aac cag	2485
Phe Leu Trp Asn Pro Pro Pro Gln Gln Phe Ile Asn Gly Ile Asn Gln	
750 755 760 765	
gga tac aag ctt ctg gca tgg ccg gca gat gcc ccc gag gct gtc act	2533
Gly Tyr Lys Leu Leu Ala Trp Pro Ala Asp Ala Pro Glu Ala Val Thr	
770 775 780	
gtg gtc act att gcc cca gat ttc cac gga gtc cac cat gga cac ata	2581
Val Val Thr Ile Ala Pro Asp Phe His Gly Val His His Gly His Ile	
785 790 795	
acg aac ctg aag aag ttt acc gcc tac ttc act tcc gtt ctg tgc ttc	2629
Thr Asn Leu Lys Lys Phe Thr Ala Tyr Phe Thr Ser Val Leu Cys Phe	
800 805 810	
acc acc cct ggg gac ggg cct ccc agc aca cct cag ctg gtc tgg act	2677
Thr Thr Pro Gly Asp Gly Pro Pro Ser Thr Pro Gln Leu Val Trp Thr	
815 820 825	
cag gaa gac aaa cca gga gct gtg gga cat ctg agt ttc aca gag atc	2725
Gln Glu Asp Lys Pro Gly Ala Val Gly His Leu Ser Phe Thr Glu Ile	
830 835 840 845	
ttg gac aca tct ctc aag gtc agc tgg cag gag ccc ctg gag aaa aat	2773
Leu Asp Thr Ser Leu Lys Val Ser Trp Gln Glu Pro Leu Glu Lys Asn	
850 855 860	
ggc atc att act ggc tat cag atc tct tgg gaa gtg tac ggc agg aac	2821
Gly Ile Ile Thr Gly Tyr Gln Ile Ser Trp Glu Val Tyr Gly Arg Asn	
865 870 875	
gac tct cgt ctc acg cac acc ctg aac agc acg acg cac gag tac aag	2869
Asp Ser Arg Leu Thr His Thr Leu Asn Ser Thr Thr His Glu Tyr Lys	
880 885 890	
atc caa ggc ctc tca tct ctc acc acc tac acc atc gac gtg gcc gct	2917
Ile Gln Gly Leu Ser Ser Leu Thr Thr Tyr Thr Ile Asp Val Ala Ala	
895 900 905	
gtg act gcc gtg ggc act ggc ctg gtg act tca tcc acc att tct tct	2965
Val Thr Ala Val Gly Thr Gly Leu Val Thr Ser Ser Thr Ile Ser Ser	
910 915 920 925	
gga gtg ccc cca gac ctt cct ggt gcc cca tcc aac ctg gtc att tcc	3013
Gly Val Pro Pro Asp Leu Pro Gly Ala Pro Ser Asn Leu Val Ile Ser	
930 935 940	
aac atc agc cct cgc tcc gcc acc ctt cag ttc cgg cca ggc tat gac	3061
Asn Ile Ser Pro Arg Ser Ala Thr Leu Gln Phe Arg Pro Gly Tyr Asp	
945 950 955	

ggg aaa acg tcc atc tcc agg tgg att gtt gag ggg cag atg aga cat 3109
 Gly Lys Thr Ser Ile Ser Arg Trp Ile Val Glu Gly Gln Met Arg His
 960 965 970

caa ggt gtt gga tta cct gcc gag gtc aca cag cca agc cat gaa gcc 3157
 Gln Gly Val Gly Leu Pro Ala Glu Val Thr Gln Pro Ser His Glu Ala
 975 980 985

gga ttg gag cct gca aac ctc gga agt ctg tgg ctg ctc agc ctg gtg 3205
 Gly Leu Glu Pro Ala Asn Leu Gly Ser Leu Trp Leu Leu Ser Leu Val
 990 995 1000 1005

tat tgg tgt tac agc cag aaa ctt tgg gaa ttc tct tgt tagttggtta 3254
 Tyr Trp Cys Tyr Ser Gln Lys Leu Trp Glu Phe Ser Cys
 1010 1015

gttttactgt aattttctat aaagaattca tatcatctgt taatggcgac agtttttgtt 3314

tcttcctttg aattttttat attccttctt tctctttttt gtttcttctt ctttgagtat 3374

tttgtaatct tactgggagg gctaaagcgt cttctatcat atcgaattgg gacaatgata 3434

gaagacaatc ttgtttttgt cactctaaag aaattattgt aagattttat catcaggtat 3494

gacatttaca ccattgatgt aggcttttta aaaaatatat ccagcctgta ttgggttaag 3554

atgattcttt tctgatcctg atttcctagg agttggtttt ttttttttta aagcataaat 3614

aaatttaatt gcatcag 3631

<210> 180
 <211> 1018
 <212> PRT
 <213> Homo sapiens

<400> 180
 Met Arg Asp Asp Ser Glu Leu Thr Thr Tyr Ser Ser Glu Tyr Lys Tyr
 1 5 10 15

Ile Ile Pro Ser Leu Gln Lys Leu Asp Ala Gly Phe Tyr Arg Cys Val
 20 25 30

Val Arg Asn Arg Met Gly Ala Leu Leu Gln Arg Lys Ser Glu Val Gln
 35 40 45

Val Ala Tyr Met Gly Ser Phe Met Asp Thr Asp Gln Arg Lys Thr Val
 50 55 60

Ser Gln Gly Arg Ala Ala Ile Leu Asn Leu Leu Pro Ile Thr Ser Tyr
 65 70 75 80

Pro Arg Pro Gln Val Thr Trp Phe Arg Glu Gly His Lys Ile Ile Pro
 85 90 95

Ser Asn Arg Ile Ala Ile Thr Leu Glu Asn Gln Leu Val Ile Leu Ala

100	105	110
Thr Thr Thr Ser Asp Ala Gly Ala Tyr Tyr Val Gln Ala Val Asn Glu		
115	120	125
Lys Asn Gly Glu Asn Lys Thr Ser Pro Phe Ile His Leu Ser Ile Ala		
130	135	140
Arg Asp Val Gly Thr Pro Glu Thr Met Ala Pro Thr Ile Val Val Pro		
145	150	155
Pro Gly Asn Arg Ser Val Val Ala Gly Ser Ser Glu Thr Thr Leu Glu		
165	170	175
Cys Ile Ala Ser Ala Arg Pro Val Glu Asp Leu Ser Val Thr Trp Lys		
180	185	190
Arg Asn Gly Val Arg Ile Thr Ser Gly Leu His Ser Phe Gly Arg Arg		
195	200	205
Leu Thr Ile Ser Asn Pro Thr Ser Ala Asp Thr Gly Pro Tyr Val Cys		
210	215	220
Glu Ala Ala Leu Pro Gly Ser Ala Phe Glu Pro Ala Arg Ala Thr Ala		
225	230	235
Phe Leu Phe Ile Ile Glu Pro Pro Tyr Phe Thr Ala Glu Pro Glu Ser		
245	250	255
Arg Ile Ser Ala Glu Val Glu Glu Thr Val Asp Ile Gly Cys Gln Ala		
260	265	270
Met Gly Val Pro Leu Pro Thr Leu Gln Trp Tyr Lys Asp Ala Ile Ser		
275	280	285
Ile Ser Arg Leu Gln Asn Pro Arg Tyr Lys Val Leu Ala Ser Gly Gly		
290	295	300
Leu Arg Ile Gln Lys Leu Arg Pro Glu Asp Ser Gly Ile Phe Gln Cys		
305	310	315
Phe Ala Ser Asn Glu Gly Gly Glu Ile Gln Thr His Thr Tyr Leu Asp		
325	330	335
Val Thr Asn Ile Ala Pro Val Phe Thr Gln Arg Pro Val Asp Thr Thr		
340	345	350
Val Thr Asp Gly Met Thr Ala Ile Leu Arg Cys Glu Val Ser Gly Ala		
355	360	365
Pro Lys Pro Ala Ile Thr Trp Lys Arg Glu Asn His Ile Leu Ala Ser		
370	375	380
Gly Ser Val Arg Ile Pro Arg Phe Met Leu Leu Glu Ser Gly Gly Leu		
385	390	395
Gln Ile Ala Pro Val Phe Ile Gln Asp Ala Gly Asn Tyr Thr Cys Tyr		

405 410 415
 Ala Ala Asn Thr Glu Gly Ser Leu Asn Ala Ser Ala Thr Leu Thr Val
 420 425 430
 Trp Asn Arg Thr Ser Ile Val His Pro Pro Glu Asp His Val Val Ile
 435 440 445
 Lys Gly Thr Thr Ala Thr Leu His Cys Gly Ala Thr His Asp Pro Arg
 450 455 460
 Val Ser Leu Arg Tyr Val Trp Lys Lys Asp Asn Val Ala Leu Thr Pro
 465 470 475 480
 Ser Ser Thr Ser Arg Ile Val Val Glu Lys Asp Gly Ser Leu Leu Ile
 485 490 495
 Ser Gln Thr Trp Ser Gly Asp Ile Gly Asp Tyr Ser Cys Glu Ile Val
 500 505 510
 Ser Glu Gly Gly Asn Asp Ser Arg Met Ala Arg Leu Glu Val Ile Glu
 515 520 525
 Leu Pro His Ser Pro Gln Asn Leu Leu Val Ser Pro Asn Ser Ser His
 530 535 540
 Ser His Ala Val Val Leu Ser Trp Val Arg Pro Phe Asp Gly Asn Ser
 545 550 555 560
 Pro Ile Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn Ser Pro Trp
 565 570 575
 Lys Val His Leu Ser Asn Val Gly Pro Glu Met Thr Gly Val Thr Val
 580 585 590
 Ser Gly Leu Thr Pro Ala Arg Thr Tyr Gln Phe Arg Val Cys Ala Val
 595 600 605
 Asn Glu Val Gly Arg Gly Gln Tyr Ser Ala Glu Thr Ser Arg Leu Met
 610 615 620
 Leu Pro Glu Glu Pro Pro Ser Ala Pro Pro Lys Asn Ile Val Ala Ser
 625 630 635 640
 Gly Arg Thr Asn Gln Ser Ile Met Val Gln Trp Gln Pro Pro Pro Glu
 645 650 655
 Thr Glu His Asn Gly Val Leu Arg Gly Tyr Ile Leu Arg Tyr Arg Leu
 660 665 670
 Ala Gly Leu Pro Gly Glu Tyr Gln Gln Arg Asn Ile Thr Ser Pro Glu
 675 680 685
 Val Asn Tyr Cys Leu Val Thr Asp Leu Ile Ile Trp Thr Gln Tyr Glu
 690 695 700
 Ile Gln Val Ala Ala Tyr Asn Gly Ala Gly Leu Gly Val Phe Ser Arg

<210> 181
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Primer

<400> 181
 cttctgctct aaaagctgcg 20

<210> 182
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Primer

<400> 182
 cgacctgcag ctcgagcaca 20

<210> 183
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 183
 ctagctagct agaaactact aaaatgtaaa tgacatag 38

<210> 184
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 184
 cgcaagcttg aaaggttgca gttagaatgt cctttc 36

<210> 185
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
double stranded nucleic acid

<220>

<223> DNA/RNA molecule

<400> 185

guccaggaua ucaugaguct t

21

<210> 186

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
double stranded nucleic acid

<220>

<223> DNA/RNA molecule

<400> 186

gacucaugau auccuggact t

21

<210> 187

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
double stranded nucleic acid

<220>

<223> DNA/RNA molecule

<400> 187

gaagucugaa gaucuaucct t

21

<210> 188

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
double stranded nucleic acid

<220>

<223> DNA/RNA molecule

<400> 188

ggauagaucu ucagacuuct t

21

<210> 189
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:synthetic
 double stranded nucleic acid

 <220>
 <223> DNA/RNA molecule

 <400> 189
 gcugaagaag agguguucct t 21

 <210> 190
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:synthetic
 double stranded nucleic acid

 <220>
 <223> DNA/RNA molecule

 <400> 190
 ggaacaccuc uucuucagct t 21

 <210> 191
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:synthetic
 double stranded nucleic acid

 <220>
 <223> DNA/RNA molecule

 <400> 191
 gaugacacag augaagccct t 21

 <210> 192
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:synthetic
 double stranded nucleic acid

<220>
 <223> DNA/RNA molecule

 <400> 192
 gggcuucauc ugugucauct t 21

 <210> 193
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:synthetic
 double stranded nucleic acid

 <220>
 <223> DNA/RNA molecule

 <400> 193
 gccucagag uccagaauct t 21

 <210> 194
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:synthetic
 double stranded nucleic acid

 <220>
 <223> DNA/RNA molecule

 <400> 194
 gauucuggac ucugagggt t 21

 <210> 195
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:synthetic
 double stranded nucleic acid

 <220>
 <223> DNA/RNA molecule

 <400> 195
 gaugacuug guaucaaact t 21

 <210> 196

<211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:synthetic
 double stranded nucleic acid

 <220>
 <223> DNA/RNA molecule

 <400> 196
 guuugauacc aaagucauct t 21

 <210> 197
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:synthetic DNA

 <400> 197
 aaaagtcag gatatcatga gtctttttta 30

 <210> 198
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:synthetic DNA

 <400> 198
 agcttaaaaa agactcatga tctcctggac 30

 <210> 199
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:synthetic DNA

 <400> 199
 aaaagaagtc tgaagatcta tcctttttta 30

 <210> 200
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 200
agcttaaaaa aggatagatc ttcagacttc 30

<210> 201
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic DNA

<400> 201
aaaagctgaa gaagaggtgt tcctttttta 30

<210> 202
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic DNA

<400> 202
agcttaaaaa aggaacacct cttcttcagc 30

<210> 203
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic DNA

<400> 203
aaaagatgac acagatgaag ccctttttta 30

<210> 204
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic DNA

<400> 204
agcttaaaaa agggcttcac ctgtgtcatc 30

<210> 205
<211> 30
<212> DNA

----- <213> Artificial Sequence -----

<220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 205

aaaagccctc agagtccaga atctttttta

30

<210> 206

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 206

agcttaaaaa agattctgga ctctgagggc

30

<210> 207

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 207

aaaagatgac tttggtatca aactttttta

30

<210> 208

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 208

agcttaaaaa agtttgatac caaagtcac

30

<210> 209

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 209

gcgaattcgg gcaggaagag ggcctatttc ccat

34

<210> 210
 <211> 44
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer

 <400> 210
 gcaagctttt tttgtcttct ttccacaaga tatataaagc caag 44

<210> 211
 <211> 32
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer

 <400> 211
 cgctcgagcc atggaattcg aacgctgacg tc 32

<210> 212
 <211> 34
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer

 <400> 212
 gcaagctttc tcatacagaa cttataagat tccc 34

<210> 213
 <211> 19
 <212> RNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:synthetic
 double stranded nucleic acid

 <400> 213
 guccaggaua ucaugaguc 19

<210> 214
 <211> 19
 <212> RNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:synthetic
 double stranded nucleic acid

<400> 214
 gacucaugau auccuggac 19

<210> 215
 <211> 19
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:synthetic
 double stranded nucleic acid

<400> 215
 gaagucugaa gaucuaucc 19

<210> 216
 <211> 19
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:synthetic
 double stranded nucleic acid

<400> 216
 ggauagaucu ucagacuuc 19

<210> 217
 <211> 19
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:synthetic
 double stranded nucleic acid

<400> 217
 gcugaagaag agguguucc 19

<210> 218
 <211> 19
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:synthetic
 double stranded nucleic acid

<400> 218
 ggaacaccuc uucuucagc 19

<210> 219
 <211> 19
 <212> RNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:synthetic
 double stranded nucleic acid

 <400> 219
 gaugacacag augaagccc 19

 <210> 220
 <211> 19
 <212> RNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:synthetic
 double stranded nucleic acid

 <400> 220
 gggcucauc ugugucauc 19

 <210> 221
 <211> 19
 <212> RNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:synthetic
 double stranded nucleic acid

 <400> 221
 gccucagag uccagaauc 19

 <210> 222
 <211> 19
 <212> RNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:synthetic
 double stranded nucleic acid

 <400> 222
 gauucuggac ucugagggc 19

 <210> 223
 <211> 19
 <212> RNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
double stranded nucleic acid

<400> 223

gaugacuuug guaucaaac

19

<210> 224

<211> 19

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
double stranded nucleic acid

<400> 224

guuugauacc aaagucauc

19